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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 23.1356 Seconds  
(Without alignments)  
4379.433 Million cell updates/sec

Title: US-10-712-654-21

Perfect score: 57  
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Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

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Post-processing: Listing first 1000 summaries

Database :

Issued Patents NA: \*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	57	100.0	2292	3	US-09-350-729A-3
4	57	100.0	2295	3	US-09-350-729A-1
5	57	100.0	2299	2	US-08-021-601-11
6	57	100.0	2709	2	US-08-082-849B-11
7	57	100.0	2709	6	PCT-US94-01624-11
8	57	100.0	4235	2	US-08-021-601-3
9	57	100.0	4235	6	PCT-US94-01624-3
10	57	100.0	4235	6	PCT-US94-01624-30
11	52	91.2	2160	2	US-08-082-849B-30
12	52	91.2	2160	6	PCT-US94-01624-30
13	18	31.6	2161	3	US-09-215-694-28
14	18	31.6	2161	3	US-10-109-310-28
15	18	31.6	31328	3	US-09-215-694-19
16	18	31.6	31328	3	US-10-109-310-19
17	18	28.1	1529	3	US-09-487-558B-21
18	18	28.1	56374	3	US-09-949-002-645
19	18	28.1	56375	3	US-09-949-002-645
20	18	28.1	23464	3	US-09-949-016-16420
21	15	26.3	344	3	US-09-513-999C-502
22	15	26.3	428	3	US-09-621-976-439
23	15	26.3	436	3	US-09-621-976-13751
24	15	26.3	437	3	US-09-621-976-13760

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28	15	26.3	601	3	US-09-949-016-170292	Sequence 170292, A
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32	15	26.3	1011	3	US-09-252-991A-14782	Sequence 14782, A
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34	15	26.3	1290	3	US-09-489-039A-4915	Sequence 4915, Ap
35	15	26.3	1296	3	US-09-328-352-110	Sequence 110, App
36	15	26.3	1297	3	US-09-347-878-53	Sequence 53, App1
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38	15	26.3	32166	3	US-09-562-919-11	Sequence 11, App1
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77	14	24.6	177	3	US-09-726-457-248	Sequence 248, App
78	14	24.6	177	3	US-09-614-1248-248	Sequence 248, App
79	14	24.6	177	3	US-09-671-325-248	Sequence 248, App
80	14	24.6	177	3	US-09-589-184-248	Sequence 248, App
81	14	24.6	177	3	US-09-658-824-248	Sequence 248, App
82	14	24.6	177	3	US-10-017-754-248	Sequence 248, App
83	14	24.6	177	3	US-09-651-563-248	Sequence 248, App
84	14	24.6	177	3	US-09-519-462-248	Sequence 248, App
85	14	24.6	291	3	US-09-270-767-11133	Sequence 11133, A
86	14	24.6	369	3	US-09-248-796A-8006	Sequence 8006, Ap
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88	14	24.6	473	8	US-09-636-771-12	Sequence 12, App1
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C 101	14	24.6	601.3	US-09-949-016-155253	Sequence 155253, A	C 174	14	24.6	86213.3	US-09-949-016-17242	Sequence 17242, A
C 102	14	24.6	601.3	US-09-949-016-178690	Sequence 178690, A	C 175	14	24.6	86213.3	US-09-949-016-17243	Sequence 17243, A
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106	14	24.6	601.3	US-09-949-016-180395	Sequence 180395, A	C 179	14	24.6	95402.3	US-09-949-016-12063	Sequence 12063, A
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C 114	14	24.6	795.3	US-09-248-796A-3842	Sequence 3842, Ap	C 187	14	24.6	124884.3	US-10-289-853-76	Sequence 76, Appl
C 115	14	24.6	1110.3	US-09-134-000C-2300	Sequence 2300, Ap	C 188	14	24.6	125157.3	US-09-913-514-2	Sequence 2, Appl
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C 893	12	21.1	531	3	US-09-248-796A-785	Sequence 785, App	C 966	12	21.1	601	3	US-09-949-016-34344	Sequence 34344, A
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995 12 21.1 601 3 US-09-949-016-51517 Sequence 51517, A
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## ALIGNMENTS

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US-09-350-729A-4
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Sequence 4, Application US/09350729A
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Patent No. 6770479
```

```
GENERAL INFORMATION:
```

```
APPLICANT: LEE, JOHN SCOTT
```

```
APPLICANT: PUSHKO, PETER
```

```
APPLICANT: PARKER, MICHAEL D.
```

```
APPLICANT: SMITH, JONATHAN F.
```

```
APPLICANT: WELKOS, SUSAN L.
```

```
TITLE OF INVENTION: ANTHRAX VACCINES
```

```
FILE REFERENCE: ARMY135
```

```
CURRENT APPLICATION NUMBER: US/09/350,729A
```

```
CURRENT FILING DATE: 2001-06-20
```

```
PRIOR APPLICATION NUMBER: 60/092,416
```

```
PRIOR FILING DATE: 1998-07-10
```

```
NUMBER OF SEQ ID NOS: 8
```

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SOFTWARE: PatentIn Ver. 2.1
```

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SEQ ID NO 4
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LENGTH: 1710
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TYPE: DNA
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```
ORGANISM: Bacillus anthracis
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```
US-09-350-729A-4
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Query Match
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Best Local Similarity 100.0%; Score 57; DB 3; Length 1710;
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## RESULT 2

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US-09-350-729A-2
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```
Sequence 2, Application US/09350729A
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```
Patent No. 6770479
```

```
GENERAL INFORMATION:
```

```
APPLICANT: LEE, JOHN SCOTT
```

```
APPLICANT: PUSHKO, PETER
```

```
APPLICANT: PARKER, MICHAEL D.
```

```
APPLICANT: SMITH, JONATHAN F.
```

```
APPLICANT: WELKOS, SUSAN L.
```

```
TITLE OF INVENTION: ANTHRAX VACCINES
```

```
FILE REFERENCE: ARMY135
```

```
CURRENT APPLICATION NUMBER: US/09/350,729A
```

```
CURRENT FILING DATE: 2001-06-20
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```
PRIOR APPLICATION NUMBER: 60/092,416
```

```
PRIOR FILING DATE: 1998-07-10
```

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NUMBER OF SEQ ID NOS: 8
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SOFTWARE: PatentIn Ver. 2.1
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SEQ ID NO 4
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LENGTH: 1710
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TYPE: DNA
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ORGANISM: Bacillus anthracis
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US-09-350-729A-4
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Query Match
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Best Local Similarity 100.0%; Score 57; DB 3; Length 1710;
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 11 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 67
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US-09-350-729A-3
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```
Sequence 3, Application US/09350729A
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```
Patent No. 6770479
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```
GENERAL INFORMATION:
```

```
APPLICANT: LEE, JOHN SCOTT
```

```
APPLICANT: PUSHKO, PETER
```

```
APPLICANT: PARKER, MICHAEL D.
```

```
APPLICANT: SMITH, JONATHAN F.
```

```
APPLICANT: WELKOS, SUSAN L.
```

```
TITLE OF INVENTION: ANTHRAX VACCINES
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FILE REFERENCE: ARMY135
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CURRENT APPLICATION NUMBER: US/09/350,729A
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PRIOR APPLICATION NUMBER: 60/092,416
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PRIOR FILING DATE: 1998-07-10
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US-09-350-729A-3
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## RESULT 4

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Sequence 1, Application US/09350729A
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```
Patent No. 6770479
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GENERAL INFORMATION:
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```
APPLICANT: LEE, JOHN SCOTT
```

```
APPLICANT: PUSHKO, PETER
```

```
APPLICANT: PARKER, MICHAEL D.
```

```
APPLICANT: SMITH, JONATHAN F.
```

```
APPLICANT: WELKOS, SUSAN L.
```

```
TITLE OF INVENTION: ANTHRAX VACCINES
```

```
FILE REFERENCE: ARMY135
```

```
CURRENT APPLICATION NUMBER: US/09/350,729A
```

```
CURRENT FILING DATE: 2001-06-20
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```
PRIOR APPLICATION NUMBER: 60/092,416
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PRIOR FILING DATE: 1998-07-10
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```
NUMBER OF SEQ ID NOS: 8
```

```
SOFTWARE: PatentIn Ver. 2.1
```

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SEQ ID NO 2
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LENGTH: 2211
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TYPE: DNA
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ORGANISM: Bacillus anthracis
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US-09-350-729A-2
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;; PRIOR FILING DATE: 1998-07-10  
;; NUMBER OF SEQ ID NOS: 8  
;; SOFTWARE: PatentIn Ver. 2.1  
;; SEQ ID NO 1  
;; LENGTH: 2295  
;; TYPE: DNA  
;; ORGANISM: Bacillus anthracis  
US-09-350-729A-1

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Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCGATTCAATAGAG 652

## RESULT 5

US-08-021-601-11  
; Sequence 11, Application US/08021601  
; Patent No. 5591631  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Nichols, Peter J.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
; TITLE OF INVENTION: RELATED METHODS  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Needle & Rosenberg, P.C.  
; STREET: 133 Carnegie Way, Suite 400  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30303  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/021.601  
; FILING DATE: 19930222  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Spratt, Gwendolyn D.  
; REGISTRATION NUMBER: 36,016  
; REFERENCE/DOCKET NUMBER: 1414.057  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 404/688-9880  
; TELEFAX: 404/688-9880  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2709 base pairs  
; TYPE: NUCLEIC ACID  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2709  
US-08-021-601-11

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Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 6  
US-08-082-849B-11  
; Sequence 11, Application US/08082849B  
; Patent No. 5677274  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; APPLICANT: Nichols, Peter J.  
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
; TITLE OF INVENTION: Related Methods  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082.849B  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/021.601  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-161-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
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; TOPOLOGY: linear  
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; HYPOTHETICAL: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..2709  
; OTHER INFORMATION: /product= "PA(1-725)-Human CD4  
; OTHER INFORMATION: residues (1-178)"  
US-08-082-849B-11

US-08-082-849B-11

Query Match 100.0%; Score 57; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCGATTCAATAGAG 57  
DB 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCGATTCAATAGAG 565

## RESULT 7

PCT-US94-01624-11  
; Sequence 11, Application PC/TUS9401624  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.



APPLICANT: Atora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESS: TOWNSEND AND TOWNSEND KHOURI AND CREW  
STREET: Steuart Street Tower, 20th Floor, One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624  
FILING DATE: June 25, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2709 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2709  
OTHER INFORMATION: /product= "PA(1-725)-----Human CD4  
OTHER INFORMATION: residues(1-178)"  
PCT-US94-01624-11  
Query Match 100.0%; Score 57; DB 6; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAGG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAGG 565  
RESULT 8  
US-08-021-601-3  
Sequence 3, Application US/08021601  
GENERAL INFORMATION:  
APPLICANT: Leppia, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Nichols, Peter J.  
APPLICANT: Atora, Naveen  
APPLICANT: Singh, Yogendra  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESS: Needle & Rosenberg, P.C.  
STREET: 133 Carnegie Way, Suite 400  
CITY: Atlanta

STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/021,601  
FILING DATE: 19930212  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414,057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404/688-0770  
TELEFAX: 404/688-9880  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4235 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1891..4095  
US-08-021-601-3  
Query Match 100.0%; Score 57; DB 2; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAGG 57  
Db 2399 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAGG 2455  
RESULT 9  
US-08-082-849B-3  
Sequence 3, Application US/08082849B  
Patent No. 5677274  
GENERAL INFORMATION:  
APPLICANT: Leppia, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Atora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
TITLE OF INVENTION: Related Methods  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3634  
COMPUTER READABLE FORM:  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,849B  
FILING DATE: 25-JUN-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,601



;; FILING DATE: 12-FEB-1993  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Weber, Kenneth A.  
;; REGISTRATION NUMBER: 31,677  
;; REFERENCE/DOCKET NUMBER: 15280-161-1  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (415) 576-0200  
;; TELEFAX: (415) 576-0300  
;; INFORMATION FOR SEQ ID NO: 3:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 4235 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHEetical: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Bacillus anthracis  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1891..4095  
;; OTHER INFORMATION: /product= "Protective Antigen"  
;;  
US-08-082-849B-3  
  
Query Match 100.0%; Score 57; DB 2; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGCTGACCTACGGTTCCAGACCGTGACAATGATGGAATCCCTGATTCTTGAAGG 57  
Db 2399 GTGCTGACCTACGGTTCCAGACCGTGACAATGATGGAATCCCTGATTCTTGAAGG 2455  
  
RESULT 10  
PCT-US94-01624-3  
; Sequence 3 Application PC/TUS9401624  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; APPLICANT: Nichols, Peter J.  
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
; TITLE OF INVENTION: RELATED METHODS  
; NUMBER OF SEQUENCES: 31  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW  
; STREET: Steuart Street Tower, 20th Floor, One Market  
; STREET: Plaza  
; CITY: San Francisco  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94105  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01624  
; FILING DATE: June 25, 1993  
; CLASSIFICATION:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-115  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-5043  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4235 base pairs

;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHEtical: NO  
;; ANTI-SENSE: NO  
;; ORIGINAL SOURCE:  
;; ORGANISM: Bacillus anthracis  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: 1891..4095  
;; OTHER INFORMATION: /product= "Protective Antigen"  
;;  
PCT-US94-01624-3  
  
Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GTGCTGACCTACGGTTCCAGACCGTGACAATGATGGAATCCCTGATTCTTGAAGG 57  
Db 2399 GTGCTGACCTACGGTTCCAGACCGTGACAATGATGGAATCCCTGATTCTTGAAGG 2455  
  
RESULT 11  
US-08-082-849B-30  
; Sequence 30 Application US/08082849B  
; Patent No. 5677274  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Klimpel, Kurt R.  
; APPLICANT: Arora, Naveen  
; APPLICANT: Singh, Yogendra  
; APPLICANT: Nichols, Peter J.  
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
; TITLE OF INVENTION: Related Methods  
; NUMBER OF SEQUENCES: 35  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,849B  
; FILING DATE: 25-JUN-1993  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: 08/021,601  
; FILING DATE: 12-FEB-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Kenneth A.  
; REGISTRATION NUMBER: 31,677  
; REFERENCE/DOCKET NUMBER: 15280-161-1  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 576-0200  
; TELEFAX: (415) 576-0300  
; INFORMATION FOR SEQ ID NO: 30:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 2160 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEtical: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Bacillus anthracis  
; FEATURE:



NAME/KEY: CDS  
LOCATION: 1..2157  
OTHER INFORMATION: /product= "PAHIV#2"  
US-08-082-849B-30

Query Match 91.2%; Score 52; DB 2; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGACCTACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57  
DB 526 GGACCTACGGTTCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 577

RESULT 12  
PCT-US94-01624-30  
Sequence 30, Application PC/TUS9401624  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Arora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND KHOURI and CREW  
STREET: Stewart Street Tower, 20th Floor, One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624  
FILING DATE: June 25, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-115  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2160 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2157  
OTHER INFORMATION: /product= "PAHIV#2"  
PCT-US94-01624-30

Query Match 91.2%; Score 52; DB 6; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 1.1e-19;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 GGACCTACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57  
DB 526 GGACCTACGGTTCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 577

RESULT 13  
US-09-215-694-28/C  
Sequence 28, Application US/09215694B  
Patent No. 6391583  
GENERAL INFORMATION:  
APPLICANT: Wisconsin Alumni Research Foundation  
APPLICANT: Hutchinson, Charles R.  
APPLICANT: Kennedy, Jonathan n.m.i  
APPLICANT: Park, Cheonsok n.m.i  
TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS  
FILE REFERENCE: 960296.95718  
CURRENT APPLICATION NUMBER: US/09/215,694B  
CURRENT FILING DATE: 1999-12-18  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 28  
LENGTH: 2161  
TYPE: DNA  
ORGANISM: Aspergillus terreus  
US-09-215-694-28

Query Match 31.6%; Score 18; DB 3; Length 2161;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACCGTGACATGATGGA 38  
DB 156 GACCGTGACATGATGGA 139

RESULT 14  
US-10-109-310-28/C  
Sequence 28, Application US/10109310  
Patent No. 6943017  
GENERAL INFORMATION:  
APPLICANT: Wisconsin Alumni Research Foundation  
APPLICANT: Hutchinson, Charles R.  
APPLICANT: Kennedy, Jonathan n.m.i  
APPLICANT: Park, Cheonsok n.m.i  
TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS  
FILE REFERENCE: 960296.95718  
CURRENT APPLICATION NUMBER: US/10/109,310  
CURRENT FILING DATE: 2002-03-28  
PRIOR APPLICATION NUMBER: 09/215,694  
PRIOR FILING DATE: 1998-12-18  
NUMBER OF SEQ ID NOS: 36  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 28  
LENGTH: 2161  
TYPE: DNA  
ORGANISM: Aspergillus terreus  
US-10-109-310-28

Query Match 31.6%; Score 18; DB 3; Length 2161;  
Best Local Similarity 100.0%; Pred. No. 1.2;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACCGTGACATGATGGA 38  
DB 156 GACCGTGACATGATGGA 139

RESULT 15  
US-09-215-694-19/C  
Sequence 19, Application US/09215694B  
Patent No. 6391583  
GENERAL INFORMATION:  
APPLICANT: Wisconsin Alumni Research Foundation  
APPLICANT: Hutchinson, Charles R.  
APPLICANT: Kennedy, Jonathan n.m.i  
APPLICANT: Park, Cheonsok n.m.i



```

; TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
; FILE REFERENCE: 960296.95718
; CURRENT APPLICATION NUMBER: US/09/215.694B
; CURRENT FILING DATE: 1999-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 31328
; TYPE: DNA
; ORGANISM: Aspergillus terreus
; US-09-215-694-19

Query Match          31.6%; Score 18; DB 3; Length 31328;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 GACCGTGACATGATGGA 38
Db      1555 GACCGTGACATGATGGA 1538

RESULT 16
US-10-109-310-19/c
; Sequence 19, Application US/10109310
; Patent No. 6943017
; GENERAL INFORMATION:
; APPLICANT: Wisconsin Alumni Research Foundation
; APPLICANT: Hutchinson, Charles R.
; APPLICANT: Kennedy, Jonathan n.m.i
; APPLICANT: Park, Cheonsuek n.m.i
; TITLE OF INVENTION: METHOD OF PRODUCING ANTIHYPERCHOLESTEROLEMIC AGENTS
; FILE REFERENCE: 960296.95718
; CURRENT APPLICATION NUMBER: US/10/109.310
; CURRENT FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 09/215,694
; PRIOR FILING DATE: 1998-12-18
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 19
; LENGTH: 31328
; TYPE: DNA
; ORGANISM: Aspergillus terreus
; US-10-109-310-19

Query Match          31.6%; Score 18; DB 3; Length 31328;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      21 GACCGTGACATGATGGA 38
Db      1555 GACCGTGACATGATGGA 1538

RESULT 17
US-09-487-558B-21/c
; Sequence 21, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Call, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Sumners, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130

; CURRENT APPLICATION NUMBER: US/09/487,558B
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 1629
; TYPE: DNA
; ORGANISM: Aspergillus terreus
; US-09-487-558B-21

Query Match          28.1%; Score 16; DB 3; Length 1629;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      23 CCGTGACATGATGGA 38
Db      154 CCGTGACATGATGGA 139

RESULT 18
US-09-949-002-645
; Sequence 645, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 645
; LENGTH: 56374
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-645

Query Match          28.1%; Score 16; DB 3; Length 56374;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      30 AATGATGAATCCCTG 45
Db      29957 AATGATGAATCCCTG 29972

RESULT 19
US-09-949-002-774
; Sequence 774, Application US/09949002
; Patent No. 6900016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; FILE REFERENCE: C1000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 56375
; TYPE: DNA
; ORGANISM: Human
; US-09-949-002-774
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Query Match 28.1%; Score 16; DB 3; Length 56375;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 AATGATGGAATCCCTG 45  
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Db 29957 AATGATGGAATCCCTG 29972

RESULT 20  
US-09-949-016-16420/c  
; Sequence 16420, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FASTSEQ for Windows Version 4.0  
; SEQ ID NO 16420  
; LENGTH: 234884  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(234884)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16420

Query Match 28.1%; Score 16; DB 3; Length 234884;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CAATGATGGAATCCCT 44  
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Db 22827 CAATGATGGAATCCCT 228812

RESULT 21  
US-09-513-999C-502  
; Sequence 502, Application US/09513999C  
; Patent No. 6783961  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Duclert, A.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
; Patent No. 6783961  
; FILE REFERENCE: 59, US2, REG  
; CURRENT APPLICATION NUMBER: US/09/513,999C  
; CURRENT FILING DATE: 2000-02-24  
; PRIOR APPLICATION NUMBER: US 60/122,487  
; PRIOR FILING DATE: 1999-02-26  
; NUMBER OF SEQ ID NOS: 36681  
; SOFTWARE: Patent.pm  
; SEQ ID NO 502  
; LENGTH: 344  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 173..343  
; FEATURE:

NAME/KEY: sig\_peptide  
; LOCATION: 173..253  
; OTHER INFORMATION: score 7.6  
; OTHER INFORMATION: seq L1FLGFL1A1QT/DV  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 263-  
; OTHER INFORMATION: w=a or t  
; FEATURE:  
; NAME/KEY: UNSURE  
; LOCATION: 4  
; OTHER INFORMATION: Xaa=Arg or Trp  
US-09-513-999C-502

Query Match 26.3%; Score 15; DB 3; Length 344;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 TGAATCCCTGATTC 49  
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Db 24 TGAATCCCTGATTC 38

RESULT 22  
US-09-621-976-439  
; Sequence 439, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 439  
; LENGTH: 428  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 255..428  
US-09-621-976-439

Query Match 26.3%; Score 15; DB 3; Length 428;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGAATCCCTGATTC 50  
|||||  
Db 202 GGAATCCCTGATTC 216

RESULT 23  
US-09-621-976-13751  
; Sequence 13751, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jobert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13751  
; LENGTH: 436  
; TYPE: DNA  
; ORGANISM: Homo sapiens



FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: 18,339  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-13751

Query Match 26.3%; Score 15; DB 3; Length 436;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGAATCCCTGATTCA 50  
Db 306 GGAATCCCTGATTCA 320

RESULT 24  
US-09-621-976-13760  
; Sequence 13760, Application US/09621976  
; Patent No. 6639063  
; GENERAL INFORMATION:  
; APPLICANT: Dumas Milne Edwards, J.B.  
; APPLICANT: Jodert, S.  
; APPLICANT: Giordano, J.Y.  
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.  
; FILE REFERENCE: GENSET.054PR2  
; CURRENT APPLICATION NUMBER: US/09/621,976  
; CURRENT FILING DATE: 2000-07-21  
; NUMBER OF SEQ ID NOS: 19335  
; SOFTWARE: Patent.pm  
; SEQ ID NO 13760  
; LENGTH: 437  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: 18  
; OTHER INFORMATION: n=a, g, c or t  
US-09-621-976-13760

Query Match 26.3%; Score 15; DB 3; Length 437;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGAATCCCTGATTCA 50  
Db 305 GGAATCCCTGATTCA 319

RESULT 25  
US-09-949-016-71544/c  
; Sequence 71544, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 71544  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-71544

Query Match 26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CAGACCGTGACCAATG 33  
Db 494 CAGACCGTGACCAATG 480

RESULT 26  
US-09-949-016-170290  
; Sequence 170290, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 170290  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-170290

Query Match 26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGAATCCCTGATTCA 50  
Db 464 GGAATCCCTGATTCA 478

RESULT 27  
US-09-949-016-170291  
; Sequence 170291, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 170291  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-170291

Query Match 26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GGAATCCCTGATTCA 50



Db 404 GGAATCCCTGATTC 418

## RESULT 28

US-09-949-016-170292  
; Sequence 170292, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; PRIOR FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 170292

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-170292

## Query Match

26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 GGAATCCCTGATTC 50  
|||||  
Db 327 GGAATCCCTGATTC 341

## RESULT 29

US-09-949-002-2878/c  
; Sequence 2878, Application US/09949002  
; Patent No. 6900016

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949,002

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/231,401

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 2878

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-002-2878

## Query Match

26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 AATGATGAATCCCT 44  
|||||  
Db 592 AATGATGAATCCCT 578

## RESULT 30

US-09-949-002-4884/c  
; Sequence 4884, Application US/09949002  
; Patent No. 6900016

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION

; FILE REFERENCE: CL000790

; CURRENT APPLICATION NUMBER: US/09/949,002

; PRIOR FILING DATE: 2000-01-28

; PRIOR APPLICATION NUMBER: 60/231,401

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 10823

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4884

; LENGTH: 601

; TYPE: DNA

; ORGANISM: Human

US-09-949-002-4884

## Query Match

26.3%; Score 15; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 AATGATGAATCCCT 44  
|||||  
Db 592 AATGATGAATCCCT 578

## RESULT 31

US-09-533-559-266/c  
; Sequence 266, Application US/09533559  
; Patent No. 6902887

; GENERAL INFORMATION:

; APPLICANT: Randy M. Berka

; APPLICANT: Jeffrey R. Shuster

; APPLICANT: Sakari Kauppinen

; APPLICANT: Ib Groth Clausen

; APPLICANT: Peter Bjørke Olsen

; TITLE OF INVENTION: Methods For Monitoring Multiple Gene

; FILE REFERENCE: 5849.200-US

; CURRENT APPLICATION NUMBER: US/09/533,559

; EARLIER FILING DATE: 2000-03-22

; EARLIER APPLICATION NUMBER: 09/273,623

; NUMBER OF SEQ ID NOS: 7860

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 266

; LENGTH: 633

; TYPE: DNA

; ORGANISM: Fusarium venenatum

; NAME/KEY: misc\_feature

; LOCATION: (1)...(633)

; OTHER INFORMATION: n = A,T,C or G

US-09-533-559-266

## Query Match

26.3%; Score 15; DB 3; Length 633;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCAGACCGTGAC 29  
|||||  
Db 22 GTTCAGACCGTGAC 8

## RESULT 32

US-09-252-991A-14782/c  
; Sequence 14782, Application US/09252991A  
; Patent No. 6551795  
; GENERAL INFORMATION:  
; APPLICANT: Marc J. Rubenfield et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS



;; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 107196.136  
;; CURRENT APPLICATION NUMBER: US/09/252,991A  
;; CURRENT FILING DATE: 1999-02-18  
;; PRIOR APPLICATION NUMBER: US 60/074,788  
;; PRIOR FILING DATE: 1998-02-18  
;; PRIOR APPLICATION NUMBER: US 60/094,190  
;; PRIOR FILING DATE: 1998-07-27  
;; NUMBER OF SEQ ID NOS: 33142  
;; SEQ ID NO 14782  
;; LENGTH: 1011  
;; TYPE: DNA  
;; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-14782

Query Match 26.3%; Score 15; DB 3; Length 1011;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 AATCCGATTCATT 52  
DB 966 AATCCGATTCATT 952

RESULT 33  
US-09-543-681A-3571/C  
;; Sequence 3571, Application US/09543681A  
;; Patent No. 6605709  
;; GENERAL INFORMATION:  
;; APPLICANT: GARY BRETON  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PROTEUS MIRABILIS  
;; TITLE OF INVENTION: DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 2709.1002-001  
;; CURRENT APPLICATION NUMBER: US/09/543,681A  
;; CURRENT FILING DATE: 2000-04-05  
;; PRIOR APPLICATION NUMBER: US 60/128,706  
;; PRIOR FILING DATE: 1999-04-09  
;; NUMBER OF SEQ ID NOS: 8344  
;; SEQ ID NO 3571  
;; LENGTH: 1200  
;; TYPE: DNA  
;; ORGANISM: Proteus mirabilis  
US-09-543-681A-3571

Query Match 26.3%; Score 15; DB 3; Length 1200;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 43 CTGATTCATTGAGG 57  
DB 346 CTGATTCATTGAGG 332

RESULT 34  
US-09-489-039A-4915  
;; Sequence 4915, Application US/09489039A  
;; Patent No. 6610836  
;; GENERAL INFORMATION:  
;; APPLICANT: GARY BRETON et. al  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
;; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: 2709.2004001  
;; CURRENT APPLICATION NUMBER: US/09/489,039A  
;; CURRENT FILING DATE: 2000-01-27  
;; PRIOR APPLICATION NUMBER: US 60/117,747  
;; PRIOR FILING DATE: 1999-01-29  
;; NUMBER OF SEQ ID NOS: 14342  
;; SEQ ID NO 4915  
;; LENGTH: 1290  
;; TYPE: DNA  
;; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4915

Query Match 26.3%; Score 15; DB 3; Length 1290;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 TGATGATCCCTGA 46  
DB 5 TGATGATCCCTGA 19

RESULT 35  
US-09-328-352-110  
;; Sequence 110, Application US/09328352  
;; Patent No. 6562958  
;; GENERAL INFORMATION:  
;; APPLICANT: GARY L. BRETON et al.  
;; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
;; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS  
;; FILE REFERENCE: GTC99-03BA  
;; CURRENT APPLICATION NUMBER: US/09/328,352  
;; CURRENT FILING DATE: 1999-06-04  
;; NUMBER OF SEQ ID NOS: 8252  
;; SEQ ID NO 110  
;; LENGTH: 1296  
;; TYPE: DNA  
;; ORGANISM: Acinetobacter baumannii  
US-09-328-352-110

Query Match 26.3%; Score 15; DB 3; Length 1296;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 ATGGAATCCCTGATT 48  
DB 733 ATGGAATCCCTGATT 747

RESULT 36  
US-09-347-878-53/C  
;; Sequence 53, Application US/09347878C  
;; Patent No. 6376210  
;; GENERAL INFORMATION:  
;; APPLICANT: YUAN, CHONG  
;; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ASSAYING ANALYTES  
;; FILE REFERENCE: 25885-1651  
;; CURRENT APPLICATION NUMBER: US/09/347,878C  
;; CURRENT FILING DATE: 1999-07-06  
;; NUMBER OF SEQ ID NOS: 75  
;; SOFTWARE: PatentIn Ver. 2.0  
;; SEQ ID NO 53  
;; LENGTH: 2277  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
;; FEATURE:  
;; NAME/KEY: CDS  
;; LOCATION: (3)..(1127)  
;; FEATURE:  
;; OTHER INFORMATION: Human class III alcohol dehydrogenase (ADH5) chi  
;; PUBLICATION INFORMATION:  
;; DATABASE ACCESSION NUMBER: M30471/GenBank  
US-09-347-878-53

Query Match 26.3%; Score 15; DB 3; Length 2277;  
Best Local Similarity 100.0%; Pred. No. 60;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATG 36  
DB 1432 ACCGTGACATGATG 1418

RESULT 37  
US-09-949-016-14242



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; Sequence 14242, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 14242
; LENGTH: 14477
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14242

Query Match      26.3%; Score 15; DB 3; Length 14477;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 GATGGAATCCTGAT 47
      |||||
Db      35 GATGGAATCCTGAT 49

RESULT 38
US-09-562-930-11
; Sequence 11, Application US/09562930
; Patent No. 6835812
; GENERAL INFORMATION:
; APPLICANT: Genotherapeutics Inc.
; APPLICANT: Steiner, Mitchell
; APPLICANT: Wang, Chiang
; APPLICANT: Rinaldy, Augustinus
; APPLICANT: Menon, Rama
; TITLE OF INVENTION: Isolated nucleic acids of the p-hyde family, p-hyde proteins, and
; TITLE OF INVENTION: of inducing susceptibility to induction of cell death in cancer
; FILE REFERENCE: P-2762-US2
; CURRENT APPLICATION NUMBER: US/09/562,930
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US 09/302,457
; PRIOR FILING DATE: 1999-04-29
; PRIOR APPLICATION NUMBER: US 09/499,817
; PRIOR FILING DATE: 1999-04-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 11
; LENGTH: 32166
; TYPE: DNA
; ORGANISM: Rat
US-09-562-930-11

Query Match      26.3%; Score 15; DB 3; Length 32166;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 ACAATGATGAATCC 42
      |||||
Db      26378 ACAATGATGAATCC 26392

RESULT 39
US-08-973-334-3
; Sequence 3, Application US/08973334
; Patent No. 6261551
; GENERAL INFORMATION:
```

```
; APPLICANT: Wilson, James M.
; APPLICANT: Fisher, Krishna J.
; APPLICANT: Gao, Guang-ping
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; TITLE OF INVENTION: Associated Virus, Cell Lines, and
; TITLE OF INVENTION: Methods of Production and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 6261551sttown Road
; CITY: Spring House
; STATE: PA
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release 1.0 Version 1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/973,334
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/462,014
; FILING DATE: 05-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/549,489
; FILING DATE: 27-OCT-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Bak, Mary E.
; REGISTRATION NUMBER: 31,215
; REFERENCE/DOCKET NUMBER: GNPV012CIPUSA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (215) 540-9206
; TELEFAX: (215) 540-5818
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 35408 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: other nucleic acid
US-08-973-334-3

Query Match      26.3%; Score 15; DB 3; Length 35408;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      28 ACAATGATGAATCC 42
      |||||
Db      31039 ACAATGATGAATCC 31053

RESULT 40
US-09-563-869A-3
; Sequence 3, Application US/09563869A
; Patent No. 6270996
; GENERAL INFORMATION:
; APPLICANT: Wilson, James M.
; APPLICANT: Fisher, Krishna J.
; APPLICANT: Gao, Guang-ping
; TITLE OF INVENTION: Recombinant Adenovirus and Adeno-
; TITLE OF INVENTION: Associated Virus, Cell Lines, and
; TITLE OF INVENTION: Methods of Production and Use
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Box 457, 321 No. 6270996sttown Road
; CITY: Spring House
; STATE: PA
```



```

/ COUNTRY: USA
/ ZIP: 19477
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release 1.0 Version 1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/563,869A
/ FILING DATE: 03-May-2000
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/973,334
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/549,489
/ FILING DATE: 27-OCT-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Bak, Mary E.
/ REGISTRATION NUMBER: 31,215
/ REFERENCE/DOCKET NUMBER: GNVPN012CIPUSA
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (215) 540-9206
/ TELEFAX: (215) 540-5818
/ INFORMATION FOR SEQ ID NO: 3:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 35408 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: not relevant
/ MOLECULE TYPE: other nucleic acid
/ SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-563-869A-3

Query Match 26.3%; Score 15; DB 3; Length 35408;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ACAATGATGGAATCC 42
Db 31039 ACAATGATGGAATCC 31053

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Search completed: April 11, 2006, 21:49:15  
 Job time : 61.1356 secs



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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 350.151 Seconds  
(without alignments)  
9253.359 Million cell updates/sec

Title: US-10-712-654-21

Perfect score: 57  
Sequence: 1 ggcgtgactactgcgtccca.....aatccctgattcattagagg 57

Scoring table: OLIGO\_NTIC  
Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl:.\*  
1: gb\_ba:.\*  
2: gb\_in:.\*  
3: gb\_env:.\*  
4: gb\_ov:.\*  
5: gb\_ov:.\*  
6: gb\_pac:.\*  
7: gb\_ph:.\*  
8: gb\_dr:.\*  
9: gb\_ro:.\*  
10: gb\_sts:.\*  
11: gb\_sy:.\*  
12: gb\_un:.\*  
13: gb\_vl:.\*  
14: gb\_hlg:.\*  
15: gb\_pl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	57	100.0	721	1 AB125961	AB125961 Bacillus
2	57	100.0	774	6 AX353773	AX353773 Sequence
3	57	100.0	954	6 AX353777	AX353777 Sequence
4	57	100.0	1278	6 AX353779	AX353779 Sequence
5	57	100.0	1281	6 CS135645	CS135645 Sequence
6	57	100.0	1461	6 AX353775	AX353775 Sequence
7	57	100.0	1707	6 CS135643	CS135643 Sequence
8	57	100.0	1710	6 AK570597	AK570597 Sequence
9	57	100.0	1785	6 AX353781	AX353781 Sequence
10	57	100.0	2208	6 CS135652	CS135652 Sequence
11	57	100.0	2208	6 AX353783	AX353783 Sequence
12	57	100.0	2211	6 CS061689	CS061689 Sequence
13	57	100.0	2211	6 AR570595	AR570595 Sequence
14	57	100.0	2225	1 BANA13937	BANA13937 Bacillus
15	57	100.0	2227	1 AY700758	AY700758 Bacillus
16	57	100.0	2231	1 BANA13936	BANA13936 Bacillus
17	57	100.0	2292	6 AR570596	AR570596 Sequence
18	57	100.0	2295	1 AY997299	AY997299 Bacillus

19	57	100.0	2295	6 CS135651	CS135651 Sequence
20	57	100.0	2295	6 AR570594	AR570594 Sequence
21	57	100.0	2369	1 AF306778	AF306778 Bacillus
22	57	100.0	2369	1 AF306779	AF306779 Bacillus
23	57	100.0	2369	1 AF306780	AF306780 Bacillus
24	57	100.0	2369	1 AF306781	AF306781 Bacillus
25	57	100.0	2369	1 AF306782	AF306782 Bacillus
26	57	100.0	2369	1 AF306783	AF306783 Bacillus
27	57	100.0	2549	1 AF268967	AF268967 Bacillus
28	57	100.0	2605	6 AX933603	AX933603 Sequence
29	57	100.0	2709	6 I33400	I33400 Sequence
30	57	100.0	2709	6 I69378	I69378 Sequence
31	57	100.0	4235	1 BACPAG	BACPAG Bacillus an
32	57	100.0	4235	6 I33396	I33396 Sequence
33	57	100.0	4235	6 I69374	I69374 Sequence
34	57	100.0	4235	6 I69374	I69374 Sequence
35	57	100.0	181654	1 AF065404	AF065404 Bacillus
36	57	100.0	181677	1 AE011190	AE011190 Bacillus
37	57	100.0	181677	1 AE017336	AE017336 Bacillus
38	52	91.2	2160	6 I69387	I69387 Sequence
39	44	77.2	1694	1 AY921578	AY921578 Bacillus
40	39	36.8	46	6 AX111916	AX111916 Sequence
41	21	36.8	46	6 AX111918	AX111918 Sequence
42	21	36.8	46	6 AX111920	AX111920 Sequence
43	21	36.8	52	6 AX111910	AX111910 Sequence
44	21	36.8	52	6 AX111912	AX111912 Sequence
45	21	36.8	52	6 AX111914	AX111914 Sequence
46	21	36.8	2277	11 AY428556	AY428556 Synthetic
47	20	35.1	607	11 BV307754	BV307754 S23P6337
48	19	33.3	3445	5 BC088610	BC088610 Xenopus t
49	19	33.3	183152	9 AC123877	AC123877 Mus muscu
50	19	33.3	194326	9 AC125542	AC125542 Mus muscu
51	18	31.6	2156	5 BC080130	BC080130 Xenopus ]
52	18	31.6	43328	15 ATLOVBSGC2	ATLOVBSGC2
53	18	31.6	96062	8 AL133274	AL133274 Human DNA
54	18	31.6	100405	9 AC114818	AC114818 Mus muscu
55	18	31.6	104244	9 AL805925	AL805925 Mouse DNA
56	18	31.6	125634	14 AC141713	AC141713 Adis me11
57	18	31.6	159304	8 AL606463	AL606463 Human DNA
58	18	31.6	164507	8 AC012067	AC012067 Homo sapi
59	18	31.6	170658	8 AC004072	AC004072 Human Chr
60	18	31.6	177117	9 AC115735	AC115735 Mus muscu
61	18	31.6	187070	9 AC162867	AC162867 Mus muscu
62	18	31.6	193425	9 AL732405	AL732405 Mouse DNA
63	18	31.6	225082	9 BX548065	BX548065 Mouse DNA
64	18	31.6	235519	14 AC164258	AC164258 Bos tauru
65	18	31.6	243290	9 AL663088	AL663088 Mouse DNA
66	18	31.6	243489	14 AC162622	AC162622 Bos tauru
67	18	31.6	349723	1 BX842650	BX842650 Bellovib
68	17	29.8	635	10 BV265047	BV265047 S23P6113
69	17	29.8	914	2 AF414456	AF414456 Echinosoc
70	17	29.8	1040	2 AF414458	AF414458 Echinosoc
71	17	29.8	1095	2 AF414457	AF414457 Echinosoc
72	17	29.8	1477	2 ECCCALBIND	ECCCALBIND
73	17	29.8	2202	6 CS061690	CS061690 Sequence
74	17	29.8	3522	5 XE1STAGE	XE1STAGE
75	17	29.8	4199	5 BC087548	BC087548 Xenopus l
76	17	29.8	4273	5 AU851578	AU851578 Galus ga
77	17	29.8	4862	5 BC063249	BC063249 Danio rer
78	17	29.8	10976	1 AE001127	AE001127 Borrelia
79	17	29.8	25345	2 CBT23FL	CBT23FL
80	17	29.8	64327	14 AC100013	AC100013 Mus muscu
81	17	29.8	82383	8 AL591623	AL591623 Human DNA
82	17	29.8	87427	1 AY652953	AY652953 Lyngbya m
83	17	29.8	103421	8 AC004920	AC004920 Homo sapi
84	17	29.8	114211	14 CR392022	CR392022 Danio rer
85	17	29.8	116906	8 CR855929	CR855929 Human DNA
86	17	29.8	132605	8 CR855280	CR855280 Human DNA
87	17	29.8	138128	8 AC145316	AC145316 Mus muscu
88	17	29.8	144147	8 AC145394	AC145394 Pan trogl
89	17	29.8	154101	14 AC136885	AC136885 Sus ectof
90	17	29.8	154151	14 AC121679	AC121679 Rattus no
91	17	29.8	162810	8 AC083923	AC083923 Homo sapi
91	17	29.8	167922	14 AC016085	AC016085 Homo sapi



C 92	17	29.8	173354	8	HS149A16	AL021937 Human DNA	165	16	28.1	118107	15	AC011560	AC011560 Arabidops
C 93	17	29.8	190199	14	AC120897	AC120897 Rattus no	166	16	28.1	118777	6	C0824583	C0824583 Sequence
C 94	17	29.8	193599	8	AC024382	AC024382 Homo sapi	167	16	28.1	118777	9	AF163865	AF163865 Mus muscu
C 95	17	29.8	194474	14	AC137536	AC137536 Sus scrof	C 168	16	28.1	122228	8	AC000003	AC000003 Homo sapi
C 96	17	29.8	198116	14	AC123155	AC123155 Rattus no	C 169	16	28.1	126349	15	AF006424	AF006424 Lotus cor
C 97	17	29.8	207698	8	AC114491	AC114491 Homo sapi	C 170	16	28.1	127374	9	AC107675	AC107675 Mus muscu
C 98	17	29.8	209608	14	AC153080	AC153080 Colobus g	C 171	16	28.1	128885	8	AP004318	AP004318 Homo sapi
C 99	17	29.8	212599	5	AL929222	AL929222 Zebrafish	C 172	16	28.1	130151	15	AC155794	AC155794 Oryza sat
C 100	17	29.8	216501	9	AC107795	AC107795 Mus muscu	C 173	16	28.1	130192	8	AL157832	AL157832 Human DNA
C 101	17	29.8	220522	14	AC157064	AC157064 Bos tauru	C 174	16	28.1	130226	9	AL162299	AL162299 Mus muscu
C 102	17	29.8	220939	14	AC110371	AC110371 Rattus no	C 175	16	28.1	130672	14	AC122282	AC122282 Mus muscu
C 103	17	29.8	221666	14	AC103480	AC103480 Rattus no	C 176	16	28.1	133226	14	AL151264	AL151264 Homo sapi
C 104	17	29.8	222994	14	AC094289	AC094289 Rattus no	C 177	16	28.1	141669	9	AL1805927	AL1805927 Mouse DNA
C 105	17	29.8	226557	14	AC127705	AC127705 Rattus no	C 178	16	28.1	143516	8	AC083783	AC083783 Homo sapi
C 106	17	29.8	230325	14	AC1330054	AC1330054 Rattus no	C 179	16	28.1	145111	14	AL390245	AL390245 Homo sapi
C 107	17	29.8	239240	14	AC094155	AC094155 Rattus no	C 180	16	28.1	146831	8	HS523C21	HS523C21 Human DNA
C 108	17	29.8	240531	14	AC106638	AC106638 Rattus no	C 181	16	28.1	151159	14	AC079346	AC079346 Homo sapi
C 109	17	29.8	240562	14	AC098895	AC098895 Rattus no	C 182	16	28.1	152012	9	AC155252	AC155252 Mus muscu
C 110	17	29.8	244169	14	AC107357	AC107357 Rattus no	C 183	16	28.1	153492	9	AC127255	AC127255 Mus muscu
C 111	17	29.8	244281	14	AC125891	AC125891 Rattus no	C 184	16	28.1	153792	14	AC094097	AC094097 Homo sapi
C 112	17	29.8	245024	14	AC137337	AC137337 Rattus no	C 185	16	28.1	153903	9	AC114676	AC114676 Mus muscu
C 113	17	29.8	245308	14	AC108307	AC108307 Rattus no	C 186	16	28.1	157594	14	CR854821	CR854821 Dario rer
C 114	17	29.8	252563	9	AC102091	AC102091 Mus muscu	C 187	16	28.1	160577	9	AC155638	AC155638 Mus muscu
C 115	17	29.8	257473	14	AC132663	AC132663 Rattus no	C 188	16	28.1	163322	8	AC138389	AC138389 Homo sapi
C 116	17	29.8	271370	14	AC112046	AC112046 Cryptospor	C 189	16	28.1	166991	14	AC158992	AC158992 Mus muscu
C 117	17	29.8	287050	2	BX538350	BX538350 Bacteroid	C 190	16	28.1	169265	14	AC161875	AC161875 Mus muscu
C 118	17	29.8	300297	1	AE016944	AE016944 Bacteroid	C 191	16	28.1	169482	8	AL390836	AL390836 Human DNA
C 119	17	29.8	331448	14	AC134126	AC134126 Rattus no	C 192	16	28.1	169482	8	AL390836	AL390836 Human DNA
C 120	16	28.1	481	6	AY558127	AY558127 Saccharom	C 193	16	28.1	169595	14	AC069316	AC069316 Homo sapi
C 121	16	28.1	647	10	BV070597	BV070597 Zea mays mR	C 194	16	28.1	170101	8	AC01306	AC01306 Homo sapi
C 122	16	28.1	865	15	AL608577	AL608577 S. cerevisia	C 195	16	28.1	171825	9	CT009689	CT009689 Sus scrof
C 123	16	28.1	900	15	SCBPR18C	SCBPR18C Xenopus 1	C 196	16	28.1	172134	14	CT009689	CT009689 Sus scrof
C 124	16	28.1	1306	15	SCBPR18C	SCBPR18C Xenopus 1	C 197	16	28.1	175407	9	AC132955	AC132955 Mus muscu
C 125	16	28.1	1440	8	BC004189	BC004189 Homo sapi	C 198	16	28.1	175423	14	AC159179	AC159179 Rhinolph
C 126	16	28.1	1619	6	AX523744	AX523744 Sequence	C 199	16	28.1	176462	8	AC159827	AC159827 Pan trogl
C 127	16	28.1	2449	6	AX523762	AX523762 Sequence	C 200	16	28.1	176462	8	AC159827	AC159827 Pan trogl
C 128	16	28.1	2463	6	AX684714	AX684714 Sequence	C 201	16	28.1	178643	9	AC125160	AC125160 Mus muscu
C 129	16	28.1	2463	6	AX684714	AX684714 Sequence	C 202	16	28.1	179099	8	CR450709	CR450709 Dario ter
C 130	16	28.1	2463	6	AX684714	AX684714 Sequence	C 203	16	28.1	179110	8	AC011755	AC011755 Homo sapi
C 131	16	28.1	2526	1	SMACHITT	SMACHITT	C 204	16	28.1	179927	8	AC154616	AC154616 Mus muscu
C 132	16	28.1	2532	6	AX523743	AX523743 Sequence	C 205	16	28.1	179954	8	AC007271	AC007271 Homo sapi
C 133	16	28.1	2934	5	BC067878	BC067878 Xenopus 1	C 206	16	28.1	181946	8	AP003972	AP003972 Homo sapi
C 134	16	28.1	3000	5	BC067878	BC067878 Xenopus 1	C 207	16	28.1	182662	14	CR790382	CR790382 Dario ter
C 135	16	28.1	3482	15	AF461197	AF461197 Medicago	C 208	16	28.1	183441	9	AC079956	AC079956 Mus muscu
C 136	16	28.1	6681	15	AF465648	AF465648 Aspergill	C 209	16	28.1	184566	14	AC102608	AC102608 Mus muscu
C 137	16	28.1	10640	1	AE006777	AE006777 Sulfolobu	C 210	16	28.1	185014	9	AC125169	AC125169 Homo sapi
C 138	16	28.1	11019	13	SV1318079	SV1318079 Sprng vi	C 211	16	28.1	185014	9	AC125169	AC125169 Homo sapi
C 139	16	28.1	11019	13	SVU18101	SVU18101 Spring vi	C 212	16	28.1	185014	9	AC125169	AC125169 Homo sapi
C 140	16	28.1	12800	15	SCC101B	SCC101B Saccharomyc	C 213	16	28.1	186279	9	AC160016	AC160016 Mus muscu
C 141	16	28.1	43166	9	CR936339	CR936339 Mouse DNA	C 214	16	28.1	186944	9	AC160016	AC160016 Mus muscu
C 142	16	28.1	56373	8	DO131903	DO131903 Homo sapi	C 215	16	28.1	186970	8	AL513303	AL513303 Homo sapi
C 143	16	28.1	56374	6	AR659604	AR659604 Sequence	C 216	16	28.1	187833	8	AL513303	AL513303 Homo sapi
C 144	16	28.1	56375	6	AR659604	AR659604 Sequence	C 217	16	28.1	188011	14	AC161075	AC161075 Homo sapi
C 145	16	28.1	59580	6	AC106875	AC106875 Homo sapi	C 218	16	28.1	190308	9	AC164626	AC164626 Mus muscu
C 146	16	28.1	68329	14	AC101548	AC101548 Mus muscu	C 219	16	28.1	190562	14	AC164626	AC164626 Mus muscu
C 147	16	28.1	81422	14	AP001110	AP001110 Homo sapi	C 220	16	28.1	192663	9	AC126797	AC126797 Mus muscu
C 148	16	28.1	87065	8	HSU11749	HSU11749 Zebrafish	C 221	16	28.1	192663	9	AC126797	AC126797 Mus muscu
C 149	16	28.1	89721	5	BX511069	BX511069 Zebrafish	C 222	16	28.1	192663	9	AC126797	AC126797 Mus muscu
C 150	16	28.1	90807	14	AP007924	AP007924 Arabidops	C 223	16	28.1	197916	14	AC127354	AC127354 Homo sapi
C 151	16	28.1	93985	15	ATAC013428	ATAC013428 Arabidops	C 224	16	28.1	197916	14	AC127354	AC127354 Homo sapi
C 152	16	28.1	97001	8	AC063918	AC063918 Homo sapi	C 225	16	28.1	197980	14	AC166872	AC166872 Mus muscu
C 153	16	28.1	97302	14	AP007448	AP007448 Lotus cor	C 226	16	28.1	198473	9	AC125204	AC125204 Mus muscu
C 154	16	28.1	102743	8	AL645507	AL645507 Human DNA	C 227	16	28.1	198577	14	AC163478	AC163478 Homo sapi
C 155	16	28.1	110000	1	CR555306	CR555306 Human DNA	C 228	16	28.1	198577	14	AC163478	AC163478 Homo sapi
C 156	16	28.1	110000	1	BA000019	BA000019 Human DNA	C 229	16	28.1	198577	14	AC163478	AC163478 Homo sapi
C 157	16	28.1	110000	1	CP000031	CP000031 Human DNA	C 230	16	28.1	198577	14	AC163478	AC163478 Homo sapi
C 158	16	28.1	110000	14	AC146850	AC146850 Rattus no	C 231	16	28.1	201031	9	AC154356	AC154356 Mus muscu
C 159	16	28.1	110000	14	AC158442	AC158442 Rattus no	C 232	16	28.1	202363	14	AC151284	AC151284 Mus muscu
C 160	16	28.1	110000	14	AC156935	AC156935 Rattus no	C 233	16	28.1	202363	14	AC151284	AC151284 Mus muscu
C 161	16	28.1	110000	15	AP008217	AP008217 Bos tauru	C 234	16	28.1	205759	5	BX255911	BX255911 Homo sapi
C 162	16	28.1	110000	15	CR382133	CR382133 Zebrafish	C 235	16	28.1	207295	14	AC101998	AC101998 Homo sapi
C 163	16	28.1	112501	14	AC165991	AC165991 Bos tauru	C 236	16	28.1	207295	14	AC101998	AC101998 Homo sapi
C 164	16	28.1	115198	14	AL139223	AL139223 Homo sapi	C 237	16	28.1	207927	14	AC118229	AC118229 Mus muscu



c 238	16	28.1	210378	14	AL590967	Homo sapi	c 311	15	26.3	590	13	AY180897	AY180897 Influenza
c 239	16	28.1	211025	9	AC126796	Mus muscu	c 312	15	26.3	590	13	AY180901	AY180901 Influenza
c 240	16	28.1	212305	9	AC154628	Mus muscu	c 313	15	26.3	601	6	AR661837	AR661837 Sequence
c 241	16	28.1	213599	14	AC140764	Rattus no	c 314	15	26.3	601	6	AR663843	AR663843 Sequence
c 242	16	28.1	213729	14	AC162466	Rattus no	c 315	15	26.3	618	10	BV378217	BV378217 S245P668P
c 243	16	28.1	214192	14	AL354667	Homo sapi	c 316	15	26.3	629	15	AF449792	AF449792 Fueraium
c 244	16	28.1	215780	9	AC109039	Rattus no	c 317	15	26.3	629	15	AF449793	AF449793 Fueraium
c 245	16	28.1	215180	14	AC119707	Rattus no	c 318	15	26.3	633	6	AR670765	AR670765 Sequence
c 246	16	28.1	216828	14	AC162415	Bos tauru	c 319	15	26.3	651	15	AF449796	AF449796 Fueraium
c 247	16	28.1	216662	14	AC161972	Bos tauru	c 320	15	26.3	657	15	BT006272	BT006272 Arabidops
c 248	16	28.1	219220	14	AC109435	Rattus no	c 321	15	26.3	659	15	AF449794	AF449794 Fueraium
c 249	16	28.1	221249	5	AC148811	Canis fam	c 322	15	26.3	659	15	AF449795	AF449795 Fueraium
c 250	16	28.1	223355	5	BX000700	Zebrafish	c 323	15	26.3	674	8	BC066358	BC066358 Homo sapi
c 251	16	28.1	224554	14	AC162820	Bos tauru	c 324	15	26.3	684	8	CQ743209	CQ743209 Sequence
c 252	16	28.1	226694	14	AC161915	Bos tauru	c 325	15	26.3	687	8	HOM2D53G11	HOM2D53G11
c 253	16	28.1	228472	14	AC103020	Rattus no	c 326	15	26.3	738	5	AB062638	AB062638 Seriola q
c 254	16	28.1	230568	14	AC13731	Rattus no	c 327	15	26.3	738	5	AB062639	AB062639 Seriola q
c 255	16	28.1	231288	14	AC164096	Mus muscu	c 328	15	26.3	747	10	BV486330	BV486330 S215P6051
c 256	16	28.1	234768	14	AC119436	Rattus no	c 329	15	26.3	756	10	BV472955	BV472955 G591P6190
c 257	16	28.1	234950	14	AC094003	Rattus no	c 330	15	26.3	768	2	DO087453	DO087453 Lineus vi
c 258	16	28.1	234964	14	AC094679	Rattus no	c 331	15	26.3	775	13	AY633354	AY633354 Influenza
c 259	16	28.1	235906	14	AC152270	Bos tauru	c 332	15	26.3	777	10	BV075990	BV075990 S212P6047
c 260	16	28.1	237091	14	AC162979	Bos tauru	c 333	15	26.3	793	5	AB196515	AB196515 Paralicht
c 261	16	28.1	237266	14	AC115499	Rattus no	c 334	15	26.3	808	6	BD145980	BD145980 Primer fo
c 262	16	28.1	237281	9	AC124552	Mus muscu	c 335	15	26.3	808	6	AY865918	AY865918 Sequence
c 263	16	28.1	237363	14	AC112749	Rattus no	c 336	15	26.3	819	15	CNR6767	CNR6767 Cicer ari
c 264	16	28.1	237379	14	AC163204	Bos tauru	c 337	15	26.3	827	10	BV456146	BV456146 qpm26c09.
c 265	16	28.1	238358	9	AL592465	Moube DNA	c 338	15	26.3	863	6	BD146810	BD146810 Primer fo
c 266	16	28.1	240029	14	AC133810	Rattus no	c 339	15	26.3	863	6	AX866748	AX866748 Sequence
c 267	16	28.1	244782	14	AC107351	Rattus no	c 340	15	26.3	905	2	ONGSLT	M37742 O. volvulus
c 268	16	28.1	245588	9	AC140073	Mus muscu	c 341	15	26.3	905	15	AK110751	AK110751 Oryza sat
c 269	16	28.1	246236	14	AC107534	Rattus no	c 342	15	26.3	984	6	CQ613920	CQ613920 Sequence
c 270	16	28.1	250704	14	AC130392	Rattus no	c 343	15	26.3	1022	4	DQ001760	DQ001760 Bos tauru
c 271	16	28.1	254303	14	AC162849	Bos tauru	c 344	15	26.3	1035	9	AY551091	AY551091 Rattus no
c 272	16	28.1	258823	14	AC133226	Rattus no	c 345	15	26.3	1065	6	AX594904	AX594904 Sequence
c 273	16	28.1	266441	9	AC162311	Mus muscu	c 346	15	26.3	1065	6	AX818794	AX818794 Sequence
c 274	16	28.1	269155	9	AC109138	Rattus no	c 347	15	26.3	1065	6	AX829824	AX829824 Sequence
c 275	16	28.1	273567	14	AC162342	Bos tauru	c 348	15	26.3	1065	15	AY693164	AY693164 Saccharom
c 276	16	28.1	281529	14	AC096370	Rattus no	c 349	15	26.3	1068	10	G39345	G39345 Zeb
c 277	16	28.1	284649	14	AC109044	Rattus no	c 350	15	26.3	1099	2	AY069725	AY069725 Drosophill
c 278	16	28.1	288589	14	AC162062	Bos tauru	c 351	15	26.3	1107	6	AX818940	AX818940 Sequence
c 279	16	28.1	289192	14	AC139506	Homo sapi	c 352	15	26.3	1107	6	AX829970	AX829970 Sequence
c 280	16	28.1	289791	14	AC161690	Bos tauru	c 353	15	26.3	1200	6	AR378565	AR378565 Sequence
c 281	16	28.1	300129	1	AE017309	Desulfuvi	c 354	15	26.3	1207	13	AY664789	AY664789 Influenza
c 282	16	28.1	300955	1	AE016996	Chlamydog	c 355	15	26.3	1217	13	AY664785	AY664785 Influenza
c 283	16	28.1	303424	14	AC111410	Rattus no	c 356	15	26.3	1218	13	AY664779	AY664779 Influenza
c 284	16	28.1	303774	14	AC105878	Rattus no	c 357	15	26.3	1218	13	AY664782	AY664782 Influenza
c 285	16	28.1	323475	14	AC160447	Bos tauru	c 358	15	26.3	1218	13	AY664784	AY664784 Influenza
c 286	16	28.1	330583	14	AC118024	Mus muscu	c 359	15	26.3	1218	13	AY664790	AY664790 Influenza
c 287	15	26.3	313	6	CQ453691	Sequence	c 360	15	26.3	1218	13	AY664791	AY664791 Influenza
c 288	15	26.3	344	6	BD024249	Sequence	c 361	15	26.3	1270	15	AK120073	AK120073 Oryza sat
c 289	15	26.3	344	6	AX884639	Sequence	c 362	15	26.3	1290	6	AR388186	AR388186 Sequence
c 290	15	26.3	428	6	BD108355	Sequence	c 363	15	26.3	1296	6	AR317560	AR317560 Sequence
c 291	15	26.3	428	6	AR412802	Sequence	c 364	15	26.3	1296	15	D89217	D89217 Schistosach
c 292	15	26.3	428	6	AX969636	Sequence	c 365	15	26.3	1329	5	AB051107	AB051107 Oryza sat
c 293	15	26.3	436	6	BD117807	Sequence	c 366	15	26.3	1338	9	MM0249129	MM0249129
c 294	15	26.3	436	6	AR422254	Sequence	c 367	15	26.3	1362	13	AF222637	AF222637 Influenza
c 295	15	26.3	436	6	AX982948	Sequence	c 368	15	26.3	1362	13	AF222638	AF222638 Influenza
c 296	15	26.3	437	6	BD117816	Sequence	c 369	15	26.3	1362	13	AF222639	AF222639 Influenza
c 297	15	26.3	437	6	AR422263	Sequence	c 370	15	26.3	1362	13	AF222640	AF222640 Influenza
c 298	15	26.3	437	6	AX982957	Sequence	c 371	15	26.3	1362	13	AF222641	AF222641 Influenza
c 299	15	26.3	478	6	AX308184	Sequence	c 372	15	26.3	1389	5	BC054210	BC054210 Xenopus l
c 300	15	26.3	541	15	CP0252159	Sequence	c 373	15	26.3	1392	6	CQ723376	CQ723376 Sequence
c 301	15	26.3	590	13	AY180840	Influenza	c 374	15	26.3	1497	13	AF523448	AF523448 Influenza
c 302	15	26.3	590	13	AY180843	Influenza	c 375	15	26.3	1519	6	CS086311	CS086311 Sequence
c 303	15	26.3	590	13	AY180844	Influenza	c 376	15	26.3	1519	6	AX336359	AX336359 Sequence
c 304	15	26.3	590	13	AY180851	Influenza	c 377	15	26.3	1519	8	HUMADH507	HUMADH507
c 305	15	26.3	590	13	AY180852	Influenza	c 378	15	26.3	1570	15	SCDPL100C	SCDPL100C
c 306	15	26.3	590	13	AY180854	Influenza	c 379	15	26.3	1613	8	HUMADH5C3	HUMADH5C3
c 307	15	26.3	590	13	AY180856	Influenza	c 380	15	26.3	1620	2	CQ730219	CQ730219 Sequence
c 308	15	26.3	590	13	AY180867	Influenza	c 381	15	26.3	1667	6	AY089305	AY089305 Drosophill
c 309	15	26.3	590	13	AY180873	Influenza	c 382	15	26.3	1677	9	AY692140	AY692140 Rattus no
c 310	15	26.3	590	13	AY180892	Influenza	c 383	15	26.3	1749	5	BC082399	BC082399 Xenopus l



C 384	15	26.3	1758	9	AY692141	AY692141 Rattus no	C 457	15	26.3	5175	2	DME252268	AJ252268 Drosophila
C 385	15	26.3	1809	5	BC076849	BC076849 Xenopus l	C 458	15	26.3	5256	15	BD183346	BD183346 Novel gen
C 386	15	26.3	2000	6	AX655973	AX655973 Sequence	C 459	15	26.3	5400	6	YSPC931A	M24942 Yeast (S.po
C 387	15	26.3	2066	6	CQ412688	CQ412688 Sequence	C 460	15	26.3	5569	15	AK120080	AK120080 Oryza sat
C 388	15	26.3	2080	8	BC013166	BC013166 Homo sapi	C 461	15	26.3	5609	9	BC098369	BC098369 Mus muscu
C 389	15	26.3	2084	3	DO088860	DO088860 Unculture	C 462	15	26.3	5937	15	PRIF97	AB004945 Pinus rad
C 390	15	26.3	2155	15	AK073221	AK073221 Oryza sat	C 463	15	26.3	6385	1	AY530288	AY530288 Staphyloc
C 391	15	26.3	2175	6	AX654095	AX654095 Sequence	C 464	15	26.3	6410	8	AB209129	AB209129 Homo sapi
C 392	15	26.3	2209	3	AF156423	AF156423 Influenza	C 465	15	26.3	6420	6	CQ582732	CQ582732 Sequence
C 393	15	26.3	2212	5	BC097820	BC097820 Xenopus l	C 466	15	26.3	6533	13	AF189155	AF189155 Hantaviru
C 394	15	26.3	2215	13	IAY43990	IAY43990 Influenza	C 467	15	26.3	6679	9	AK173131	AK173131 Mus muscu
C 395	15	26.3	2237	13	AF156422	AF156422 Influenza	C 468	15	26.3	6885	15	YSPADC	M66699 Yeast (S.po
C 396	15	26.3	2250	6	E07651	E07651 gDNA encodi	C 469	15	26.3	7463	8	AB056059	AB056059 Homo sapi
C 397	15	26.3	2250	13	WHTRITIN	WHTRITIN	C 470	15	26.3	8899	14	AC017290	AC017290 Drosophila
C 398	15	26.3	2253	13	AF222819	AF222819 Influenza	C 471	15	26.3	9001	1	AE003973	AE003973
C 399	15	26.3	2253	13	AF222819	AF222819 Influenza	C 472	15	26.3	10181	1	AE007867	AE007867 Clostridi
C 400	15	26.3	2259	13	AF508628	AF508628 Influenza	C 473	15	26.3	10622	1	AE007867	AE007867 Clostridi
C 401	15	26.3	2268	13	INA306863	INA306863 Influenza	C 474	15	26.3	10710	1	U32700	U32700 Haemophilus
C 402	15	26.3	2274	13	AF508627	AF508627 Influenza	C 475	15	26.3	10902	1	AE011969	AE011969
C 403	15	26.3	2274	13	AF508629	AF508629 Influenza	C 476	15	26.3	11158	1	AE004682	AE004682 Pseudomon
C 404	15	26.3	2274	13	AF508630	AF508630 Influenza	C 477	15	26.3	11439	6	CQ590870	CQ590870 Sequence
C 405	15	26.3	2274	13	AF508632	AF508632 Influenza	C 478	15	26.3	11562	1	AB031214	AB031214 Bacillus
C 406	15	26.3	2274	13	AF508633	AF508633 Influenza	C 479	15	26.3	11580	6	CQ582731	CQ582731 Sequence
C 407	15	26.3	2274	13	AF684880	AF684880 Influenza	C 480	15	26.3	11849	1	AE009364	AE009364 Agrobacte
C 408	15	26.3	2274	13	AF684880	AF684880 Influenza	C 481	15	26.3	12036	1	AE008249	AE008249 Agrobacte
C 409	15	26.3	2277	6	AR367932	AR367932 Sequence	C 482	15	26.3	13842	1	AE010388	AE010388 Methanopy
C 410	15	26.3	2277	6	AX069389	AX069389 Sequence	C 483	15	26.3	14039	1	MTU19364	MTU19364
C 411	15	26.3	2277	6	AX774868	AX774868 Sequence	C 484	15	26.3	15652	14	AC012771	AC012771
C 412	15	26.3	2277	2	HOMADH5CH	HOMADH5CH	C 485	15	26.3	15819	5	EX649369	EX649369 Zebrafish
C 413	15	26.3	2279	2	AY118355	AY118355 Drosophila	C 486	15	26.3	15041	8	AB088095	AB088095 Homo sapi
C 414	15	26.3	2295	5	BC074230	BC074230 Xenopus l	C 487	15	26.3	21460	8	AY987960	AY987960 Homo sapi
C 415	15	26.3	2323	6	BD157396	BD157396 Primer fo	C 488	15	26.3	22044	8	CR847863	CR847863 Human DNA
C 416	15	26.3	2323	6	AX878705	AX878705 Sequence	C 489	15	26.3	22693	2	AC006656	AC006656 Caenorhabd
C 417	15	26.3	2323	8	AK021823	AK021823 Homo sapi	C 490	15	26.3	24379	15	AY181248	AY181248 Kluyverom
C 418	15	26.3	2355	5	BC094077	BC094077 Xenopus l	C 491	15	26.3	27885	2	AF022984	AF022984 Caenorhab
C 419	15	26.3	2401	2	AF497828	AF497828 Caenorhab	C 492	15	26.3	28074	8	AB014077	AB014077 Homo sapi
C 420	15	26.3	2419	15	AF096992	AF096992 Euglena m	C 493	15	26.3	30452	8	AB014077	AB014077 Homo sapi
C 421	15	26.3	2453	2	AF497829	AF497829 Caenorhab	C 494	15	26.3	30488	2	AC004421	AC004421 Drosophila
C 422	15	26.3	2553	15	AK067558	AK067558 Oryza sat	C 495	15	26.3	31223	2	CEZK270	CEZK270
C 423	15	26.3	2560	6	BD094134	BD094134 Shear str	C 496	15	26.3	33166	6	AR628961	AR628961 Sequence
C 424	15	26.3	2560	6	CQ602372	CQ602372 Sequence	C 497	15	26.3	33592	6	AX084504	AX084504 Sequence
C 425	15	26.3	2560	10	BV178718	BV178718 sqm10220	C 498	15	26.3	33699	6	AX084506	AX084506 Sequence
C 426	15	26.3	2671	15	AK068618	AK068618 Oryza sat	C 499	15	26.3	33988	6	AX084517	AX084517 Sequence
C 427	15	26.3	2721	1	AF268057	AF268057 Candidatu	C 500	15	26.3	33431	6	AX084505	AX084505 Sequence
C 428	15	26.3	2722	1	AF400585	AF400585 Actinotoba	C 501	15	26.3	34448	6	AX084507	AX084507 Sequence
C 429	15	26.3	2962	5	BC090562	BC090562 Xenopus l	C 502	15	26.3	34551	8	EX248518	EX248518 Human DNA
C 430	15	26.3	3046	6	CQ613919	CQ613919 Sequence	C 503	15	26.3	34737	6	AX084518	AX084518 Sequence
C 431	15	26.3	3064	8	AK074242	AK074242 Homo sapi	C 504	15	26.3	34804	15	SPBC19C7	SPBC19C7
C 432	15	26.3	3082	8	BC024031	BC024031 Homo sapi	C 505	15	26.3	35408	6	AR163568	AR163568 Sequence
C 433	15	26.3	3107	6	AX833091	AX833091 Sequence	C 506	15	26.3	35408	6	AR166442	AR166442 Sequence
C 434	15	26.3	3107	8	AK094541	AK094541 Homo sapi	C 507	15	26.3	35724	6	AX084516	AX084516 Sequence
C 435	15	26.3	3182	6	CS130795	CS130795 Sequence	C 508	15	26.3	35871	2	AR403724	AR403724 Sequence
C 436	15	26.3	3208	5	XU067190	U67190 Xenopus lae	C 509	15	26.3	35888	6	CERT19B10	CERT19B10
C 437	15	26.3	3269	15	S45035	S45035 Kt11=Kuntiz	C 510	15	26.3	35934	13	AY339865	AY339865 Human ade
C 438	15	26.3	3362	15	CQ602354	CQ602354 Sequence	C 511	15	26.3	35935	6	AR091533	AR091533 Sequence
C 439	15	26.3	3364	15	AY136481	AY136481 Arabidops	C 512	15	26.3	35935	6	AR102266	AR102266 Sequence
C 440	15	26.3	3373	5	BC094405	BC094405 Xenopus l	C 513	15	26.3	35935	6	AR116313	AR116313 Sequence
C 441	15	26.3	3393	5	XU109135	XU109135 Sequence	C 514	15	26.3	35935	6	CQ584907	CQ584907 Sequence
C 442	15	26.3	3764	6	CQ842873	CQ842873 Sequence	C 515	15	26.3	35935	6	AR230724	AR230724 Sequence
C 443	15	26.3	3764	6	AK125920	AK125920 Homo sapi	C 516	15	26.3	35935	6	AX451988	AX451988 Sequence
C 444	15	26.3	3766	13	AD5E3	X03002 Adenovirus	C 517	15	26.3	35935	6	AX683770	AX683770 Sequence
C 445	15	26.3	4197	9	AY623757	AY623757 Rattus no	C 518	15	26.3	35935	13	ADRCOMPEN	ADRCOMPEN
C 446	15	26.3	4522	9	MMU278191	MU278191 Mus muscu	C 519	15	26.3	35938	6	AR403723	AR403723 Sequence
C 447	15	26.3	4673	15	V8CUGA35	M6498 S. cerevisia	C 520	15	26.3	36114	6	AX084519	AX084519 Sequence
C 448	15	26.3	4876	5	AY454396	AY454396 Hippoglo	C 521	15	26.3	36310	15	SPAC9C9	SPAC9C9
C 449	15	26.3	5019	6	CQ872891	CQ872891 Sequence	C 522	15	26.3	36620	6	AR534337	AR534337 Sequence
C 450	15	26.3	5058	9	BC045602	BC045602 Mus muscu	C 523	15	26.3	36724	8	AC009174	AC009174 Homo sapi
C 451	15	26.3	5069	9	BC039979	BC039979 Mus muscu	C 524	15	26.3	37474	6	AR534332	AR534332 Sequence
C 452	15	26.3	5169	6	AX512631	AX512631 Sequence	C 525	15	26.3	37777	14	AC145645	AC145645 Homo sapi
C 453	15	26.3	5169	6	AX512637	AX512637 Sequence	C 526	15	26.3	38516	15	SCCHR1VLA	SCCHR1VLA
C 454	15	26.3	5169	6	AX522282	AX522282 Sequence	C 527	15	26.3	38519	6	AR534335	AR534335 Sequence
C 455	15	26.3	5169	6	AX522288	AX522288 Sequence	C 528	15	26.3	39461	15	AC152115	AC152115 Pichia et
C 456	15	26.3	5171	15	AF364179	AF364179 Fusarium	C 529	15	26.3	39466	14	AC015131	AC015131 Drosophila



530	15	26.3	39489	15	SPBC1709	AL01852 S. pombe c	C 603	15	26.3	109110	9	AL672231	AL672231 Mouse DNA
531	15	26.3	41122	8	HSAC000109	AC0000109 Human Cos	604	15	26.3	109228	14	AC138190	AC138190 Mus muscu
532	15	26.3	41211	8	AL591545	AL591545 Human DNA	605	15	26.3	110000	1	CP000099_05	Continuation (6 of
533	15	26.3	41338	8	AC093760	AC093760 Homo sapi	606	15	26.3	110000	1	CP000099_06	Continuation (7 of
534	15	26.3	42565	15	AC149313	AC149313 Phakopsor	607	15	26.3	110000	1	CP000107_02	Continuation (3 of
535	15	26.3	42793	15	SC9168	Z38061 S. cerevisia	608	15	26.3	110000	1	CR628337_21	Continuation (22 o
536	15	26.3	43205	8	AC126123	AC126123 Homo sapi	609	15	26.3	110000	1	AE017220_03	Continuation (4 of
537	15	26.3	43600	8	AC004209	AC004209 Homo sapi	610	15	26.3	110000	1	AE017340_07	Continuation (8 of
538	15	26.3	44362	6	CG613865	CG613865 Sequence	611	15	26.3	110000	1	AY586296_2	Continuation (3 of
539	15	26.3	46900	7	AT736146	AT736146 Salmoneil	612	15	26.3	110000	1	BA000004_06	Continuation (7 of
540	15	26.3	47364	8	AC008809	AC008809 Homo sapi	613	15	26.3	110000	1	BA000031_25	Continuation (26 o
541	15	26.3	47533	14	AC101284	AC101284 Mus muscu	614	15	26.3	110000	1	BA000035_28	Continuation (29 o
542	15	26.3	53537	15	P26C17	AP177535 Arabidops	615	15	26.3	110000	1	BA000041_09	Continuation (9 of
543	15	26.3	54488	15	AF359360	AF359360 Fusarium	616	15	26.3	110000	1	EX908798_21	Continuation (2 of
544	15	26.3	56379	14	AC023447	AC023447 Homo sapi	617	15	26.3	110000	1	CP000020_26	Continuation (27 o
545	15	26.3	57000	8	AC069278	AC069278 Homo sapi	618	15	26.3	110000	1	CP000050_29	Continuation (30 o
546	15	26.3	57085	14	AC017905	AC017905 Drosophil	619	15	26.3	110000	1	CP000057_02	Continuation (13 o
547	15	26.3	57213	14	AC104415	AC104415 Mus muscu	620	15	26.3	110000	1	CP000083_12	Continuation (3 of
548	15	26.3	58301	14	AC014987	AC014987 Drosophil	621	15	26.3	110000	6	BD426631_01	Continuation (2 of
549	15	26.3	58320	14	AC133850	AC133850 Rattus no	622	15	26.3	110000	6	AR274513_01	Continuation (2 of
550	15	26.3	58641	14	AC087401	AC087401 Homo sapi	623	15	26.3	110000	6	AR632719_01	Continuation (2 of
551	15	26.3	59465	15	AY007367	AY007367 Lycopersi	624	15	26.3	110000	8	BA000025_13	Continuation (14 o
552	15	26.3	59605	14	AC103926	AC103926 Mus muscu	625	15	26.3	110000	8	BA000041_09	Continuation (10 o
553	15	26.3	63423	9	BX571778	BX571778 Mouse DNA	626	15	26.3	110000	14	AC010257_1	Continuation (2 of
554	15	26.3	63518	14	AC095260_4	Continuation (5 of	627	15	26.3	110000	14	AC095260_3	Continuation (4 of
555	15	26.3	64172	8	EX000357	Continuation (5 of	628	15	26.3	110000	14	AC098332_0	Continuation (2 of
556	15	26.3	68137	14	AC079966	AC079966 Homo sapi	629	15	26.3	110000	14	AC106675_0	Continuation (2 of
557	15	26.3	68378	14	AC113131	AC113131 Homo sapi	630	15	26.3	110000	14	AC108280_0	Continuation (5 of
558	15	26.3	68723	14	AC125941_3	Continuation (4 of	631	15	26.3	110000	14	AC110930_4	Continuation (5 of
559	15	26.3	68726	15	AB017063	AB017063 Arabidops	632	15	26.3	110000	14	AC125941_1	Continuation (12 of
560	15	26.3	70397	2	AC150256	AC150256 Aedes aeg	633	15	26.3	110000	14	AL390202_07	Continuation (18 of
561	15	26.3	70448	8	CR388372	CR388372 Human DNA	634	15	26.3	110000	14	AP006489_1	Continuation (2 of
562	15	26.3	72245	8	HS93C23	AL008713 Human DNA	635	15	26.3	110000	14	BX284653_0	BX284653 Homo Sapi
563	15	26.3	76031	9	AL928548	AL928548 Mouse DNA	636	15	26.3	110000	14	CEX10263_2	Continuation (3 of
564	15	26.3	79469	15	AC010852	AC010852 Arabidops	637	15	26.3	110000	14	CT005269_04	Continuation (5 of
565	15	26.3	80247	8	AL512406	AL512406 Human DNA	638	15	26.3	110000	14	CT005269_05	Continuation (6 of
566	15	26.3	80393	15	AP000382	AP000382 Arabidops	639	15	26.3	110000	14	LMFLCHR32_19	Continuation (20 o
567	15	26.3	80725	8	AL137078	AL137078 Human DNA	640	15	26.3	110000	14	TANN11_04	Continuation (5 of
568	15	26.3	81768	8	AL662825	AL662825 Human DNA	641	15	26.3	110000	15	AP008214_052	Continuation (53 o
569	15	26.3	82700	14	AC015635	AC015635 Homo sapi	642	15	26.3	110000	15	AP008214_206	Continuation (207
570	15	26.3	82700	14	AC015635	AC015635 Homo sapi	643	15	26.3	110000	15	AP008216_012	Continuation (133 o
571	15	26.3	82724	8	BX927220	BX927220 Human DNA	644	15	26.3	110000	15	AP008216_121	Continuation (122
572	15	26.3	83859	15	AB024038	AB024038 Arabidops	645	15	26.3	110000	15	AP008217_147	Continuation (148
573	15	26.3	84194	15	AB006701	AB006701 Arabidops	646	15	26.3	110000	15	AP008218_072	Continuation (73 o
574	15	26.3	84896	15	AB025639	AB025639 Arabidops	647	15	26.3	110000	15	AP008218_154	Continuation (155
575	15	26.3	84931	14	AC139389	AC139389 Rattus no	648	15	26.3	110000	15	AP008218_212	Continuation (213
576	15	26.3	85439	2	AC004728	AC004728 Drosophil	649	15	26.3	110000	15	CR382129_00	CR382129 Yarrowia
577	15	26.3	86737	15	BX842632	BX842632 Neurospor	650	15	26.3	110000	15	CR382132_37	Continuation (38 o
578	15	26.3	86987	14	AC1449920	AC1449920 Mus muscu	651	15	26.3	110000	15	AC145127_12	Continuation (13 o
579	15	26.3	87333	8	BX537154	BX537154 Human DNA	652	15	26.3	110000	15	AP008207_034	Continuation (35 o
580	15	26.3	88236	14	AP007807	AP007807 Lotus cor	653	15	26.3	110000	15	AP008207_041	Continuation (41 o
581	15	26.3	88734	14	AP007871	AP007871 Lotus cor	654	15	26.3	110000	15	AP008207_040	Continuation (42 o
582	15	26.3	88736	8	AC010420	AC010420 Homo sapi	655	15	26.3	110000	15	AP008207_186	Continuation (187
583	15	26.3	88869	8	AF130247	AF130247 Homo sapi	656	15	26.3	110000	15	AP008208_187	Continuation (188
584	15	26.3	90816	14	AC017493	AC017493 Drosophil	657	15	26.3	110000	15	AP008209_050	Continuation (51 o
585	15	26.3	91040	5	BX248094	BX248094 Zebrafish	658	15	26.3	110000	15	AP008209_178	Continuation (179
586	15	26.3	91286	2	CEY102A5C	AL0031627 Caenorhab	659	15	26.3	110000	15	AP008210_011	Continuation (112 o
587	15	26.3	92189	15	AC130798	AC130798 Medicago	660	15	26.3	110000	15	AP008210_016	Continuation (17 o
588	15	26.3	92563	6	AX695695	AX695695 Sequence	661	15	26.3	110000	15	AP008211_026	Continuation (27 o
589	15	26.3	92648	14	AP007853	AP007853 Lotus cor	662	15	26.3	110000	15	AP008211_087	Continuation (88 o
590	15	26.3	92719	14	AC165477	AC165477 Bos tauru	663	15	26.3	110000	15	AP008211_145	Continuation (146
591	15	26.3	93965	8	AL353132	AL353132 Human DNA	664	15	26.3	110000	15	AP008211_249	Continuation (1250
592	15	26.3	96570	14	AP0077418	AP0077418 Lotus cor	665	15	26.3	110000	15	AP008212_134	Continuation (1135
593	15	26.3	98126	14	AP008019	AP008019 Lotus cor	666	15	26.3	110000	15	AP008212_174	Continuation (1175
594	15	26.3	98581	15	P8K7	AC007727 Arabidops	667	15	26.3	110000	15	AP008212_226	Continuation (1227
595	15	26.3	101981	8	AC003001	AC003001 Homo sapi	668	15	26.3	110000	15	AP008212_227	Continuation (228
596	15	26.3	102178	15	AP003803	AP003803 Oryza sat	669	15	26.3	110000	15	AP008212_303	Continuation (304
597	15	26.3	102387	8	AC022114	AC022114 Homo sapi	670	15	26.3	110000	15	AP008213_162	Continuation (163
598	15	26.3	103842	9	AL840633	AL840633 Mouse DNA	671	15	26.3	110000	15	AP008213_169	Continuation (1170
599	15	26.3	104515	15	AP002903	AP002903 Oryza sat	672	15	26.3	110000	15	AP008213_237	Continuation (1238
600	15	26.3	105218	15	AC130652	AC130652 Medicago	673	15	26.3	111614	5	BX571719	BX571719 Zebrafish
601	15	26.3	106762	14	AP004141	AP004141 Oryza sat	674	15	26.3	112356	8	AL138812	AL138812 Human DNA
602	15	26.3	108365	15	AC015447	AC015447 Arabidops	675	15	26.3	113345	15	AC141110	AC141110 Medicago



676	15	26.3 114897	14	AP003624	AP003624 Oryza sat	c 749	15	26.3 141159	14	AP000754	AP000754 Homo sapi
677	15	26.3 115497	9	AL772304	AL772304 Mouse DNA	750	15	26.3 141427	15	CNS08CAJ	AL831806 Oryza sat
678	15	26.3 115397	8	AL157902	AL157902 Human DNA	751	15	26.3 141578	15	CNS08CAJ	AL831806 Oryza sat
679	15	26.3 116419	15	AC146743	AC146743 Medicago	752	15	26.3 141833	8	AL442063	AL442063 Human DNA
680	15	26.3 116874	8	AL590304	AL590304 Human DNA	753	15	26.3 142087	9	AC092773	AC092773 Homo sapi
681	15	26.3 119255	8	AL535614	AL535614 Human DNA	754	15	26.3 142333	8	AC131798	AC131798 Homo sapi
682	15	26.3 119657	15	AC149578	AC149578 Medicago	755	15	26.3 142527	8	AL589843	AL589843 Human DNA
683	15	26.3 120236	14	AC157562	AC157562 Mus muscu	756	15	26.3 142576	8	AC010609	AC010609 Homo sapi
684	15	26.3 120469	14	AC156875	AC156875 Bos tauru	757	15	26.3 142680	15	AP004611	AP004611 Oryza sat
685	15	26.3 120871	8	AC016605	AC016605 Homo sapi	758	15	26.3 142896	15	AP009641	AP009641 Oryza sat
686	15	26.3 121243	15	CNS08CCY	AL954160 Oryza sat	759	15	26.3 143328	15	AC151598	AC151598 Medicago
687	15	26.3 121421	14	AC148341	AC148341 Medicago	760	15	26.3 144457	15	AC119290	AC119290 Oryza sat
688	15	26.3 122167	15	BX511009	BX511009 Zebrafish	761	15	26.3 145415	8	HSBA388X2	AL121584 Human DNA
689	15	26.3 122479	2	CERY113G7A	AL132858 Caenorhab	762	15	26.3 145526	15	AC079179	AC079179 Oryza sat
690	15	26.3 123050	8	AC008917	AC008917 Homo sapi	763	15	26.3 145574	8	AC104151	AC104151 Homo sapi
691	15	26.3 123851	8	AL844903	AL844903 Mouse DNA	764	15	26.3 146087	14	CR925721	CR925721 Danio rer
692	15	26.3 125042	14	AC164944	AL616944 Sus scrofa	765	15	26.3 147052	8	AL1590640	AL1590640 Human DNA
693	15	26.3 125192	9	AL805920	AL805920 Mouse DNA	766	15	26.3 147225	14	AC134892	AC134892 Oryza sat
694	15	26.3 125378	8	AL391416	AL391416 Human DNA	767	15	26.3 148158	15	AP005181	AP005181 Homo sapi
695	15	26.3 125690	9	AC129780	AC129780 Mus muscu	768	15	26.3 148167	9	AC141879	AC141879 Homo sapi
696	15	26.3 126534	15	AP006233	AP006233 Oryza sat	769	15	26.3 148342	8	AC010140	AC010140 Homo sapi
697	15	26.3 126582	8	AC010241	AC010241 Homo sapi	770	15	26.3 148385	14	AC166243	AC166243 Mus muscu
698	15	26.3 126680	15	CNS07YQC	AL173911 Oryza sat	771	15	26.3 148642	8	HS580G13	AL034426 Human DNA
699	15	26.3 126793	14	AC148912	AC148912 Otolenmur	772	15	26.3 149389	8	AL590731	AL590731 Human DNA
700	15	26.3 126931	14	AC161740	AC161740 Daelypus n	773	15	26.3 149398	15	AC146946	AC146946 Homo sapi
701	15	26.3 127330	15	AC124142	AC124142 Oryza sat	774	15	26.3 149654	15	AC080019	AC080019 Genomic s
702	15	26.3 127643	5	BX322791	BX322791 Zebrafish	775	15	26.3 149772	9	AC154466	AC154466 Mus muscu
703	15	26.3 127939	8	AF165138	AF165138 Homo sapi	776	15	26.3 149839	9	AC153496	AC153496 Mus muscu
704	15	26.3 129246	8	AL929073	AL929073 Mouse DNA	777	15	26.3 150437	6	CS086345	CS086345 Sequence
705	15	26.3 129413	8	AC020992	AC020992 Homo sapi	778	15	26.3 150516	14	AC022946	AC022946 Homo sapi
706	15	26.3 130069	8	AC010988	AC010988 Homo sapi	779	15	26.3 150892	5	AL929190	AL929190 Zebrafish
707	15	26.3 130080	8	AP003160	AP003160 Homo sapi	780	15	26.3 150925	8	AC125282	AC125282 Homo sapi
708	15	26.3 130271	14	AP007320	AP007320 Lotus cor	781	15	26.3 150925	8	AL662800	AL662800 Human DNA
709	15	26.3 131000	8	AP001017	AP001017 Homo sapi	782	15	26.3 151228	8	HS0730H16	AL322006 Human DNA
710	15	26.3 131250	8	AC008062	AC008062 Homo sapi	783	15	26.3 151391	8	AL934770	AL934770 Zebrafish
711	15	26.3 131371	14	BX901982	BX901982 Danio rer	784	15	26.3 151426	15	AL934770	AL934770 Zebrafish
712	15	26.3 131423	8	AC116609	AC116609 Homo sapi	785	15	26.3 151494	14	AC132989	AC132989 Homo sapi
713	15	26.3 132169	14	AC026814	AC026814 Mus muscu	786	15	26.3 151699	15	AP003916	AP003916 Oryza sat
714	15	26.3 132263	14	AC155405	AC155405 Zee mayu	787	15	26.3 151830	15	BX255962	BX255962 Zebrafish
715	15	26.3 132987	8	AC026870	AC026870 Homo sapi	788	15	26.3 151933	14	AC046118	AC046118 Homo sapi
716	15	26.3 133104	8	AL451070	AL451070 Human DNA	789	15	26.3 152188	14	AP004617	AP004617 Oryza sat
717	15	26.3 133381	9	AC109308	AC109308 Mus muscu	790	15	26.3 152460	15	AC046172	AC046172 Homo sapi
718	15	26.3 133516	8	AL591409	AL591409 Human DNA	791	15	26.3 152492	5	CR524821	CR524821 Zebrafish
719	15	26.3 134074	15	AC145325	AC145325 Oryza sat	792	15	26.3 152728	8	AC092767	AC092767 Homo sapi
720	15	26.3 134159	7	AP003625	AP003625 Oryza sat	793	15	26.3 153652	14	AC092767	AC092767 Homo sapi
721	15	26.3 134416	14	AP020713	AP020713 Bacterioph	794	15	26.3 153746	8	AC108125	AC108125 Homo sapi
722	15	26.3 134878	8	AC140847	AC140847 Homo sapi	795	15	26.3 153887	8	AC093830	AC093830 Homo sapi
723	15	26.3 135417	8	HS041217	HS041217 Human DNA	796	15	26.3 154051	14	AC142357	AC142357 Homo sapi
724	15	26.3 135816	15	AP005505	AP005505 Oryza sat	797	15	26.3 154212	14	AC149952	AC149952 Strongylo
725	15	26.3 135925	5	BX927203	BX927203 Zebrafish	798	15	26.3 154354	14	RN470J21	AL627239 Rattus no
726	15	26.3 136131	8	BQ000063	BQ000063 Pan trogl	799	15	26.3 154393	14	AC162793	AC162793 Mus muscu
727	15	26.3 136799	15	AP003506	AP003506 Oryza sat	800	15	26.3 154482	9	AC164662	AC164662 Mus muscu
728	15	26.3 136975	8	AC068831	AC068831 Homo sapi	801	15	26.3 154714	15	BX927222	BX927222 Zebrafish
729	15	26.3 137389	5	BX901884	BX901884 Zebrafish	802	15	26.3 154957	14	AC080126	AC080126 Homo sapi
730	15	26.3 137474	9	AC155944	AC155944 Mus muscu	803	15	26.3 155024	5	BX649446	BX649446 Zebrafish
731	15	26.3 137571	15	CNS07YPD	AL173932 Oryza sat	804	15	26.3 155037	15	AC164626	AC164626 Genomic s
732	15	26.3 137730	8	HS36582	AL009177 Human DNA	805	15	26.3 155189	14	AC102397	AC102397 Homo sapi
733	15	26.3 137894	14	AL138829	AL138829 Homo sapi	806	15	26.3 155382	8	AP006152	AP006152 Homo sapi
734	15	26.3 137910	8	AL157764	AL157764 Human DNA	807	15	26.3 155525	14	AP006152	AP006152 Homo sapi
735	15	26.3 138037	15	AP003685	AP003685 Oryza sat	808	15	26.3 155564	5	AB078884	AB078884 Colutnrix
736	15	26.3 138473	9	AC003019	AC003019 Mus muscu	809	15	26.3 155616	14	CR933398	CR933398 Danio rer
737	15	26.3 138533	8	AC001357	AC001357 Homo sapi	810	15	26.3 155805	8	AL359265	AL359265 Human DNA
738	15	26.3 138633	8	AP002028	AP002028 Homo sapi	811	15	26.3 155919	5	BX548246	BX548246 Zebrafish
739	15	26.3 138969	8	AC060771	AC060771 Homo sapi	812	15	26.3 156419	15	AP002524	AP002524 Oryza sat
740	15	26.3 139103	15	AP003898	AP003898 Oryza sat	813	15	26.3 156574	9	AC141504	AC141504 Homo sapi
741	15	26.3 139123	15	AC145480	AC145480 Genomic B	814	15	26.3 156794	8	AP005211	AP005211 Homo sapi
742	15	26.3 139351	5	BX465184	BX465184 Zebrafish	815	15	26.3 157224	9	AC132925	AC132925 Homo sapi
743	15	26.3 139829	15	AC130601	AC130601 Oryza sat	816	15	26.3 157249	8	AC133329	AC133329 Homo sapi
744	15	26.3 140381	14	AC0011634	AC0011634 Homo sapi	817	15	26.3 157442	14	AC079929	AC079929 Homo sapi
745	15	26.3 140491	15	AP003276	AP003276 Oryza sat	818	15	26.3 157577	8	CNS05TFF	AL359212 Homo chr
746	15	26.3 140791	15	AP002912	AP002912 Oryza sat	819	15	26.3 157656	14	AC104124	AC104124 Homo sapi
747	15	26.3 140838	15	AP006130	AP006130 Lotus cor	820	15	26.3 158073	8	AC093756	AC093756 Homo sapi
748	15	26.3 141099	15	OSJN00296	BX482607 Oryza sat	821	15	26.3 158410	15	AP005497	AP005497 Homo sapi



C 822	15	26.3	158663	14	AC161010	AC161010 Pan trogl	C 895	15	26.3	172868	14	AC024321	AC024321 Homo sapi
C 823	15	26.3	158980	6	CO895750	CO895750 Sequence	C 896	15	26.3	173198	9	AC124440	AC124440 Mus muscu
C 824	15	26.3	158980	8	HSDF6P5	AL080315 Human DNA	C 897	15	26.3	173253	9	AC102898	AC102898 Mus muscu
C 825	15	26.3	159382	15	AC116601	AC116601 Oryza sat	C 898	15	26.3	173358	14	AC145050	AC145050 Canis fam
C 826	15	26.3	159490	14	AC152356	AC152356 Oryza sat	C 899	15	26.3	173513	8	HS125H2	298949 Human DNA s
C 827	15	26.3	159901	14	AP004226	AP004226 Oryza sat	C 900	15	26.3	173603	8	AC132222	AC132222 Mus muscu
C 828	15	26.3	160014	8	AL133325	AL133325 Human DNA	C 901	15	26.3	173627	8	AC004963	AC004963 Homo sapi
C 829	15	26.3	160184	8	AC015821	AC015821 Homo sapi	C 902	15	26.3	173735	9	AC158956	AC158956 Mus muscu
C 830	15	26.3	160275	8	AC013701	AC013701 Homo sapi	C 903	15	26.3	173881	8	AL162388	AL162388 Human DNA
C 831	15	26.3	160280	14	AC146628	AC146628 Papio anu	C 904	15	26.3	173903	15	AC148814	AC148814 Oryza sat
C 832	15	26.3	160366	8	AC069457	AC069457 Drosophi1	C 905	15	26.3	173975	14	AC123030	AC123030 Mus muscu
C 833	15	26.3	160582	8	AL138693	AL138693 Human DNA	C 906	15	26.3	173975	14	AC068960	AC068960 Homo sapi
C 834	15	26.3	160808	8	AC108096	AC108096 Homo sapi	C 907	15	26.3	174375	14	AC128360	AC128360 Rattus no
C 835	15	26.3	161115	14	AC101939	AC101939 Mus muscu	C 908	15	26.3	174632	14	CR450773	CR450773 Danio rer
C 836	15	26.3	161487	8	AC158944	AC158944 Mus muscu	C 909	15	26.3	174724	9	AC122532	AC122532 Mus muscu
C 837	15	26.3	161538	8	AL131818	AL131818 Human DNA	C 910	15	26.3	174725	8	AC093545	AC093545 Homo sapi
C 838	15	26.3	161927	2	AC006330	AC006330 Drosophi1	C 911	15	26.3	174755	8	AC007486	AC007486 Homo sapi
C 839	15	26.3	162037	9	AC137516	AC137516 Mus muscu	C 912	15	26.3	174752	14	AC015841	AC015841 Homo sapi
C 840	15	26.3	162658	14	AC018617	AC018617 Homo sapi	C 913	15	26.3	174856	14	BX296555	BX296555 Homo sapi
C 841	15	26.3	162762	14	AC112942	AC112942 Mus muscu	C 914	15	26.3	175075	8	AC113346	AC113346 Homo sapi
C 842	15	26.3	162841	8	AC099504	AC099504 Homo sapi	C 915	15	26.3	175076	14	AC048365	AC048365 Homo sapi
C 843	15	26.3	163160	15	AC129050	AC129050 Medicago	C 916	15	26.3	175079	8	AC114982	AC114982 Homo sapi
C 844	15	26.3	163165	15	AC124953	AC124953 Medicago	C 917	15	26.3	175144	14	AC068502	AC068502 Mus muscu
C 845	15	26.3	163377	15	AP004684	AP004684 Oryza sat	C 918	15	26.3	175174	15	AP003339	AP003339 Oryza sat
C 846	15	26.3	163722	14	CR848783	CR848783 Danio rer	C 919	15	26.3	175261	5	BX469891	BX469891 Zebrafish
C 847	15	26.3	163848	8	HS1056L3	AL031727 Human DNA	C 920	15	26.3	175386	9	AC119815	AC119815 Mus muscu
C 848	15	26.3	163887	14	AC156379	AC156379 Rhinoloph	C 921	15	26.3	175707	14	AC022030	AC022030 Homo sapi
C 849	15	26.3	164026	14	AC147535	AC147535 Felis cat	C 922	15	26.3	175994	8	AC079460	AC079460 Homo sapi
C 850	15	26.3	164368	2	AC150255	AC150255 Aedes aeg	C 923	15	26.3	175998	8	AC087238	AC087238 Homo sapi
C 851	15	26.3	164486	8	CNS05TES	AL359332 Human chr	C 924	15	26.3	176183	9	AL589766	AL589766 Mus muscu
C 852	15	26.3	164628	8	CNS01D42	AL121542 Mus muscu	C 925	15	26.3	176258	8	AC026955	AC026955 Homo sapi
C 853	15	26.3	164639	9	AC122738	AL135858 Human chr	C 926	15	26.3	176532	14	AC161924	AC161924 Mus muscu
C 854	15	26.3	164639	9	AC122738	AC122738 Mus muscu	C 927	15	26.3	176616	14	AC007449	AC007449 Homo sapi
C 855	15	26.3	164701	14	AC084202	AC084202 Mus muscu	C 928	15	26.3	176641	14	AC023753	AC023753 Homo sapi
C 856	15	26.3	165049	14	AC149561	AC149561 Papio anu	C 929	15	26.3	176823	8	AC146138	AC146138 Par trogl
C 857	15	26.3	165202	14	AC157462	AC157462 Rhinoloph	C 930	15	26.3	177080	14	AC084875	AC084875 Homo sapi
C 858	15	26.3	165697	2	AC092222	AC092222 Drosophi1	C 931	15	26.3	177382	14	AC125953	AC125953 Rattus no
C 859	15	26.3	165904	14	AL158148	AL158148 Homo sapi	C 932	15	26.3	177412	14	CR974565	CR974565 Sus scrof
C 860	15	26.3	166012	14	AC166986	AC166986 Mus muscu	C 933	15	26.3	177722	8	AL158053	AL158053 Human DNA
C 861	15	26.3	166120	14	AC091963	AC091963 Homo sapi	C 934	15	26.3	177978	8	AC009073	AC009073 Homo sapi
C 862	15	26.3	166240	9	AL1713897	AL1713897 Mouse DNA	C 935	15	26.3	177978	8	AC009126	AC009126 Homo sapi
C 863	15	26.3	166642	2	AC008364	AC008364 Drosophi1	C 936	15	26.3	178033	8	AC107025	AC107025 Homo sapi
C 864	15	26.3	166801	9	AC132948	AC132948 Mus muscu	C 937	15	26.3	178075	14	AC021615	AC021615 Homo sapi
C 865	15	26.3	166847	8	CNS06C75	AL39801 Human chr	C 938	15	26.3	178190	14	CR536613	CR536613 Danio rer
C 866	15	26.3	167108	8	CNS01RHA	AL161666 Human chr	C 939	15	26.3	178208	14	AC136432	AC136432 Homo sapi
C 867	15	26.3	167334	9	AC124428	AC124428 Mus muscu	C 940	15	26.3	178309	8	AL596326	AL596326 Human DNA
C 868	15	26.3	167382	14	AC140739	AC140739 Rattus no	C 941	15	26.3	178415	14	AC023547	AC023547 Homo sapi
C 869	15	26.3	167886	14	AC166031	AC166031 Sus scrof	C 942	15	26.3	178456	9	AL544716	AL544716 Mus muscu
C 870	15	26.3	167895	15	OSJN00001	AL606450 Oryza sat	C 943	15	26.3	178656	9	AL844556	AL844556 Mouse DNA
C 871	15	26.3	167925	14	AC126993	AC126993 Rattus no	C 944	15	26.3	178691	5	BX571836	BX571836 Zebrafish
C 872	15	26.3	167940	9	AL1773517	AL1773517 Mouse DNA	C 945	15	26.3	178866	14	BX294193	BX294193 Homo sapi
C 873	15	26.3	168135	14	AC120654	AC120654 Rattus no	C 946	15	26.3	178992	9	AC124690	AC124690 Mus muscu
C 874	15	26.3	168544	8	AL133344	AL133344 Human DNA	C 947	15	26.3	179187	8	AC073583	AC073583 Homo sapi
C 875	15	26.3	168851	8	AC079336	AC079336 Homo sapi	C 948	15	26.3	179216	9	AC104832	AC104832 Mus Muscu
C 876	15	26.3	169206	9	AC123550	AC123550 Mus muscu	C 949	15	26.3	179343	8	AC007281	AC007281 Homo sapi
C 877	15	26.3	169510	9	AC102461	AC102461 Mus muscu	C 950	15	26.3	179585	8	AC117544	AC117544 Mus muscu
C 878	15	26.3	169913	14	AC016481	AC016481 Homo sapi	C 951	15	26.3	179859	8	AC007563	AC007563 Homo sapi
C 879	15	26.3	170163	2	AC009457	AC009457 Drosophi1	C 952	15	26.3	179918	9	AC1021037	AC1021037 Homo sapi
C 880	15	26.3	170427	8	AP005328	AP005328 Homo sapi	C 953	15	26.3	180079	8	AC114678	AC114678 Mus muscu
C 881	15	26.3	170470	8	AC146392	AC146392 Pan trogl	C 954	15	26.3	180084	9	AC140372	AC140372 Mus muscu
C 882	15	26.3	170610	14	AC033935	AC033935 Homo sapi	C 955	15	26.3	180425	2	AC008229	AC008229 Drosophi1
C 883	15	26.3	171187	8	BS000062	BS000062 Pan trogl	C 956	15	26.3	180555	8	AC079384	AC079384 Homo sapi
C 884	15	26.3	171230	14	AC140013	AC140013 Homo sapi	C 957	15	26.3	180664	14	AC145277	AC145277 Xenopus t
C 885	15	26.3	171388	5	BX294181	BX294181 Zebrafish	C 958	15	26.3	180674	14	AC148565	AC148565 Papio anu
C 886	15	26.3	171653	8	AC080162	AC080162 Homo sapi	C 959	15	26.3	180742	9	AC122867	AC122867 Mus muscu
C 887	15	26.3	171896	14	AC117003	AC117003 Rattus no	C 960	15	26.3	181050	14	AC141642	AC141642 Mus muscu
C 888	15	26.3	171973	14	AC155770	AC155770 Mus muscu	C 961	15	26.3	181066	14	AC144606	AC144606 Canis fam
C 889	15	26.3	172161	15	AP003301	AP003301 Oryza sat	C 962	15	26.3	181303	9	AC155815	AC155815 Mus muscu
C 890	15	26.3	172652	14	AC144852	AC144852 Mus muscu	C 963	15	26.3	181345	9	AL626774	AL626774 Mouse DNA
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C 969	15	26.3 182400	14	AC124010	Mus muscu
C 970	15	26.3 182726	9	AL691444	Mouse DNA
C 971	15	26.3 182942	9	AC135110	Mus muscu
C 972	15	26.3 183390	14	AC162536	Bos tauru
C 973	15	26.3 183455	9	AL713978	Mouse DNA
C 974	15	26.3 183778	14	AC011004	Homo sapi
C 975	15	26.3 183827	8	AC005899	Homo sapi
C 976	15	26.3 183922	14	AC151021	Callithr
C 977	15	26.3 184201	9	EX088698	Mouse DNA
C 978	15	26.3 184276	9	AC115917	Mus muscu
C 979	15	26.3 184391	8	AL592043	Human DNA
C 980	15	26.3 184854	8	AC114488	Homo sapi
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C 982	15	26.3 185107	14	AC118513	Rattus no
C 983	15	26.3 185211	14	AC018707	Homo sapi
C 984	15	26.3 185268	9	AC122458	Mus muscu
C 985	15	26.3 185378	9	AL772367	Mouse DNA
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C 988	15	26.3 185892	5	CR293514	Zebrafish
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C 990	15	26.3 186045	9	AL837505	Mouse DNA
C 991	15	26.3 186137	9	AC110895	Mus muscu
C 992	15	26.3 186278	8	AL928717	Human DNA
C 993	15	26.3 186433	8	AL162231	Human DNA
C 994	15	26.3 186490	2	AC092234	Drosophi
C 995	15	26.3 187126	14	AC156983	Mus muscu
C 996	15	26.3 187131	9	AL365317	Mouse DNA
C 997	15	26.3 187273	15	AP005966	Oryza sat
C 998	15	26.3 187635	5	BX465208	Zebrafish
C 999	15	26.3 187938	14	AC117973	Rattus no
C1000	15	26.3 188504	6	AR659670	Sequence

## ALIGNMENTS

RESULT 1  
AB125961/c 721 bp DNA linear BCT 02-APR-2004

LOCUS AB125961  
DEFINITION *Bacillus anthracis* plasmid PX01 pagA gene, partial cds.  
ACCESSION AB125961  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE  
AUTHORS Inoue, S., Noguichi, A., Tanabayashi, K. and Yamada, A.  
TITLE Preparation of a positive control DNA for molecular diagnosis of  
JOURNAL *Bacillus anthracis*  
REFERENCE Unpublished  
AUTHORS 2 (bases 1 to 721)  
TITLE Inoue, S. and Noguichi, A.  
JOURNAL Direct Submission  
Submitted (06-NOV-2003) Satoshi Inoue, National Institute of Infectious Diseases, Laboratory of Transmission Control of Zoonosis, Department of Veterinary Science, 1-23-1 Toyama, Shinjuku-ku, Tokyo 162-8640, Japan (E-mail: sinouehi@nii.go.jp, Tel:81-3-5285-1111(ex.2620), Fax:81-3-5285-1179)

FEATURES  
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complement(1..721)  
gene

CDS  
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NNSSTVAIDHSISLAGEKRTWAEITMGNTADTARLNADIRYVNTGTAPTYVLPFTSL  
VLGKQTLATIKAKENQLSQIL"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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708 GTGCTGACCTACCGTTCCAGACCGTGACATGATGTAATCCCTGATTCTAGAG 652

RESULT 2  
AX353773 774 bp DNA linear PAT 06-FEB-2002

LOCUS AX353773  
DEFINITION Sequence 4 from Patent WO0204646.  
ACCESSION AX353773  
VERSION AX353773.1 GI:18618826  
KEYWORDS  
SOURCE  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Williamson, R.D., Miller, J., Walker, N.J., Baillie, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 4 17-JAN-2002;  
The Secretary of State for Defense (GB)  
Location/Qualifiers  
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/db\_xref="taxon:32630"  
/note="DNA sequence used to encode SEQ ID NO: 3"

ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGTAATCCCTGATTCTAGAG 565

RESULT 3  
AX353777 954 bp DNA linear PAT 06-FEB-2002

LOCUS AX353777  
DEFINITION Sequence 8 from Patent WO0204646.  
ACCESSION AX353777  
VERSION AX353777.1 GI:18618828  
KEYWORDS  
SOURCE  
synthetic construct  
other sequences; artificial sequences.

REFERENCE  
AUTHORS Williamson, R.D., Miller, J., Walker, N.J., Baillie, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 8 17-JAN-2002;  
The Secretary of State for Defense (GB)  
Location/Qualifiers



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source
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/mol_type="unassigned DNA"
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 2 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 58

RESULT 4
AX353779 1278 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 10 from Patent WO204646.
ACCESSION AX353779
VERSION AX353779.1 GI:18618829
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
1 Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,
  Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.
  Expression system
  Patent: WO 0204646-A 10 17-JAN-2002;
  The Secretary of State for Defense (GB)
  Location/Qualifiers
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  /note="DNA sequence used to encode SEQ ID NO: 9"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 57
    |||||
Db 2 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 58

RESULT 5
CS135645 1281 bp DNA linear PAT 09-AUG-2005
LOCUS Sequence 10 from Patent WO2005068493.
ACCESSION CS135645
VERSION CS135645.1 GI:72056311
KEYWORDS
SOURCE
ORGANISM
Bacillus anthracis
Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
AUTHORS
1 Cutting,S.M.
  Anthrax vaccine in the form of a spore
  Patent: WO 2005068493-A 10 28-JUL-2005;
  Royal Holloway and Bedford New College (GB)
  Location/Qualifiers
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  /db_xref="taxon:1392"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 57
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Db 8 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 64

RESULT 6
AX353775 1461 bp DNA linear PAT 06-FEB-2002
LOCUS Sequence 6 from Patent WO204646.
ACCESSION AX353775
VERSION AX353775.1 GI:18618827
KEYWORDS
SOURCE
ORGANISM
synthetic construct
other sequences; artificial sequences.
REFERENCE
AUTHORS
1 Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,
  Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.
  Expression system
  Patent: WO 0204646-A 6 17-JAN-2002;
  The Secretary of State for Defense (GB)
  Location/Qualifiers
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  /mol_type="unassigned DNA"
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 57
    |||||
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 565

RESULT 7
CS135643 1707 bp DNA linear PAT 09-AUG-2005
LOCUS Sequence 8 from Patent WO2005068493.
ACCESSION CS135643
VERSION CS135643.1 GI:72056309
KEYWORDS
SOURCE
ORGANISM
Bacillus anthracis
Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
AUTHORS
1 Cutting,S.M.
  Anthrax vaccine in the form of a spore
  Patent: WO 2005068493-A 8 28-JUL-2005;
  Royal Holloway and Bedford New College (GB)
  Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 57
    |||||
Db 8 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAGG 64
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RESULT 8  
AR570597  
LOCUS AR570597 1710 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 4 from patent US 6770479.  
ACCESSION AR570597  
VERSION AR570597.1 GI:56571410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1710)  
AUTHORS Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 4 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOX;  
FEATURES  
source location/Qualifiers  
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11 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 67  
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RESULT 9  
AX353781  
LOCUS AX353781 1785 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 12 from Patent WO204646.  
ACCESSION AX353781  
VERSION AX353781.1 GI:18618830  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,  
Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 12 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source location/Qualifiers  
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OY 1 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 57  
509 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 565  
Db  
RESULT 10  
CS135652  
LOCUS CS135652 2208 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 17 from Patent WO2005068493.  
ACCESSION CS135652  
VERSION CS135652.1 GI:72056316  
KEYWORDS  
SOURCE Bacillus anthracis

ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus  
cereus group.  
REFERENCE 1  
AUTHORS Cutting,S.M.  
JOURNAL Anthrax vaccine in the form of a spore  
Patent: WO 2005068493-A 17 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
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ORIGIN  
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 57  
509 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 565  
Db  
RESULT 11  
AX353783  
LOCUS AX353783 2208 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 14 from Patent WO204646.  
ACCESSION AX353783  
VERSION AX353783.1 GI:18618831  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,  
Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 14 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source location/Qualifiers  
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/note="DNA sequence used to encode SEQ ID NO: 13"  
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Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 57  
509 GTGCTGACCTACGGTTCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 565  
Db  
RESULT 12  
CS061689  
LOCUS CS061689 2211 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 9 from Patent WO2005026203.  
ACCESSION CS061689  
VERSION CS061689.1 GI:62553664  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus  
cereus group.  
REFERENCE 1  
AUTHORS Kopecko,D.J., Osorio,M., Bhattacharyya,S., Girt,C.P. and Blake,M.  
TITLE DNA promoters and anthrax vaccines  
JOURNAL Patent: WO 2005026203-A 9 24-MAR-2005;  
Department of Health and Human Services (US)



FEATURES  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
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512 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTAGAGG 568

RESULT 13  
AR570595 2211 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 2 from patent US 6770479.  
ACCESSION AR570595  
VERSION AR570595.1 GI:56571408  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
1 (bases 1 to 2211)  
AUTHORS Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 2 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOX;

FEATURES  
source  
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/organism="unknown"  
/mol\_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTAGAGG 57  
|||||  
512 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTAGAGG 568

RESULT 14  
BAN413937 2225 bp DNA linear BCT 22-MAY-2002  
LOCUS Bacillus anthracis partial pag gene, isolate IT-Card1-6241.  
DEFINITION  
ACCESSION AY413937.1 GI:16031494  
VERSION AY413937.1  
KEYWORDS pag gene.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE  
1  
AUTHORS Adone,R., Pasquali,P., La Rosa,G., Marianelli,C., Muscillo,M.,  
Pasanella,A., Francia,M. and Cinchini,F.  
TITLE Sequence analysis of the gene encoding for the major virulence  
factors of Bacillus anthracis vaccine strain 'Carbosap  
JOURNAL J. Appl. Microbiol. 92, 1-5 (2002)  
REFERENCE 2 (bases 1 to 2225)  
AUTHORS Muscillo,M.  
TITLE Direct Submission  
JOURNAL Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,  
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199,  
Italy

FEATURES  
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Location/Qualifiers

/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
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KKEVISDNLQLELKOSSNSRKRSTSGAPVPDNDNGIIPDILEVEGYTVVKNK  
RTPLSPWISNIHEKGLTKYKSPKSKSTADPYSDPEKTYGRIDKNVSPARPLVA  
APRVHVDMENTIILSKNDSQNTDSTPTSKNTSSTRTHNSRVAGNAEVHAFPD  
IGGSVAGPENSNSSTVAIDHSLSAGERVMAETMGINTADTARLANAIRVYGTAP  
IYNVPTTSLVLKNOPLATIKAKENQLSGLAPNNYPSKNIAPIALNADQSTTP  
ITANNQFLELETKQLRLDTDVYGNIAIYFNENGRVYDTGSNMBEVLPOIQUETTA  
RIIFNGKDLNLVERRIAAVSPDPLETKPDMTLKEALKIAFGNENGMNQYQKDI  
TEDEPNPDQOSTQNIKNQALVELWNTNYTLDIKIKNAKNMILIRDRFRYDRNIIY  
GADESIVKAEHREIVINSSTREGLINIDKOIRKILISGIVYIEDEGEKVIYNDPYDM  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2225;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTAGAGG 57  
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566 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTAGAGG 622

RESULT 15  
AY700758 2227 bp DNA linear BCT 18-AUG-2004  
LOCUS Bacillus anthracis Sterne plasmid pXO1 protective antigen  
DEFINITION  
ACCESSION AY700758  
VERSION AY700758.1 GI:51235129  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2227)  
AUTHORS Aziz,M.A. and Bhatnagar,R.  
TITLE Mature protective antigen gene with prokaryotic ribosomal binding  
site  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2227)  
AUTHORS Aziz,M.A. and Bhatnagar,R.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUL-2004) Centre for Biotechnology, Jawaharlal Nehru  
University, New Mehrauli Road, New Delhi, Delhi 110067, India

FEATURES  
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CDS

17..2227  
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SSNKRKSTASGPTVPRDNDGIPDSLVEVGTYVDVYKRTPLSPWISNHEKGLT  
KYKSPKEMSTASDPYSDPEKYTGIDKNSPEARHPVAAVPIVHVMENIISKNE  
DOSTQNDQSTRTISKNTSTRTSHSVHNAEVAASFDDIGSVSAFSSNSSTVA  
IDHSLSLAGERMTAETMGLNADTARLANRNVYTGAPYVLPPTSLVLRKQTL  
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LDTOYVGNLNTVNGRVRVDGSMSEVLPOIQTETARIIINGNDLVERRIIA  
VNPSDPLETTPDMTLKALAKIAGFNEPNNLQYQKDIPEPDPFOQTSQNKQ  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2227;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 57  
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Db 528 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 584

RESULT 16  
BAN413936 2231 bp DNA linear BCT 22-MAY-2002  
LOCUS Bacillus anthracis partial pag gene, isolate IT-Carb3-6254.  
DEFINITION AJ413936  
ACCESSION AJ413936.1 GI:16031492  
VERSION AJ413936.1  
KEYWORDS pag gene.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE  
1 Adone, R., Paequali, P., Ia Rosa, G., Marianielli, C., Muscillo, M.,  
Pasanello, A., Francia, M., and Ciuchini, F.  
Sequence analysis of the gene encoding for the major virulence  
factors of bacillus anthracis vaccine strain 'Carbosap  
J. Appl. Microbiol. 92, 1-5 (2002)  
2 (bases 1 to 2231)  
Muscillo, M.  
Direct Submission  
Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,  
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199,  
Italy

FEATURES  
source Location/Qualifiers  
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/db\_xref="GI:16031493"

gene  
CDS

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QNKKEVSISSNQLPELKKRSNSKRKSTASGPTVPRDNDGIPDSLVEVGTYVDV  
NKRFTPLSPWISNHEKGLTKYKSPKEMSTASDPYSDPEKYTGIDKNSPEARHP  
VAAVPIVHVMENIISKNEPSTQNDQSTRTISKNTSTRTSHSVHNAEVAASF  
FDIGSVSAFSSNSSTVAIDHSLSLAGERMTAETMGLNADTARLANRNVYTG  
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INGNDLVERRIIAVNPSDPLETTPDMTLKALAKIAGFNEPNNLQYQKDIPEPDP  
FOQTSQNKQLAELATNTVTVLDKIKLANMNLIRKRHYDNNIAVADSVVEARHE  
VINS TEGLLNTDKDIRKILSGYIVEIEDTEGLKEVINDRYDMNIISSLRQKGF  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2231;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 57  
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Db 573 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 629

RESULT 17  
AR570596 2292 bp DNA linear PAT 14-DEC-2004  
LOCUS AR570596  
DEFINITION Sequence 3 from patent US 6770479.  
ACCESSION AR570596  
VERSION AR570596.1 GI:56571409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 2292)  
Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
Anthrax vaccine  
Patent: US 6770479-A 3 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOX;

FEATURES  
source Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 57  
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Db 593 GTGCTGACCTACCGTTCCAGACCGTGACAATGATGATCCCTGATTCATTAGAG 649

RESULT 18  
AY997299 2295 bp DNA linear BCT 26-APR-2005  
LOCUS AY997299  
DEFINITION Bacillus anthracis strain A18r protective antigen (pag) gene,  
complete cds.  
ACCESSION AY997299  
VERSION AY997299.1 GI:62823103  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2295)  
Xu, J., Dong, D. and Chen, W.



TITLE Protective antigen gene of *Bacillus anthracis* strain A16R  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2295)  
AUTHORS Xu, J., Dong, D., and Chen, W.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-2005) Department of Molecular Biology, Beijing  
Institute of Microbiology and Epidemiology, 20 Dongdajie, Fengtai,  
Beijing 100071, China

FEATURES  
source Location/Qualifiers  
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/strain="A16R"  
/db\_xref="taxon:1392"

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/db\_xref="GI:62823104"

CDS

1 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 57  
596 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 652

## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 57  
DB 596 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 652

RESULT 19  
LOCUS CS135651 2295 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 16 from Patent WO2005068493.  
ACCESSION CS135651  
VERSION CS135651.1 GI:72056315

KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 16 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)

FEATURES  
source Location/Qualifiers  
1..2295  
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/db\_xref="taxon:1392"

## ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 57  
DB 596 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 652

RESULT 20  
LOCUS AR570594 2295 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6770479.  
ACCESSION AR570594  
VERSION AR570594.1 GI:56571407

KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 2295)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 1 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army, Washington, DC;  
WOX;

FEATURES  
source Location/Qualifiers  
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/organism="unknown"  
/mol\_type="genomic DNA"

## ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 57  
DB 596 GTGCTGACCTACGCTTCCAGACCGTGACATGATGAATCCTGATTCTTAGAG 652

RESULT 21  
LOCUS AF306778 2369 bp DNA linear BCT 01-OCT-2003  
DEFINITION Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306778  
VERSION AF306778.1 GI:10880942

KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of *Bacillus*  
JOURNAL anthracis  
Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

FEATURES  
source Location/Qualifiers  
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49..2343  
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FKLYWTDSONKKEVISDNLQLELKOKSSNSRKRSTAGPTVPDRDNGIPDSLE  
EGYTVDKNKRFTLSPWISNIHKKGLTKYKSPKRWSTADPSPDEKVTGRIDKNV  
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NAEVASFPIGGSVSAGFSNSSTVAIDHSLAGERTMAETMGLNTADTARLAN  
IRVNTGTAPITVAVLPPTSLVLGKQTLATIKKENQLSQILAPNNYPSKNIAPIAL  
NAODPSSSTPIITWNYQFLERKQRLDPTDQVGNIAITNENRVRVDTGSNMB  
VLPOIETTARILFNGKDLNVERRIAIVAPSPDLFTTKEDMTLKEALKAFGEFNEP  
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FHYDRNNIIVAGADESVYKAEHREVIINSSTEGLLNTDKOIRKLSGIYVIEBTBGLK  
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ENDSTINGIKKILIPSKGYEIG"

## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTATTAGAG 57  
|||||  
Db 644 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTATTAGAG 700

RESULT 22  
AF306779 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate 28 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306779  
VERSION AF306779.1 GI:10880944  
KEYWORDS  
SOURCE .  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
2 (bases 1 to 2369)  
REFERENCE Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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SPARHPVLAAPYIVHVDMENTILSKNEDOSTONTOSQRTTISKNTSTSTHTSEVHG  
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ENDSTINGIKKILIPSKGYEIG"

## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTATTAGAG 57  
|||||  
Db 644 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTATTAGAG 700

SPARHPVLAAPYIVHVDMENTILSKNEDOSTONTOSQRTTISKNTSTSTHTSEVHG  
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EVINDRDMINISLSLQDGKTFIDFKTKYNDKPLPLYISNPYKVNVAIVKENTINPS  
ENDSTINGIKKILIPSKGYEIG"

RESULT 23  
AF306780 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate BAI035 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306780  
VERSION AF306780.1 GI:10880946  
KEYWORDS  
SOURCE .  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
2 (bases 1 to 2369)  
REFERENCE Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
AUTHORS  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
source  
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49..2343  
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EGYTVDKNKRFTLSPWISNIHKKGLTKYKSPKRWSTADPSPDEKVTGRIDKNV  
SPARHPVLAAPYIVHVDMENTILSKNEDOSTONTOSQRTTISKNTSTSTHTSEVHG  
NAEVASFPIGGSVSAGFSNSSTVAIDHSLAGERTMAETMGLNTADTARLAN  
IRVNTGTAPITVAVLPPTSLVLGKQTLATIKKENQLSQILAPNNYPSKNIAPIAL  
NAODPSSSTPIITWNYQFLERKQRLDPTDQVGNIAITNENRVRVDTGSNMB  
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FHYDRNNIIVAGADESVYKAEHREVIINSSTEGLLNTDKOIRKLSGIYVIEBTBGLK  
EVINDRDMINISLSLQDGKTFIDFKTKYNDKPLPLYISNPYKVNVAIVKENTINPS  
ENDSTINGIKKILIPSKGYEIG"

gene  
CDS



## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 57  
|||||  
Db 644 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 700

## RESULT 24

AF306781 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS  
DEFINITION Bacillus anthracis isolate 33 protective antigen (pag) gene,  
complete cds.

ACCESSION AF306781  
VERSION AF306781.1 GI:10880948

## KEYWORDS

## SOURCE

## ORGANISM

Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)

## PUBMED

2 (bases 1 to 2369)  
PRICE, L.B., HUGH-JONES, M., JACKSON, P.J. AND KEIM, P.

## AUTHORS

## TITLE

## JOURNAL

Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

Location/Qualifiers

## FEATURES

## source

1..2369  
/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
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/plasmid="pX01"  
1..2369  
/gene="pag"  
49..2343  
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/transl\_table=1  
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/db\_xref="GI:10880948"

## gene

## CDS

## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 57  
|||||  
Db 644 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 700

## RESULT 25

AF306782

LOCUS

DEFINITION

complete cds.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Bacillus anthracis

Bacillus anthracis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus

cereus group.

REFERENCE 1 (bases 1 to 2369)

PRICE, L.B., HUGH-JONES, M., JACKSON, P.J. AND KEIM, P.

Genetic diversity in the protective antigen gene of Bacillus anthracis

J. Bacteriol. 181 (8), 2358-2362 (1999)

10197996

2 (bases 1 to 2369)

PRICE, L.B., HUGH-JONES, M., JACKSON, P.J. AND KEIM, P.

Direct Submission

Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

Location/Qualifiers

1..2369

/organism="Bacillus anthracis"

/mol\_type="genomic DNA"

/db\_xref="taxon:1392"

/plasmid="pX01"

1..2369

/gene="pag"

49..2343

/gene="pag"

/codon\_start=1

/transl\_table=1

/product="protective antigen"

/protein\_id="AAG24450.1"

/db\_xref="GI:10880951"

/translation="MKRRKVLIPMLSTILVSTGNLEVIQAEVKQENRLNLSSESS

SGGLGYYFSDLNFOAPMVVTSSTGDLSPSELENI PSENOYFQSAIWGPIKVK

SDRYTPTSADNHNTVMVDQEVINKNSNKKRLKGRLOYIKIORYENPTKGLD

PKLYWDSQNKKEVISDNIQLPELKOKSSNRKSTSGAPTYPDNDNGIPSLAV

EGTYVDYKNTKRTPLSPWISNHEKKGITKYSPEKSTASDPYDEPKYGRIDKAV

SPKARHPVLAAYPIVHVDMENIILSKNEDSTQNTDSQRTISKNTSRTHTSEVHG

NAEVHASFPDVGVSAGFNSNSSTVAIHSLSLAERTMAETMGANTADTALNN

IRYVNTGAPLYNVLPPTSLVLGKQTLATIKAKENOLSOILAENNYPSKNLAPIL

NAODDSSPTITMNVNOFLEKTKOLRLTDQVYGNIAATYFNENGRVAVDTGSNMS

VLPOIOTTRARIIFNGDLNVERRIAANVPSDPLRTTKPDMTLKALIAFGNEEN

GNLOYQCKDITFDFNPDQTSQNIKNQALBLVNTNITYVLDDIKLAKAKNMLIRDR

PHYDRNNIAGADESVVKEAREVINSSTEGLLNLDKDIRKILSGYIVIEIDTEGKL

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## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 57  
|||||  
Db 644 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCGATTCTATTAGAGG 700

## RESULT 26

AF306783

LOCUS

DEFINITION

complete cds.

ACCESSION

VERSION

KEYWORDS

Bacillus anthracis

Bacillus anthracis

Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus



SOURCE  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus

REFERENCE  
AUTHORS 1 (bases 1 to 2369)  
TITLE Price, J.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
JOURNAL Genetic diversity in the protective antigen gene of Bacillus anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996

REFERENCE  
AUTHORS 2 (bases 1 to 2369)  
TITLE Price, J.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
JOURNAL Direct Submission  
Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

FEATURES  
Source Location/Qualifiers  
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49..2343  
/gene="pag"  
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/transl\_table=1  
/product="protective antigen"  
/protein\_id="AAG24451.1"  
/db\_xref="GI:10880953"  
/translation="MKRRKVLIPMLASTLIVSSTGNLEVIQAEVKQENRLNSESBS  
SQGLGYFDFDLNFOAPMVVTSSTGDLSPSELENIPENOYFOGAIWGFYKVK  
SDETFATSDNHTVMVDQEVINKSNKRIEKGRLYOIKIYORENPTKGLD  
PKLYWDSQNKKEVYISDNLOLPELKQSSNSRKRSTASDPYDPDNDGIPSLRY  
EGYVDVKNKRTFISPMISNHEKGLTKYKSSPEKSTASDPYDPDNDGIPSLRY  
SPEARHPVAAPYPIVHVDMENTILSKNEDSTONTDSQRTISNRTSRTSEVNG  
NAEYHAFPIFGSVSAGFSNSNSTVAIDHSLSIAGERTWAETMGINTADTALNAN  
IRVYNTGAPILYVNLPTTSLVLAGNQTATIKAKENQLSQILAPNNYPSKNLPIAL  
NAODFSTPTIMVNOFLIEKTKQRLDIDVOYGNATYVFNENGRVRYDGSNME  
VLPOIGETTAIIINGKDLNVERRIAIVNSDPELTTPMTLKEALKIAPGNESN  
GNLQYQGDITTEFPNFDQSTONIKQDLAEIANTNITYVLDKIKNAKNMILRDKR  
FHYDRNNIAGVADSVVKEAREVINSTBGLNIDIDIRKILISGYIVEIDTEGLK  
EVIDRDMINISLSRODKTFIDFKKYNKDLPLYISNPNYKVVVAVTKENTLINS  
ENGDTSTNGIKILIFSKKGYEIG"

ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  
1 GTGCTGGACCTACGGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
|||||  
DB 644 GTGCTGGACCTACGGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 700

RESULT 27  
AF268967 2549 bp DNA linear BCT 31-JUL-2000  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
DEFINITION Complete cds.  
ACCESSION AF268967  
VERSION AF268967.1 GI:9280532  
KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus

REFERENCE  
AUTHORS 1 (bases 1 to 2549)  
TITLE Cohen, S., Mendelson, I., Altboum, Z., Kobiler, D., Elhanany, E.,  
Bino, T., Leitner, M., Inbar, I., Rosenberg, H., Gezev, Y., Barak, R.,  
Fisher, M., Kromann, C., Velan, B. and Shafferman, A.  
JOURNAL Attenuated nontoxicogenic and nonencapsulated recombinant Bacillus

JOURNAL anthracis spore vaccines protect against anthrax  
INfect. Immun. 68 (8), 4549-4558 (2000)  
PUBMED 10899854

REFERENCE  
AUTHORS 2 (bases 1 to 2549)  
TITLE Cohen, S., Mendelson, I. and Shafferman, A.  
JOURNAL Direct Submission  
Submitted (18-MAY-2000) Department of Biochemistry, Israel  
Institute for Biological Research, P.O. Box 19, Ness Ziona 74100,  
Israel

FEATURES  
Source Location/Qualifiers  
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/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:1392"  
/plasmid="pX01"  
152..2446  
/gene="pagA"  
152..2446  
/gene="pagA"  
/note="Common internalizing receptor binding protein of  
the two binary exotoxins; similar to protective antigen  
precursor product encoded by Genbank Accession Number  
M2589"

ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2549;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY  
1 GTGCTGGACCTACGGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
|||||  
DB 747 GTGCTGGACCTACGGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 803

RESULT 28  
AX933603 2605 bp DNA linear PAT 22-DEC-2003  
LOCUS Sequence 3 from Patent WO03087378.  
DEFINITION AX933603  
ACCESSION AX933603  
VERSION AX933603.1 GI:40312826  
KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus

REFERENCE  
AUTHORS 1  
TITLE Schmaljohn, C.U. and Fuller, J.  
JOURNAL Nucleic acid immunization  
Patent: WO 03087378-A 3 23-OCT-2003;  
PowderJect Research Limited (GB)  
FEATURES  
Source Location/Qualifiers  
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/db\_xref="GI:40312827"  
/translation="MKRRKVLIPMALSTLVSSGTNLEVIQAEVQENLLNESSSS  
SGLIGYFSDINFOAPMVVTSITGDISIPSSLENIPENOYFQSAISGFIKYK  
SDEYFATISADNHTVMVDQEVINRKSNSNKIRLEKRLYOIKI OYRENPEKGLD  
FKLYMTDSOKKKEVISSDNLQPELKOKSNSRKSSTAGPTVPDNDNDIPDSLEV  
EGYTVQKMRTPISPWISHERKGLTRYKSPKRSSTASDPSPDEKRTGBIDKRV  
SPRRHPVAAIPIVHVDMENTILSKKEDSTONTSETRTTISKSTSKRTSHVHG  
NAEVHASFPIGVSAGFSNSNSTVALIDHSLSLAGERTWAEITGLNTADYARLAN  
IRVYNGTAPIYAVLPTTSLVLGNQTLATIKAKENLSQILA PNNVYPSKNIAPAL  
NAODDSSTPIYVNVQFLEKTKQLRDTDOYGNIAFYENSVRVDTSNMS  
VLPOIDETTARIIFNGKDLVVERIAAVVPSDPLETTKPDMLKEALKIAPGNEPN  
GNLOYGKOTIETPDNPDOOTSONIKQALNAATNTVYVLDIKIKANAKNIIIPDKR  
PHYDRNNIAGADESVYKAEHREYINSSTGGLINTDKDRIKILSGIYIEETBGLK  
EVINDRYDMNIISSLRQDKFTIDFKKYNDKLPLYISNPNYKVNVAIVKENTINPS  
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1241..1246  
/note="EcoRI restriction site"

ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 57  
|||||  
Db 769 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 825  
|||||

RESULT 29

LOCUS 133400 2709 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 11 from patent US 5591631.  
ACCESSION 133400  
VERSION 133400.1 GI:1824191  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2709)  
AUTHORS Leppla,S.H., Kimpel,K.R., Arora,N., Singh,Y. and Nicholas,P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 11 07-JAN-1997;  
FEATURES  
location/Qualifiers  
1..2709  
/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 57  
|||||  
Db 509 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 565  
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RESULT 30

LOCUS 169378 2709 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 11 from patent US 5677274.  
ACCESSION 169378  
VERSION 169378.1 GI:2831500  
KEYWORDS

SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2709)  
AUTHORS Leppla,S.H., Kimpel,K.R., Arora,N., Singh,Y. and Nicholas,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 11 14-OCT-1997;  
FEATURES  
location/Qualifiers  
1..2709  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 57  
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Db 509 GTGCTGACCTACCGTTCAGACCGGTGACATGATGGAATCCCTGATTCATTAGAG 565  
|||||

RESULT 31

LOCUS BACPAG 4235 bp DNA linear BCT 02-AUG-1999  
DEFINITION Bacillus anthracis cryptic protein and protective antigen precursor  
(paga) genes, complete cds.  
ACCESSION M22589  
VERSION M22589.1 GI:143280  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
REFERENCE 1 (bases 1 to 4235)  
AUTHORS Welkos,S.L., Lowe,J.R., Eden-McCutchan,F., Vodkin,M., Leppla,S.H.  
and Schmidt,J.J.  
TITLE Sequence and analysis of the DNA encoding protective antigen of  
Bacillus anthracis  
JOURNAL Gene 69 (2), 287-300 (1988)  
PUBMED 3148491  
REFERENCE 2 (bases 1 to 4235)  
AUTHORS Welkos,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-1989) Bacteriology, USAMRIID, Ft. Detrick,  
Frederick, MD 21702, USA  
FEATURES  
source  
1..4235  
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/clone="pPA26"  
416..994  
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/transl\_table=11  
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DEVDNALSGMYQIKKPSNHLTNSPTTITLAKGDSGVEIYVLSDGAFLEPNED  
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NIFVWPIIYLLFYIISIVFANHVIVLSM"

gene

1804..4098  
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1804..4098  
/note="protective antigen precursor"  
/codon\_start=1  
/transl\_table=11  
/protein\_id="AA22637.1"  
/db\_xref="GI:143282"

CDS



/translation="MKRRKVLPIPLMALSTIVSSTGNLEVIQAEVKQENRLNSESSE  
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SDEYTPATSDNHTMMVDDQEVINKASNSKILKRGRLVYOIKIYORENPTEKGLD  
FKLYWDSQNKKEVYISSDNQLPELKOKSSNRKRSTASAGPTYPDDNDNGIPLSLEY  
EGYTVDPKAKRTPLSPWISNHEKKGKTKIKSSPEKKSSTADPSIDPEKVTGRIDKRV  
SPEARHPLVAAPYPIVHVDMENTILSKNEDOSTQMTDETRTISNKTSTSRHTSEVIG  
NAEVHASFDPDGSSVAGFSNSNSVTVAIDHSLIABERTWAEFTMGANTADTALNAN  
IRVNTGTAPYVNLPTTSLVLAGKQTLATIKAKENOLSIAPENNYRPSKNIAPLAL  
NAODFSTPTIMVNOFLIEKTKOIRLDQOYGNLQATYFENGSGNVRDVTGSNMBE  
VLPOIESTTARIIFNGKDLNVERBIAVNSRDELETTKPDMTKEALKIARFGBNBN  
GNLOYOKDITFEPDNPDOQTSQNIKQALBNANTNTYTLVDKIKLAKNKTILIDRK  
FHYDRNINAVGADSVVEKAREVINSSTBELNLINDKIRKILSGYIVETIDEGK  
EVIDRYDMNISLRQDKTFIDFKKYNDELPLYISNPYKVVVAVTKENTININS  
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1804. .1890  
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1891. .4095  
mac\_peptide  
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/product="protective antigen"

ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 57  
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Db 2399 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 2455

RESULT 32

LOCUS 133396 4235 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5591631.  
ACCESSION 133396 GI:1824187  
VERSION 133396.1  
KEYWORDS  
ORGANISM Unknown.  
SOURCE Unknown.  
REFERENCE 1 (bases 1 to 4235)  
AUTHORS Leppia,S.H., Kimpel,K.R., Aroora,N., Singh,Y. and Nicholls,P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNML Patent: US 5591631-A 3 07-JAN-1997;  
FEATURES Location/Qualifiers  
source 1. .4235  
/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 57  
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Db 2399 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 2455

RESULT 33

LOCUS 169374 4235 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 3 from patent US 5677274.  
ACCESSION 169374  
VERSION 169374.1 GI:2831496  
KEYWORDS  
ORGANISM Unknown.  
SOURCE Unknown.  
REFERENCE 1 (bases 1 to 4235)  
AUTHORS Leppia,S.H., Kimpel,K.R., Aroora,N., Singh,Y. and Nicholls,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNML Patent: US 5677274-A 3 14-OCT-1997;

FEATURES

Location/Qualifiers  
1. .4235  
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/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 7.3e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 57  
|||||  
Db 2399 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCAATGAGG 2455

RESULT 34

LOCUS AF065404/c 181654 bp DNA circular BCT 01-OCT-2003  
DEFINITION Bacillus anthracis virulence plasmid pX01, complete sequence.  
ACCESSION AF065404  
VERSION AF065404.1 GI:4894216  
KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A.R., Hill,K.K., Kelm,P., Koehler,T.M., Lamke,G., Kumano,S., Mahillon,J., Menter,D., Martinez,Y., Rieke,D., Svensson,R. and Jackson,P.  
TITLE Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes  
JOURNML J. Bacteriol. 181 (20), 6509-6515 (1999)  
10515943  
2 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A., Hill,K., Kelm,P., Koehler,T., Kumano,S., Lamke,G., Menter,D., Martinez,Y., Rieke,D.O., Svensson,R. and Jackson,P.  
TITLE Direct Submission  
JOURNML Submitted (14-MAY-1998) Life Sciences Division, Los Alamos National Laboratory, T443, LS-6, HRL-1, MS N688, Los Alamos, NM 87545, USA  
FEATURES Location/Qualifiers  
source 1. .181654  
/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
/strain="Sterne"  
/db\_xref="taxon:1392"  
/plasmid="virulence plasmid pX01"  
/note="Hypothetical protein, Methanobacterium thermoautotrophicum, (AE000831)"  
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/protein\_id="AA032305.1"  
/db\_xref="GI:4894217"  
/translation="MEVILFELILIAVLIPUNSVKKHVPKMGKAGKSLVKRMLSKL  
DKSYVLAHNTVYTEYGDPTQIDHIVIAATGAVTVTKNREGIYISSEKAARPTQGI  
FRKSSFQNPFPQHYKHAIEWLIHQQLPCISMAAPHSCLARVAVHSKERHVKYL  
HNKFAKO"  
complement (1639. .1644)  
2751. .2755  
2760. .3338  
/codon\_start=1  
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/product="pX01-02"  
/protein\_id="AA032306.1"  
/db\_xref="GI:4894218"  
/translation="MLEHTILFSLIVOLVPLIVSGIYILBLTDEMTKMFVSYGIF  
AIEFLIRPOVFNQKSIISINQHEKFSCLNTFVLSFIVLPASIPTLKIAIQLGM  
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YFIVTAVYLSGIIISPISSEVFESEYERNNLNMR"  
complement (3389. .4024)

REFERENCE

1 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A.R., Hill,K.K., Kelm,P., Koehler,T.M., Lamke,G., Kumano,S., Mahillon,J., Menter,D., Martinez,Y., Rieke,D., Svensson,R. and Jackson,P.  
TITLE Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes  
JOURNML J. Bacteriol. 181 (20), 6509-6515 (1999)  
10515943

TITLE

JOURNML 2 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A., Hill,K., Kelm,P., Koehler,T., Kumano,S., Lamke,G., Menter,D., Martinez,Y., Rieke,D.O., Svensson,R. and Jackson,P.  
TITLE Direct Submission  
JOURNML Submitted (14-MAY-1998) Life Sciences Division, Los Alamos National Laboratory, T443, LS-6, HRL-1, MS N688, Los Alamos, NM 87545, USA  
FEATURES Location/Qualifiers  
source 1. .181654  
/organism="Bacillus anthracis"  
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RBS  
CDS

CDS



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100.0%; Score 57; DB 1; Length 181654;



Best Local Similarity 100.0%; Pred. No. 7, 2e-25;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 35  
AE011190 181677 bp DNA circular BCT 14-JUN-2002

LOCUS AE011190  
DEFINITION Bacillus anthracis str. A2012 plasmid pXOI, complete sequence.

ACCESSION AE011190  
VERSION AE011190.1 GI:20520075

KEYWORDS  
SOURCE Bacillus anthracis str. A2012  
ORGANISM Bacillus anthracis str. A2012  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 181677)

AUTHORS Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L.,

Holtzapple, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D.,

Keim, P. and Fraser, C.M.  
Comparative genome sequencing for discovery of novel polymorphisms

in Bacillus anthracis

Science 296 (5575), 2028-2033 (2002)

JOURNAL 2 (bases 1 to 181677)

PUBMED Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L.,

Holtzapple, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D.,

Keim, P. and Fraser, C.M.  
Direct Submission

TITLE Submitted (09-MAY-2002) The Institute for Genomic Research, 9712

Medical Center Dr, Rockville, MD 20850, USA

FEATURES  
Location/Qualifiers

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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 144374 GTGCTGACCTACCGTTCCAGACCGTGACAAATGATGAATCCTGATTCATTAGAGG 144430

RESULT 36  
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VERSION  
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QY 1 GTGCTGGACCTACGGTTCCAGACCGTGACGATGAGTAATCCCGATTCAATTAGAGG 57  
DB 144374 GTGCTGGACCTACGGTTCCAGACCGTGACGATGAGTAATCCCGATTCAATTAGAGG 144430  
RESULT 37  
169387 169387 2160 bp DNA linear PAT 04-FEB-1998  
LOCUS Sequence 30 from patent US 5677274.  
DEFINITION 169387  
ACCESSION 169387  
VERSION 169387.1 GI:2831509



KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2160)  
AUTHORS Leppla,S.H., Klimpel,K.R., Arora,N., Singh,Y. and Nichols,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5672724-A 30-14-OCT-1997;  
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Best Local Similarity 100.0%; Pred. No. 1.1e-21;  
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Db 526 GGACCTACGGTTCACGACCGTGACATGATGGAATCCCTGATTCATTAGAG 577  
RESULT 38  
AY921578 1694 bp DNA linear BCT 16-APR-2005  
LOCUS Bacillus anthracis isolate 34F2 plasmid pXOI protective antigen  
DEFINITION (pa) gene, partial cds.  
ACCESSION AY921578  
VERSION AY921578.1 GI:62467684  
KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 1694)  
AUTHORS Vahedi,F., Moazeni Julia,G. and Mahmoudi,M.  
TITLE Humoral immunity in mice induced by vaccination with a plasmid  
encoding anthrax protective antigen  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1694)  
AUTHORS Vahedi,F., Moazeni Julia,G. and Mahmoudi,M.  
TITLE Direct Submission  
JOURNAL Submitted (06-FEB-2005) Immunology Research Center, Buall Research  
Institute, Mashhad University of Medical Sciences, Buall Sq.,  
Mashhad, Iran  
FEATURES  
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Db 1 GGTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 44  
RESULT 39  
AX111916 46 bp DNA linear PAT 30-APR-2001  
LOCUS Sequence 16 from Patent WO0121656.  
DEFINITION AX111916  
ACCESSION AX111916  
VERSION AX111916.1 GI:13928020  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Leppla,S.H., Liu,S.H., Netzel-Arnett,S., Hansen-Birkedal,H. and  
Bugge,T.  
TITLE Mutated anthrax toxin protective antigen proteins that specifically  
target cells containing high amounts of cell-surface  
metalloproteinases or plasminogen activator receptors  
JOURNAL Patent: WO 0121656-A 16-29-MAR-2001;  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
FEATURES  
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Db 26 GTGCTGACCTACGCTTCAG 46  
RESULT 40  
AX111918 46 bp DNA linear PAT 30-APR-2001  
LOCUS Sequence 18 from Patent WO0121656.  
DEFINITION AX111918  
ACCESSION AX111918  
VERSION AX111918.1 GI:13928021  
KEYWORDS  
SOURCE  
ORGANISM synthetic construct  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Leppla,S.H., Liu,S.H., Netzel-Arnett,S., Hansen-Birkedal,H. and  
Bugge,T.  
TITLE Mutated anthrax toxin protective antigen proteins that specifically  
target cells containing high amounts of cell-surface  
metalloproteinases or plasminogen activator receptors  
JOURNAL Patent: WO 0121656-A 16-29-MAR-2001;  
THE SECRETARY OF THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)  
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Search completed: April 11, 2006, 18:05:53  
Job time : 417.151 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using bw model

Run on: April 11, 2006, 14:24:17 ; Search time 79.4164 Seconds  
(Without alignments)  
4783.489 Million cell updates/sec

Title: US-10-712-654-21

Perfect score: 57

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Gapop 60.0 , Gapext 60.0

Searched: 4996997 segs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seg length: 0

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Post-Processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	57	13	ADR48523
2	57	100.0	774	6	ADD29116
3	57	100.0	954	6	ADD29118
4	57	100.0	1108	13	ADR48535
5	57	100.0	1278	6	ADD29119
6	57	100.0	1281	14	ABE63722
7	57	100.0	1461	6	ADD29117
8	57	100.0	1704	14	ADZ51325
9	57	100.0	1707	14	ABE63720
10	57	100.0	1710	3	AAZ56877
11	57	100.0	1722	12	ADL16356
12	57	100.0	1785	6	ADD29120
13	57	100.0	2205	14	ADZ51331
14	57	100.0	2208	6	ADD29121
15	57	100.0	2208	6	AAI99904
16	57	100.0	2208	12	ADL16343
17	57	100.0	2208	12	ADL16346
18	57	100.0	2208	14	ADW05484
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21	57	100.0	2211	14	ADY84835	ADY84835 Bacillus
22	57	100.0	2220	13	ADY96726	ADY96726 Gene of c
23	57	100.0	2292	3	AAZ56876	AAZ56876 B. anthra
24	57	100.0	2295	3	AAZ56874	AAZ56874 B. anthra
25	57	100.0	2295	4	AAZ56874	AAZ56874 B. anthra
26	57	100.0	2295	14	ACB6016	ACB6016 Wild type
27	57	100.0	2295	14	ABE63728	ABE63728 DNA encod
28	57	100.0	2295	14	ABE63728	ABE63728 DNA encod
29	57	100.0	2605	10	ABE63728	ABE63728 Bacillus
30	57	100.0	2605	14	ABE63728	ABE63728 Bacillus
31	57	100.0	2709	2	AAQ70184	AAQ70184 PA(1-725)
32	57	100.0	4235	2	AAQ70180	AAQ70180 Sequence
33	57	100.0	4235	10	ACF58207	ACF58207 B. anthrac
34	57	100.0	4235	12	ADL72868	ADL72868 Anthrax v
35	57	100.0	8198	12	ADL16342	ADL16342 pBP103 ex
36	57	100.0	9286	12	ADL16345	ADL16345 pBP103 ex
37	52	91.2	2160	2	AAQ70189	AAQ70189 Sequence
38	52	91.2	2235	13	ADR40459	ADR40459 Bacillus
39	52	91.2	2235	10	ADP44806	ADP44806 Internal
40	43	75.4	240	10	ADP44812	ADP44812 Internal
41	43	75.4	348	10	ADP44815	ADP44815 Internal
42	43	75.4	415	10	ADP44822	ADP44822 Internal
43	43	75.4	427	10	ADP44828	ADP44828 Internal
44	43	75.4	521	10	ADP44816	ADP44816 Internal
45	38	66.7	153	10	ADP44794	ADP44794 Bacillus
46	32	56.1	32	13	ADR48504	ADR48504 paga prob
47	25	43.9	25	13	ADR48503	ADR48503 paga prob
48	23	40.4	30	14	ADX97631	ADX97631 Adenovira
49	22	38.6	262	10	ADP44832	ADP44832 Internal
50	22	38.6	272	10	ADP44838	ADP44838 Internal
51	22	38.6	548	10	ADP44842	ADP44842 Internal
52	22	38.6	21	10	ADP44799	ADP44799 Internal
53	21	36.8	21	10	ADP44844	ADP44844 Internal
54	21	36.8	46	5	AAFS7419	AAFS7419 Protective
55	21	36.8	46	5	AAFS7420	AAFS7420 Protective
56	21	36.8	46	5	AAFS7421	AAFS7421 Protective
57	21	36.8	46	10	ACC58222	ACC58222 Primer H3
58	21	36.8	46	10	ACC58223	ACC58223 Primer H4
59	21	36.8	52	5	AAFS7415	AAFS7415 NMP subet
60	21	36.8	52	5	AAFS7413	AAFS7413 NMP subet
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62	21	36.8	52	10	ACC58217	ACC58217 Primer H1
63	21	36.8	52	10	ACC58219	ACC58219 Primer H2
64	21	36.8	52	10	ACC58220	ACC58220 Primer H1
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66	21	36.8	1782	12	ADL72870	ADL72870 Anthrax v
67	21	36.8	1782	12	ADL72866	ADL72866 Anthrax v
68	21	36.8	1788	12	ADL72882	ADL72882 Anthrax v
69	21	36.8	2277	12	ADL72872	ADL72872 Anthrax v
70	21	36.8	2295	12	ADL72888	ADL72888 Anthrax v
71	19	33.3	19	13	ADSV75424	ADSV75424 Anthrax P
72	18	31.6	2161	3	AAAS1304	AAAS1304 A. terreu
73	18	31.6	31328	3	AAAS1295	AAAS1295 A. terreu
74	18	31.6	70215	11	ACN43992	ACN43992 Mouse gen
75	17	29.8	45	10	ADP44830	ADP44830 Internal
76	17	29.8	25	13	ADSV96724	ADSV96724 PCR prime
77	17	29.8	2202	14	ADY84836	ADY84836 Bacillus
78	17	29.8	2292	12	ADL72889	ADL72889 Anthrax v
79	17	29.8	110000	2	AAZ20248	AAZ20248 07
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82	16	28.1	481	6	ABN26538	ABN26538 Human ORF
83	16	28.1	648	11	ADM39970	ADM39970 E. coli OP
84	16	28.1	907	13	ADM53701	ADM53701 Plant ful
85	16	28.1	922	13	ADX36914	ADX36914 Plant ful
86	16	28.1	1321	8	ACA25311	ACA25311 Prokaryot
87	16	28.1	1571	14	AAZ33584	AAZ33584 Thale cre
88	16	28.1	1781	13	ADT17349	ADT17349 Plant CDN
89	16	28.1	2000	12	ADU41575	ADU41575 Plant CDN
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91	16	28.1	2463	6	ABSV70005	ABSV70005 ApepGill
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C 93	16	28.1	2532	6	ABST70003	Abst70003 DNA seque	166	15	26.3	3362	4	ABL21914	AbI21914 Drosophila
C 94	16	28.1	61396	13	ABD33379	Abd33379 Murine ca	C 167	15	26.3	3764	12	ADO64459	AdO64459 Novel hum
C 95	16	28.1	118777	12	ADP44620	Adp44620 Murine al	C 168	15	26.3	4333	13	ACN41023	AcN41023 Tumour-as
C 96	15	26.3	28	10	ADF44885	Adf44885 Internal	C 169	15	26.3	5019	13	ADP05468	AdP05468 Haemophil
C 97	15	26.3	48	10	ADF44800	Adf44800 Internal	C 170	15	26.3	5076	13	ADP47805	AdP47805 Bacterioid
C 98	15	26.3	26	10	ACC58221	Acc58221 Primer H2	C 171	15	26.3	5169	6	ABO75483	AbO75483 Plasmid p
C 99	15	26.3	111	10	ACC85218	Acc85218 Anthrax t	C 172	15	26.3	5169	6	ABO75480	AbO75480 FHV-Brecl
C 100	15	26.3	278	8	ABZ19425	Abz19425 Group IIT	C 173	15	26.3	6204	6	ABD33371	AbD33371 Staphyloc
C 101	15	26.3	313	6	ABN25487	Abn25487 Human ORF	C 174	15	26.3	6420	4	ABL08883	AbI08883 Drosophila
C 102	15	26.3	344	3	AAC00504	Aac00504 Human sec	C 175	15	26.3	7595	13	ADR84439	AdR84439 Aspergill
C 103	15	26.3	391	5	AAS66455	Aas66455 DNA encod	C 176	15	26.3	9235	13	ADR84305	AdR84305 Aspergill
C 104	15	26.3	406	14	ACL55836	ACL55836 Human col	C 177	15	26.3	11439	4	ABL14258	AbI14258 Drosophila
C 105	15	26.3	414	9	ACH30334	Ach30334 Human tes	C 178	15	26.3	11580	4	ABL08832	AbI08832 Drosophila
C 106	15	26.3	478	6	ABN75638	Abn75638 Human ATP	C 179	15	26.3	32165	3	AAA09092	AAA09092 AdMTV-D8
C 107	15	26.3	484	6	ABO56585	Abv56585 Human COL	C 180	15	26.3	32165	3	AAA14723	AAA14723 Nucleotid
C 108	15	26.3	557	6	ABV97230	Abv97230 Human pol	C 181	15	26.3	32166	3	AAA09090	AAA09090 AdPSA-bet
C 109	15	26.3	609	4	AAK74747	AAk74747 Human pan	C 182	15	26.3	32166	4	AAK89170	AAK89170 AdRSPHD
C 110	15	26.3	633	3	AAF07743	AAf07743 Fusarium	C 183	15	26.3	32167	14	ADM11287	AdM11287 Adenovira
C 111	15	26.3	633	13	ADU51784	AdU51784 Fusarium	C 184	15	26.3	32167	3	AAA14803	AAA14803 Nucleotid
C 112	15	26.3	633	14	ADZ89787	AdZ89787 Fusarium	C 185	15	26.3	32167	3	AAA09086	AAA09086 AdRSV-bet
C 113	15	26.3	636	4	AAK74749	AAk74749 Human imm	C 186	15	26.3	32886	3	AAO9086	AAO9086 Adenoviru
C 114	15	26.3	808	4	AAH03988	AAh03988 Human CDN	C 187	15	26.3	33592	4	AAK85020	AAK85020 Adenoviru
C 115	15	26.3	863	4	AAH04818	AAh04818 Human CDN	C 188	15	26.3	33639	4	AAK85020	AAK85020 Adenoviru
C 116	15	26.3	954	13	ADO84670	AdO84670 Plant full	C 189	15	26.3	33988	4	AAK85023	AAK85023 Adenoviru
C 117	15	26.3	984	4	ABL29625	AbI29625 Drosophila	C 190	15	26.3	34302	3	AAZ94163	AAZ94163 Adenoviru
C 118	15	26.3	1011	11	ABD16178	ABd16178 Pseudomon	C 191	15	26.3	34341	4	AAK85021	AAK85021 Adenoviru
C 119	15	26.3	1065	10	ACC60888	Acc60888 Gene seque	C 192	15	26.3	34448	4	AAK85021	AAK85021 Adenoviru
C 120	15	26.3	1065	10	ADK62293	ADk62293 Disease t	C 193	15	26.3	34737	4	AAK85024	AAK85024 Adenoviru
C 121	15	26.3	1107	10	ADK62439	ADk62439 Disease t	C 194	15	26.3	35408	2	AAK59272	AAK59272 Recombina
C 122	15	26.3	1146	8	ACA34031	AAc53236 Haemophil	C 195	15	26.3	35620	14	ADP80723	AdP80723 DNA seque
C 123	15	26.3	1146	8	ACA34031	AAc53236 Haemophil	C 196	15	26.3	35700	14	ADP93032	AdP93032 Human ade
C 124	15	26.3	1170	8	ACA44809	AAc44809 Prokaryot	C 197	15	26.3	35712	14	ADZ45246	AdZ45246 Human ade
C 125	15	26.3	1200	10	ADP03286	AdP03286 Bacterioid	C 198	15	26.3	35724	4	AAK85022	AAK85022 Adenoviru
C 126	15	26.3	1290	11	ACH99120	ACH99120 Klebsiell	C 199	15	26.3	35871	6	AAD27972	AAZ27972 Recombina
C 127	15	26.3	1296	9	ADA28823	AdA28823 DNA encod	C 200	15	26.3	35882	14	ADZ47950	AdZ47950 delcra923-
C 128	15	26.3	1314	10	ADP88558	AdP88558 Ribosome	C 201	15	26.3	35887	14	ADP77562	AdP77562 Artificia
C 129	15	26.3	1315	4	AAI86569	AAI86569 Human pol	C 202	15	26.3	35909	14	ADZ45247	AdZ45247 Human ade
C 130	15	26.3	1329	8	ACA27730	ACA27730 Prokaryot	C 203	15	26.3	35934	2	AAV07258	AAV07258 Adenoviru
C 131	15	26.3	1416	3	AACT6158	AAc76158 Human ORF	C 204	15	26.3	35935	8	AAK85026	AAK85026 Complete
C 132	15	26.3	1500	8	ACA21004	AAc21004 Prokaryot	C 205	15	26.3	35935	4	ABK659882	ABK659882 Human ade
C 133	15	26.3	1519	6	ABL68531	ABl68531 Kidney ca	C 206	15	26.3	35935	6	ABK659883	ABK659883 Human ade
C 134	15	26.3	1519	14	ADM14645	Adm14645 Human alc	C 207	15	26.3	35935	6	ABK659883	ABK659883 Human ade
C 135	15	26.3	1542	13	ADR85613	AdR85613 Aspergill	C 208	15	26.3	35935	8	ACA61117	ACA61117 Adenoviru
C 136	15	26.3	1595	13	ADR85026	AdR85026 Aspergill	C 209	15	26.3	35935	8	ACA61117	ACA61117 Adenoviru
C 137	15	26.3	1613	14	ADM14637	Adm14637 Human ADH	C 210	15	26.3	35935	10	ACA60761	ACA60761 Human ade
C 138	15	26.3	1813	5	ADM19235	Adm19235 Novel hum	C 211	15	26.3	35935	13	ADR41672	AdR41672 Wild type
C 139	15	26.3	1971	13	ADX28533	Adx28533 Plant full	C 212	15	26.3	35978	6	AAZ27971	AAZ27971 Recombina
C 140	15	26.3	1974	13	ADX49266	Adx49266 Plant full	C 213	15	26.3	36019	14	ADZ03804	AdZ03804 DNA seque
C 141	15	26.3	2000	8	ADA72518	AdA72518 Rice gene	C 214	15	26.3	36114	4	AAK85025	AAK85025 Adenoviru
C 142	15	26.3	2066	5	ADL45869	AdL45869 Human ova	C 215	15	26.3	36620	6	ADE71172	AdE71172 pMRKAdSHI
C 143	15	26.3	2076	13	ADX63023	Adx63023 Plant full	C 216	15	26.3	36620	10	ACD27673	ACD27673 Adenoviru
C 144	15	26.3	2175	8	ADA70642	AdA70642 Rice gene	C 217	15	26.3	36620	14	ADY80522	ADY80522 Plasmid p
C 145	15	26.3	2225	6	ABQ54634	ABq54634 Human ova	C 218	15	26.3	37035	12	ADJ82985	ADJ82985 Adenovect
C 146	15	26.3	2250	2	AAQ96001	AAq96001 Wheat emb	C 219	15	26.3	37339	5	AAI51612	AAI51612 Mouse orb
C 147	15	26.3	2277	4	AAF31118	AAf31118 Alcohol d	C 220	15	26.3	37474	6	ADE71169	AdE71169 pMRKAdSHI
C 148	15	26.3	2277	10	ADP84965	ADp84965 Farnesyl	C 221	15	26.3	37474	10	ADP19699	ADP19699 pMRKAdSHI
C 149	15	26.3	2323	4	AAH15404	AaH15404 Human CDN	C 222	15	26.3	37474	13	ADP800146	ADP800146 pMRKAdSHI
C 150	15	26.3	2492	13	ACN38145	ACn38145 Tumour-as	C 223	15	26.3	37474	13	ADP800147	ADP800147 pMRKAdSHI
C 151	15	26.3	2496	14	ADM14638	Adm14638 Human ADH	C 224	15	26.3	37474	13	ADP800147	ADP800147 pMRKAdSHI
C 152	15	26.3	2560	4	AAH02968	AAh02968 Human she	C 225	15	26.3	37474	13	ADU15248	ADU15248 Viral vec
C 153	15	26.3	2560	4	ABL21926	AbI21926 Drosophila	C 226	15	26.3	37474	14	ADY80517	ADY80517 Plasmid p
C 154	15	26.3	2613	3	AACT7614	AAc77614 Human can	C 227	15	26.3	38518	10	ACD27672	ACD27672 Adenoviru
C 155	15	26.3	2743	8	ABT19780	ABt19780 Aspergill	C 228	15	26.3	38519	6	ADE71171	AdE71171 pMRKAdSHI
C 156	15	26.3	2743	8	ABT19780	ABt19780 Aspergill	C 229	15	26.3	38519	14	ADY80520	ADY80520 Plasmid p
C 157	15	26.3	2743	8	ABT19780	ABt19780 Aspergill	C 230	15	26.3	44362	4	ABL29588	ABL29588 Drosophila
C 158	15	26.3	3007	6	ABZ35391	ABz35391 Human gen	C 231	15	26.3	80393	13	ADT89084	ADT89084 Arabidops
C 159	15	26.3	3015	13	ADR85479	AdR85479 Aspergill	C 232	15	26.3	81098	11	ACN45202	ACN45202 Human gen
C 160	15	26.3	3046	4	ABL29624	AbI29624 Drosophila	C 233	15	26.3	92562	10	ADC85284	ADC85284 Human tk
C 161	15	26.3	3107	11	ADM01530	Adm01530 Human CDN	C 234	15	26.3	92563	9	ADA02804	AdA02804 Human tk
C 162	15	26.3	3107	10	ADV85654	Adv85654 Human Mel	C 235	15	26.3	92563	10	ADM72542	AdM72542 Human tk
C 163	15	26.3	3150	14	ACF71487	ACf71487 Photocorb	C 236	15	26.3	92563	12	ADM74399	AdM74399 Human cat
C 164	15	26.3	3182	14	AEB22786	AEb22786 Human col	C 237	15	26.3	110000	2	AAT42063_01	Continuation (2 of
C 165	15	26.3	3235	13	ADR84892	AdR84892 Aspergill	C 238	15	26.3	110000	10	ACF67367_46	Continuation (47 o



239	15	26.3	110000	10	ACF65388_01	Continuation (2 of	C 312	14	24.6	477	4	AA184234	AA184234 Human pol
240	15	26.3	110000	11	ADM27081_09	Continuation (10 of	C 313	14	24.6	483	9	ACH37288	Ach37288 Human end
241	15	26.3	110000	11	AD242285_2	Continuation (3 of	C 314	14	24.6	497	8	ADL38916	Adl38916 Human ova
242	15	26.3	110000	14	ABE42401_21	Continuation (22 of	C 315	14	24.6	501	8	ACA52850	Acas52850 Prokaryot
243	15	26.3	145985	12	ADQ97164	Adq97164 Human can	C 316	14	24.6	509	13	ACN47863	Acn47863 Coton pr
244	15	26.3	158980	13	AD244537	Adz44537 Human bre	C 317	14	24.6	522	14	ADX97716	Adx97716 Human man
245	15	26.3	160361	12	AD108116	Adl08116 Human gen	C 318	14	24.6	527	11	ADP96637	Adp96637 Colon can
246	15	26.3	349980	12	ADT05648	Adt05648 Haemophil	C 319	14	24.6	527	11	ADX43119	Adx43119 Human cdn
247	14	24.6	14	3	AAZ11043	AAz11043 HIV gene	C 320	14	24.6	534	12	ACH79583	Ach79583 Human gen
248	14	24.6	25	9	ACK18115	ACK18115 Human mic	C 321	14	24.6	536	4	AA117800	AA117800 Probe #77
249	14	24.6	32	11	ADM39871	Adm39871 Multigenic	C 322	14	24.6	546	4	ABA62751	Abas62751 Human foe
250	14	24.6	51	4	AAH89339	Aah89339 Human eph	C 323	14	24.6	546	4	AA142765	AA142765 Probe #11
251	14	24.6	51	4	AAH89338	Aah89338 Human eph	C 324	14	24.6	546	4	ABA30051	Abas30051 Probe #85
252	14	24.6	65	6	ABN54083	Abn54083 Mouse epl	C 325	14	24.6	546	4	AAK36955	Aak36955 Human bon
253	14	24.6	74	10	ABT33888	Abt33888 TALL-1 re	C 326	14	24.6	546	4	AAK11139	Aak11139 Human bra
254	14	24.6	74	10	ABT33865	Abt33865 TALL-1 re	C 327	14	24.6	546	4	ABS36630	Abbs36630 Human liv
255	14	24.6	76	10	ABT33889	Abt33889 TALL-1 re	C 328	14	24.6	546	6	ABS10961	Abse10961 Human gen
256	14	24.6	146	13	ACF91234	Acf91234 Human SIR	C 329	14	24.6	549	3	AAAC94925	Aac94925 Cat flea
257	14	24.6	162	4	AA126997	AA126997 Probe #16	C 330	14	24.6	550	3	AAAC93647	Aac93647 Cat flea
258	14	24.6	162	4	AAH75263	Aah75263 Human foe	C 331	14	24.6	552	12	ADN99008	Adn99008 Novel hum
259	14	24.6	162	4	AAI55825	AAI55825 Probe #24	C 332	14	24.6	552	12	ADN00576	Adn00576 Novel hum
260	14	24.6	162	4	ABA33923	Abas33923 Probe #18	C 333	14	24.6	552	12	ADN00577	Adn00577 Novel hum
261	14	24.6	162	4	AAK49896	Aak49896 Human bon	C 334	14	24.6	552	12	ADN99007	Adn99007 Novel hum
262	14	24.6	162	4	AAK23807	Aak23807 Human bra	C 335	14	24.6	554	9	ADA21177	Ada21177 Human sec
263	14	24.6	162	4	ABS49537	Abs49537 Human liv	C 336	14	24.6	556	12	ACH68234	Ach68234 Human gen
264	14	24.6	162	6	ABS23391	Abs23391 Human gen	C 337	14	24.6	557	13	ADOS5121	Ados5121 Novel can
265	14	24.6	164	12	ACH93283	Ach93283 Human gen	C 338	14	24.6	570	12	AAH09457	Aah09457 Human cdn
266	14	24.6	170	12	ACH85317	Ach85317 Human gen	C 339	14	24.6	577	12	ACH71561	Ach71561 Human gen
267	14	24.6	174	2	AAQ76522	Aaq76522 Human gen	C 340	14	24.6	582	13	ACN46166	Acn46166 Coton pr
268	14	24.6	175	3	AAAC26142	Aac26142 Human sec	C 341	14	24.6	584	4	AA117821	AA117821 Probe #77
269	14	24.6	177	5	AAF68330	Aaf68330 Human lun	C 342	14	24.6	584	4	ABA62776	Abas62776 Human foe
270	14	24.6	177	6	ABK38241	Abk38241 cDNA enco	C 343	14	24.6	584	4	AA142792	AA142792 Probe #11
271	14	24.6	177	8	ACA10570	Acas10570 Human lun	C 344	14	24.6	584	4	ABA30068	Abas30068 Probe #85
272	14	24.6	177	8	ABX95921	Abx95921 Lung canc	C 345	14	24.6	584	4	AAK36977	Aak36977 Human bon
273	14	24.6	177	10	ADH45767	Adh45767 Human lun	C 346	14	24.6	584	4	AAK11167	Aak11167 Human bra
274	14	24.6	177	12	ADH72304	Adh72304 Human lun	C 347	14	24.6	584	4	ABS36657	Abbs36657 Human liv
275	14	24.6	177	13	ADJ19686	Adj19686 Human lun	C 348	14	24.6	593	6	ABV96061	Abv96061 Human pan
276	14	24.6	236	2	AAAT21683	Aat21683 Human gen	C 349	14	24.6	594	13	ACNS3388	Acns3388 Coton an
277	14	24.6	250	10	ADB67983	Adb67983 Human lun	C 350	14	24.6	596	13	ADU12168	Adu12168 Solid tum
278	14	24.6	275	2	AAQ76781	Aaq76781 Human gen	C 351	14	24.6	601	14	ABE34218	Abes34218 Human DNA
279	14	24.6	291	10	ABZ37919	Abz37919 N. gonorr	C 352	14	24.6	617	10	ADD146784	Add146784 Bacteri
280	14	24.6	303	6	AAAS16466	Aas16466 Human Apo	C 353	14	24.6	617	13	ADT44361	Adt44361 Bacteri
281	14	24.6	331	2	AAAT19542	Aat19542 Human gen	C 354	14	24.6	651	11	ADM39972	Adm39972 E. coli op
282	14	24.6	331	2	AAAS36000	Aas36000 Human car	C 355	14	24.6	651	11	ADM39972	Adm39972 E. coli op
283	14	24.6	331	10	ADBE4694	Adbe4694 Human car	C 356	14	24.6	655	4	AA124222	AA124222 Human bre
284	14	24.6	331	13	ADJ08112	Adj08112 Human car	C 357	14	24.6	668	10	ADD17604	Add17604 Human epi
285	14	24.6	348	13	ACF91356	Acf91356 Human SIR	C 358	14	24.6	677	13	AAZ33286	Aaz33286 Human gen
286	14	24.6	352	4	AAAS35263	Aas35263 Human car	C 359	14	24.6	680	10	ACRF66030	Acrf66030 Photorhab
287	14	24.6	352	10	ADBA5342	Adba5342 Human car	C 360	14	24.6	685	3	AAAF12385	Aaf12385 Aspergill
288	14	24.6	352	13	ADU06760	Adu06760 Human car	C 361	14	24.6	685	13	ADUS6426	Adus6426 Aspergill
289	14	24.6	362	4	AAH12396	Aah12396 Human cdn	C 362	14	24.6	685	14	ADZ94429	Adz94429 Aspergill
290	14	24.6	363	5	ABV07595	Abv07595 Human pro	C 363	14	24.6	702	10	ADBE1649	Adbe1649 Human gen
291	14	24.6	365	5	ABV08012	Abv08012 Human pro	C 364	14	24.6	705	13	ADRB1898	Adrb1898 Coton cd
292	14	24.6	378	12	ADP93592	Adp93592 Coton ex	C 365	14	24.6	732	5	AAAS86654	Aas86654 DNA enco
293	14	24.6	393	6	ABN95499	Abn95499 Gene #199	C 366	14	24.6	734	4	AAH33141	Aah33141 Human col
294	14	24.6	400	9	ACH18799	Ach18799 Human adu	C 367	14	24.6	753	8	ACA27574	Aca27574 Prokaryot
295	14	24.6	417	3	AAA69577	Aaa69577 Eucalyptu	C 368	14	24.6	767	5	AAAS76877	Aas76877 DNA enco
296	14	24.6	417	3	ACH30550	Ach30550 Human tes	C 369	14	24.6	767	10	AD121491	Ad121491 Novel hum
297	14	24.6	420	9	ACH22353	Ach22353 Human adu	C 370	14	24.6	778	10	ACRF66859	Acrf66859 Photorhab
298	14	24.6	424	10	ABR83458	Abz83458 Toxicolog	C 371	14	24.6	785	4	AAAF22856	Aaf22856 Human pro
299	14	24.6	425	8	ABX52908	Abx52908 Bovine ES	C 372	14	24.6	803	10	ADDS6321	Adds6321 Rat gene
300	14	24.6	429	8	ABV37527	Abv37527 Human pro	C 373	14	24.6	803	10	ADD45311	Add45311 Rat gene
301	14	24.6	434	5	AAAS6414	Aas6414 DNA enco	C 374	14	24.6	822	5	ADL63794	Adl63794 Human ova
302	14	24.6	442	5	ACH24012	Ach24012 Human adu	C 375	14	24.6	825	13	ACN42554	Acn42554 Human dfa
303	14	24.6	444	5	ABV37933	Abv37933 Human pro	C 376	14	24.6	835	5	AAH08510	Aah08510 Human cdn
304	14	24.6	456	8	ABZ53501	Abz53501 Aspergill	C 377	14	24.6	863	5	AAAC85560	Aac85560 cDNA enco
305	14	24.6	456	8	ACH49368	Ach49368 Human leu	C 378	14	24.6	912	5	AAAS90175	Aas90175 DNA enco
306	14	24.6	472	8	ABQ83323	Abq83323 Mitochond	C 379	14	24.6	912	5	AAAS9267	Aas9267 DNA enco
307	14	24.6	472	9	ACH33897	Ach33897 Human end	C 380	14	24.6	912	5	AAAS9810	Aas9810 DNA enco
308	14	24.6	473	2	AAQ78289	Aaq78289 The compl	C 381	14	24.6	948	8	ACA28906	Aca28906 Prokaryot
309	14	24.6	473	6	ABL65785	Ab165785 Lung canc	C 382	14	24.6	963	8	AAH67228	Aah67228 C glutami
310	14	24.6	473	11	ADP65756	Adp65756 Human apo	C 383	14	24.6	980	10	AD121980	Ad121980 Novel hum
311	14	24.6	475	13	ACF83022	Acf83022 Human SIR	C 384	14	24.6	993	8	ACA52689	Aca52689 Prokaryot



385	14	24.6	1025	13	ADSS1191	AdS51191 Bacterial	458	14	24.6	2393	6	ABL67247	ABL67247 Thyroid c
386	14	24.6	1025	13	ADSS1189	AdS51189 Bacterial	459	14	24.6	2393	6	AAI49806	AAI49806 Human chl
387	14	24.6	1025	13	ADSS1190	AdS51190 Bacterial	460	14	24.6	2393	6	ABZ35076	ABZ35076 Human gen
388	14	24.6	1028	5	ABV24841	Abv24841 Human pro	461	14	24.6	2468	13	ACNA1031	ACNA1031 Tumour-as
389	14	24.6	1028	5	ADL63118	AdL63118 Human ova	462	14	24.6	2483	4	AAIS8943	AAIS8943 Human pol
390	14	24.6	1081	3	ACA48330	ACa48330 Arabidops	463	14	24.6	2483	4	ADQ99165	ADQ99165 DNA encod
C 391	14	24.6	1083	3	AAAS52856	AAAS52856 Enterococ	464	14	24.6	2483	9	ADB48925	ADB48925 Novel hum
C 392	14	24.6	1110	10	ADH84415	Adh84415 Enterococ	465	14	24.6	2487	5	AAAS88829	AAAS88829 DNA encod
C 393	14	24.6	1151	13	ACNA1030	ACNA1030 Tumour-as	466	14	24.6	2505	12	ADMA45829	ADMA45829 TME -alpha
394	14	24.6	1176	13	ADX14049	Adx14049 Plant ful	C 467	14	24.6	2505	12	ADDO0873	ADDO0873 Human hom
395	14	24.6	1208	3	AAAC42735	AAAC42735 Arabidops	C 468	14	24.6	2505	12	ADDO0874	ADDO0874 Mouse hom
C 396	14	24.6	1221	12	ADP84837	ADP84837 Cellodiox	C 469	14	24.6	2540	6	ABA90850	ABA90850 Bacillus
397	14	24.6	1235	8	ABX63125	ABx63125 Human CDN	C 470	14	24.6	2560	4	AAI60729	AAI60729 Human pol
C 398	14	24.6	1241	13	ADT98298	ADt98298 E. coli 1	C 471	14	24.6	2560	4	AAI60730	AAI60730 Human pol
C 399	14	24.6	1245	6	ABZ78273	Abz78273 A. niger	C 472	14	24.6	2569	12	ADOI9549	ADOI9549 Human PRO
400	14	24.6	1260	9	ADB69771	Adb69771 C. neofor	C 473	14	24.6	2595	13	ADSS7808	AdSS7808 Bacterial
C 401	14	24.6	1314	9	ADB12586	ADB12586 Altiolococ	C 474	14	24.6	2604	4	AAH18535	AAH18535 Human CDN
C 402	14	24.6	1314	12	ADU27156	ADj27156 Altiolococ	C 475	14	24.6	2604	4	AAH18535	AAH18535 Human CDN
C 403	14	24.6	1315	2	AAAT65022	AAAT65022 Human nuc	C 476	14	24.6	2647	2	AAAT76739	AAAT76739 CDNA enco
C 404	14	24.6	1359	3	AAAC46828	AAc46828 Arabidops	C 477	14	24.6	2677	2	AAAX13455	AAAX13455 Enterococ
405	14	24.6	1389	8	ACA46710	ACa46710 Prokaryot	C 478	14	24.6	2677	6	ABS99250	ABS99250 Enterococ
406	14	24.6	1395	11	ABD14130	ABd14130 Pseudomon	C 479	14	24.6	2682	13	ADX14228	ADx14228 Plant ful
407	14	24.6	1404	6	AAN91279	Ahn91279 Staphyloc	C 480	14	24.6	2722	13	ADX55006	ADX55006 Plant ful
408	14	24.6	1404	13	ADS00947	AdS00947 Staphyloc	C 481	14	24.6	2727	5	AAAS93059	AAAS93059 DNA encod
409	14	24.6	1434	11	ABD13981	ABd13981 Pseudomon	C 482	14	24.6	2739	11	ACL26131	ACL26131 Rice abio
C 410	14	24.6	1454	4	AAAF81762	AAAF81762 Human mem	C 483	14	24.6	2763	8	ACA43661	ACA43661 Prokaryot
411	14	24.6	1532	13	ADX28597	ADx28597 Plant ful	C 484	14	24.6	2764	11	ADPE5755	ADPE5755 Human lec
412	14	24.6	1566	10	ACF69649	ACf69649 Photoforb	C 485	14	24.6	2764	11	ADPE5747	ADPE5747 Human lec
413	14	24.6	1590	10	ADB69410	Adb69410 C. neofor	C 486	14	24.6	2764	13	ADRE6148	ADRE6148 Human pro
414	14	24.6	1631	12	ADQ08621	Adq08621 Clona int	C 487	14	24.6	2764	13	ADX97717	ADx97717 Human man
415	14	24.6	1672	4	AAH17157	AAh17157 Human CDN	C 488	14	24.6	2764	14	ADY15043	ADy15043 DNA encod
C 416	14	24.6	1740	6	ABQ90148	ABq90148 M. capaul	C 489	14	24.6	2764	14	ADY15043	ADy15043 DNA encod
417	14	24.6	1740	6	ACA28640	ACa28640 Prokaryot	C 490	14	24.6	2766	14	ADZ48989	ADz48989 Insulin s
418	14	24.6	1755	6	AAAS16465	AAAS16465 Human Apo	C 491	14	24.6	2766	12	ADK41940	ADk41940 DNA encod
419	14	24.6	1757	4	AAH57461	AAH57461 Human liv	C 492	14	24.6	2783	5	AAAS91372	AAAS91372 DNA encod
420	14	24.6	1859	4	AAK68991	AAK68991 Human imm	C 493	14	24.6	2808	5	AAAS8838	AAAS8838 DNA encod
C 421	14	24.6	1866	3	AAAS7375	AAAS7375 CDNA sequ	C 494	14	24.6	2858	10	ABT42426	ABT42426 Toxicity
C 422	14	24.6	1876	10	ABZ56958	ABZ56958 Splicing	C 495	14	24.6	2858	13	ADRI4985	ADRI4985 Rat elect
C 423	14	24.6	1887	6	ACA00696	ACA00696 C. glutam	C 496	14	24.6	2858	13	ADV14662	ADv14662 Rat card1
C 424	14	24.6	1928	6	ABO80867	ABO80867 Burkaryoti	C 497	14	24.6	2928	14	ADZ99563	ADZ99563 Human apo
425	14	24.6	1944	8	ABX63782	ABx63782 Human CDN	C 498	14	24.6	2950	5	ADL45187	ADL45187 Human ova
426	14	24.6	1949	10	ADG10717	ADg10717 Human STA	C 499	14	24.6	2950	5	AAK68990	AAK68990 Human imm
427	14	24.6	1978	2	AAAX56953	AAAX56953 Human GBF	C 500	14	24.6	2995	4	ABL07033	ABL07033 Drosophill
428	14	24.6	1978	6	ABQ60781	ABq60781 Human SKD	C 501	14	24.6	3030	4	ABL20740	ABL20740 Drosophill
C 429	14	24.6	2000	8	ADA73130	AdA73130 Rice gene	C 502	14	24.6	3054	11	ACL30612	ACL30612 Rice abio
C 430	14	24.6	2000	8	ADA71885	AdA71885 Rice gene	C 503	14	24.6	3056	6	ABL99947	ABL99947 Human sia
431	14	24.6	2000	11	ACL37603	ACL37603 Rice stre	C 504	14	24.6	3122	8	ACA45676	ACA45676 Prokaryot
C 432	14	24.6	2000	11	ACL35091	ACL35091 Rice stre	C 505	14	24.6	3150	8	ACA43500	ACA43500 Prokaryot
C 433	14	24.6	2032	2	AAAT42073	AAAT42073 Human nuc	C 506	14	24.6	3169	14	ADY20286	ADy20286 DNA encod
C 434	14	24.6	2036	3	AAZ92672	AAZ92672 Murine al	C 507	14	24.6	3207	8	ACA25497	ACA25497 Prokaryot
435	14	24.6	2046	6	ABQ68933	ABq68933 Listeria	C 508	14	24.6	3215	5	AAAS88841	AAAS88841 DNA encod
436	14	24.6	2146	5	AAAS71015	AAAS71015 DNA encod	C 509	14	24.6	3273	3	AAAC48406	AAAC48406 Arabidops
437	14	24.6	2146	5	AAAS69456	AAAS69456 DNA encod	C 510	14	24.6	3277	6	ABL88427	ABL88427 Pain regu
C 438	14	24.6	2146	5	AAAS83284	AAAS83284 DNA encod	C 511	14	24.6	3277	10	ADPE0662	ADPE0662 Human CLC
C 439	14	24.6	2146	5	AAAS90960	AAAS90960 DNA encod	C 512	14	24.6	3277	12	ADQ18240	ADQ18240 Human sof
C 440	14	24.6	2170	3	AAZ92645	AAZ92645 Murine al	C 513	14	24.6	3293	4	ABA09077	ABA09077 Human Cl
C 441	14	24.6	2172	4	AAH16497	AAH16497 Human CDN	C 514	14	24.6	3318	10	ADH84846	ADH84846 Enterococ
442	14	24.6	2194	11	ADP65833	ADp65833 Human man	C 515	14	24.6	3370	13	ACNA1259	ACNA1259 Human dia
443	14	24.6	2194	11	ADP65825	ADp65825 Human man	C 516	14	24.6	3421	13	ACNA1258	ACNA1258 Human dia
C 444	14	24.6	2215	4	AAI04846	AAI04846 Human tes	C 517	14	24.6	3425	13	ACNA1257	ACNA1257 Human dia
C 445	14	24.6	2215	4	ABL97740	ABL97740 Human rep	C 518	14	24.6	3450	12	ADL06832	ADL06832 Streptomy
C 446	14	24.6	2220	10	AD140316	AD140316 Human pur	C 519	14	24.6	3465	14	AEH13128	AEH13128 C. glutam
C 447	14	24.6	2253	5	AAAS93060	AAAS93060 DNA encod	C 520	14	24.6	3465	14	AEH13128	AEH13128 C. glutam
C 448	14	24.6	2255	4	AAH18290	AAH18290 Human CDN	C 521	14	24.6	3487	12	ADQ22213	ADQ22213 Human sof
C 449	14	24.6	2287	6	ABZ78216	Abz78216 A. niger	C 522	14	24.6	3532	4	ABL04513	ABL04513 Drosophill
450	14	24.6	2288	4	AAIS58944	AAIS58944 Human pol	C 523	14	24.6	3546	4	AAHS4962	AAHS4962 S. epider
451	14	24.6	2288	5	ADQ9166	ADQ9166 DNA encod	C 524	14	24.6	3576	4	ABL02191	ABL02191 Drosophill
452	14	24.6	2288	9	ADB48926	ADB48926 Novel hum	C 525	14	24.6	3589	4	ABL28610	ABL28610 Drosophill
C 453	14	24.6	2298	5	ABV29020	ABv29020 Human pro	C 526	14	24.6	3590	10	ADB69049	ADB69049 C. neofor
C 454	14	24.6	2298	5	AAV23180	AAV23180 Human pro	C 527	14	24.6	3595	10	ADJ87396	ADJ87396 DNA rep1
455	14	24.6	2346	5	AAAS89993	AAAS89993 DNA encod	C 528	14	24.6	3684	10	ADA53429	ADA53429 Human God
456	14	24.6	2346	5	AAAS88883	AAAS88883 DNA encod	C 529	14	24.6	3697	2	AAAT72153	AAAT72153 Drosophill
457	14	24.6	2358	4	AAAF26081	AAAF26081 FIV gp140	C 530	14	24.6	3752	4	AAIS7852	AAIS7852 Human pol



C 531	14	24.6	3753	4	AAI59638	AAI59638 Human pol	C 604	14	24.6	13810	4	ABL06020	ABL06020 Drosophill
532	14	24.6	3769	13	ACN39923	Acn39923 Tumour-as	C 605	14	24.6	17303	13	ADR66579	Adr66579 Human pro
533	14	24.6	3776	12	ADK70385	Adk70385 Respirato	C 606	14	24.6	17303	13	ADR66527	Adr66527 Human pro
534	14	24.6	3777	13	ADK70385	Adk70385 Human tum	C 607	14	24.6	17300	12	ADK70385	Adk70385 Human pro
535	14	24.6	3849	11	ACI28344	AcI28344 Rice abio	C 608	14	24.6	19024	6	AAI13116	AAI13116 Enterococ
536	14	24.6	3849	12	ADL45252	AdI45252 Rice isop	C 609	14	24.6	19024	6	AAI13116	AAI13116 Enterococ
537	14	24.6	3865	5	ABAI6594	ABAI6594 Human ner	C 610	14	24.6	22297	13	ABD33236	ABD33236 Human can
538	14	24.6	3865	5	ABAI6594	ABAI6594 Human ner	C 611	14	24.6	22297	13	ABD33236	ABD33236 Human can
539	14	24.6	3882	8	ACAI8464	ACAI8464 Prokaryot	C 612	14	24.6	22934	8	ACF64542	ACF64542 Propionib
C 540	14	24.6	3903	4	AAI55172	AAI55172 Enterococ	C 613	14	24.6	26064	11	ACN44812	ACN44812 Mouse gen
C 541	14	24.6	3903	4	AAI55172	AAI55172 Enterococ	C 614	14	24.6	30306	11	ACN44196	ACN44196 Mouse gen
C 542	14	24.6	3974	11	ACN44759	Acn44759 Human mRN	C 615	14	24.6	30471	11	ACN44448	ACN44448 Human gen
C 543	14	24.6	3990	13	ADSA6478	Adsa6478 Bacterial	C 616	14	24.6	31737	10	ACF67743	ACF67743 Phototrab
C 544	14	24.6	4091	12	ADQ23949	Adq23949 Human sof	C 617	14	24.6	31840	13	ABD33005	ABD33005 Human can
C 545	14	24.6	4097	12	ADQ22784	Adq22784 Human sof	C 618	14	24.6	32159	10	ADH80454	ADH80454 Human can
C 546	14	24.6	4107	14	ADZ62685	Adz62685 Murine Ra	C 619	14	24.6	32160	6	ABF78887	ABF78887 E. coli C
547	14	24.6	4139	6	ABLI2616	ABLI2616 Drosophill	C 620	14	24.6	32177	4	AAI04279	AAI04279 Human mus
548	14	24.6	4178	6	ABZ35296	Abz35296 Human gen	C 621	14	24.6	32177	4	AAI04279	AAI04279 Human rep
549	14	24.6	4190	10	ADBS8003	Adbs8003 Toxicity-	C 622	14	24.6	32177	8	ABX59874	ABX59874 Drosophill
550	14	24.6	4190	11	ADW21874	Adw21874 Rat hepat	C 623	14	24.6	32177	12	ADJ30624	ADJ30624 Human mus
551	14	24.6	4260	13	ADBS9263	Adbs9263 Bacterial	C 624	14	24.6	32207	4	AAI04278	AAI04278 Human rep
552	14	24.6	4269	5	ACN42865	Acn42865 Human dia	C 625	14	24.6	32207	8	ABX59873	ABX59873 CDNA enco
553	14	24.6	4413	13	AAI833662	AAI833662 DNA encod	C 626	14	24.6	32207	12	ADJ30623	ADJ30623 Human mus
C 554	14	24.6	4532	6	ABLO4512	ABLO4512 Drosophill	C 627	14	24.6	35832	4	ABLI8726	ABLI8726 Drosophill
C 555	14	24.6	4532	6	ABZ35261	Abz35261 Human gen	C 628	14	24.6	35832	4	ABLI8726	ABLI8726 Drosophill
C 556	14	24.6	4561	13	ADP54762	Adp54762 Human PRO	C 629	14	24.6	37620	12	ADQ43240	ADQ43240 Human mus
557	14	24.6	4820	13	ADRE6644	Adre6644 Human pro	C 630	14	24.6	38136	4	AAK82172	AAK82172 Human imm
558	14	24.6	4820	13	ADRE6560	Adre6560 Human pro	C 631	14	24.6	38140	4	AAK82171	AAK82171 Human imm
559	14	24.6	4825	8	ABX56980	ABX56980 DNA encod	C 632	14	24.6	39052	4	ABLO2664	ABLO2664 Drosophill
560	14	24.6	4850	5	ABV24759	Abv24759 Human pro	C 633	14	24.6	42738	4	AAK68992	AAK68992 Human imm
C 561	14	24.6	4887	6	ABO70940	ABO70940 Listeria	C 634	14	24.6	44979	10	ADC86188	ADC86188 Human GPC
562	14	24.6	5039	11	ADM33263	Adm33263 Candida a	C 635	14	24.6	45244	11	ACN45044	ACN45044 Human gen
563	14	24.6	5194	2	AAK25885	AAK25885 C.albican	C 636	14	24.6	47686	12	ADQ59461	ADQ59461 Human can
564	14	24.6	5194	6	AAI031519	AAI031519 Candida a	C 637	14	24.6	47774	14	ADZ13790	ADZ13790 Murine ca
565	14	24.6	5194	6	ABK48292	ABK48292 DNA encod	C 638	14	24.6	52562	4	AAK86671	AAK86671 Human imm
566	14	24.6	5194	10	ADCT3266	Adct3266 Yeast DNA	C 639	14	24.6	53075	14	AAK86671	AAK86671 Human imm
C 567	14	24.6	5373	4	ABLO7032	ABLO7032 Drosophill	C 640	14	24.6	53974	14	ABR35707	ABR35707 L. pneumo
C 568	14	24.6	5722	4	ABLO2190	ABLO2190 Drosophill	C 641	14	24.6	79786	10	ADQ2909	ADQ2909 Mouse jak
569	14	24.6	5871	4	AAI26075	AAI26075 PIV gp140	C 642	14	24.6	79786	10	ADH72647	ADH72647 Mouse jak
C 571	14	24.6	6049	12	ABX97140	ABX97140 Human NOV	C 643	14	24.6	79786	10	ADH72647	ADH72647 Mouse jak
C 572	14	24.6	6049	12	ADN61996	ADN61996 Human NOV	C 644	14	24.6	79786	10	ADH72647	ADH72647 Mouse jak
C 573	14	24.6	6129	11	ABD01107	ABD01107 Klebsiell	C 645	14	24.6	81679	12	ADQ59189	ADQ59189 Human can
574	14	24.6	6143	13	ADJ33482	Adj33482 Mouse leu	C 646	14	24.6	84826	13	ABD32594_6	ABD32594_6 Human can
575	14	24.6	6149	14	ADK06898	Adk06898 Cyclin-de	C 647	14	24.6	85859	11	ACN44888	ACN44888 Human gen
576	14	24.6	6541	10	ADBS2922	Adbs2922 Primary r	C 648	14	24.6	85859	11	ACN44888	ACN44888 Human gen
C 577	14	24.6	6571	13	ADSO9864	ADSO9864 Human the	C 649	14	24.6	92427	11	ACN44266	ACN44266 Human gen
578	14	24.6	6628	6	AAI45691	AAI45691 Human LBD	C 650	14	24.6	92427	11	ACN44266	ACN44266 Human gen
579	14	24.6	6628	10	ADH28769	Adh28769 Human LBD	C 651	14	24.6	96638	12	ADQ97919	ADQ97919 Human can
580	14	24.6	6677	10	ADD29631	Add29631 Human chr	C 652	14	24.6	96638	12	ADQ97919	ADQ97919 Human can
C 581	14	24.6	6708	10	ADCS6730	Adcs6730 Human tum	C 653	14	24.6	96638	12	ADQ97919	ADQ97919 Human can
C 582	14	24.6	6708	10	ADCS6730	Adcs6730 Human cre	C 654	14	24.6	99918	13	ABD33009	ABD33009 Human can
583	14	24.6	6931	9	ACF06240	ACF06240 Human NOV	C 655	14	24.6	100660	13	ABD33009	ABD33009 Human can
584	14	24.6	7010	3	AAZ36927	AAZ36927 Nucleotid	C 656	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 585	14	24.6	7060	10	ADC30132	Adc30132 Human nov	C 657	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 586	14	24.6	7149	10	ADC56728	Adc56728 Human nov	C 658	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 587	14	24.6	7287	10	AAH57428	Aah57428 Human int	C 659	14	24.6	100660	13	ABD33009	ABD33009 Human can
588	14	24.6	7312	2	AAH84324	AAH84324 Stealch v	C 660	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 589	14	24.6	7402	2	ABL05304	ABl05304 Drosophill	C 661	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 590	14	24.6	7743	5	ABV24883	ABV24883 Human pro	C 662	14	24.6	100660	13	ABD33009	ABD33009 Human can
591	14	24.6	7743	5	ABV25138	ABV25138 Human pro	C 663	14	24.6	100660	13	ABD33009	ABD33009 Human can
592	14	24.6	8162	6	ABQ71064	Abq71064 Listeria	C 664	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 593	14	24.6	8802	8	AAI59586	AAI59586 Propionib	C 665	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 594	14	24.6	8802	8	AAI59586	AAI59586 Propionib	C 666	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 595	14	24.6	9704	8	ABX93511	ABX93511 Genomic d	C 667	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 596	14	24.6	9704	8	ABX93511	ABX93511 Genomic d	C 668	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 597	14	24.6	11000	10	ADCS6726	Adcs6726 Thale cre	C 669	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 598	14	24.6	11917	12	ADIC1564	Adic1564 Human cdn	C 670	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 599	14	24.6	11917	14	ABE43829	ABe43829 Human cdn	C 671	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 600	14	24.6	11950	10	ADBS3871	Adbs3871 Human pro	C 672	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 601	14	24.6	11965	10	ADFP90735	Adfp90735 Human hep	C 673	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 602	14	24.6	12004	12	ADNO4560	Adno4560 Antipori	C 674	14	24.6	100660	13	ABD33009	ABD33009 Human can
C 603	14	24.6	12117	3	AAA96368	AAA96368 Polymorph	C 675	14	24.6	100660	13	ABD33009	ABD33009 Human can
							C 676	14	24.6	110000	12	ADN46123_15	ADN46123_15 Human can



677	14	24.6	110000	12	ADN47209_05	Continuation (6 of	750	13	22.8	47	14	ADW08998	Adw08998 PCR prime	
678	14	24.6	110000	12	ADNA6464_15	Continuation (16 o	751	13	22.8	60	6	ABN44425	Abn44425 Human sp1	
679	14	24.6	110000	12	ADNA7960_05	Continuation (6 of	752	13	22.8	60	6	ABN38057	Abn38057 Human sp1	
680	14	24.6	110000	12	ADQ59446_1	Continuation (2 of	753	13	22.8	65	6	ABN27765	Abn27765 Rat sp1ic	
681	14	24.6	110000	12	ADQ97328_0	Adq97328 Mouse can	754	13	22.8	65	6	ABN29443	Abn29443 Rat sp1ic	
682	14	24.6	110000	13	ABD32921_1	Continuation (2 of	755	13	22.8	81	3	AAZ94798	Aaz94798 Soybean A	
683	14	24.6	110000	13	ABD32629_1	Continuation (2 of	756	13	22.8	100	8	ABZ24662	Abz24662 Interleuk	
684	14	24.6	110000	14	ADZ13631_0	Adz13631 Human can	757	13	22.8	112	4	AAI24337	Aai24337 Probe #14	
685	14	24.6	110000	14	ADZ13620_0	Adz13620 Human can	758	13	22.8	112	4	ABA69475	Aba69475 Human foe	
686	14	24.6	110000	14	ADZ13757_1	Continuation (2 of	759	13	22.8	112	4	AAI49607	Aai49607 Probe #18	
687	14	24.6	110000	14	ADZ12821_3	Continuation (4 of	760	13	22.8	112	4	ABA51447	Aba51447 Human bre	
688	14	24.6	110000	14	AEB39175_06	Continuation (7 of	761	13	22.8	112	4	ABA36400	Aba36400 Probe #14	
689	14	24.6	110000	14	AEB39175_11	Continuation (12 o	762	13	22.8	112	4	AAK43551	Aak43551 Human bon	
690	14	24.6	110000	14	AEBA4201_11	Continuation (12 o	763	13	22.8	112	4	AAK17730	Aak17730 Human bra	
691	14	24.6	124884	5	AAH74201	AAh74201 Nucleotid	764	13	22.8	112	4	ABS43196	Abs43196 Human liv	
692	14	24.6	124884	10	ADA14878	Ada14878 Human her	765	13	22.8	112	5	AAI09879	Aai09879 Probe #98	
693	14	24.6	124884	11	ADL99489	Adl99489 Varicella	766	13	22.8	112	6	ABS17690	Abs17690 Human gen	
694	14	24.6	125157	5	AAH74202	AAh74202 Nucleotid	767	13	22.8	131	6	ABA73180	Aba73180 Human foe	
695	14	24.6	126488	14	ADZ12943	Adz12943 Human can	768	13	22.8	131	4	AAI53611	Aai53611 Probe #22	
696	14	24.6	127943	12	ADQ97651	Adq97651 Human can	769	13	22.8	131	4	AAK47779	Aak47779 Human bon	
697	14	24.6	150130	11	ACNA4394	Acna4394 Human gen	770	13	22.8	131	4	AAK21615	Aak21615 Human bra	
698	14	24.6	155937	12	ADQ19389	Adq19389 Human sof	771	13	22.8	131	4	ABS47505	Abs47505 Human liv	
699	14	24.6	171324	11	ACNA3892	Acna3892 Mouse gen	772	13	22.8	131	6	ABS21793	Abs21793 Human gen	
700	14	24.6	172569	11	ACNA4758	Acna4758 Human gen	773	13	22.8	139	3	AAL19572	Aal19572 Human bre	
701	14	24.6	201766	10	ADL13771	Adl13771 Osteocarth	774	13	22.8	147	3	AAK18942	Aak18942 Human sec	
702	14	24.6	209612	12	ADQ59395	Adq59395 Human can	775	13	22.8	164	10	ACD96366	Acd96366 Human col	
703	14	24.6	209612	12	ADZ13662	Adz13662 Murine ca	776	13	22.8	178	12	ACH84409	Ach84409 Human gen	
704	14	24.6	248999	12	ADQ97365	Adq97365 Human can	777	13	22.8	201	13	ADS438531	Ads438531 Human aut	
705	14	24.6	252907	13	ABD32694	Abd32694 Human can	778	13	22.8	201	13	ADS41330	Ads41330 Human aut	
706	14	24.6	254868	14	ADZ13236	Adz13236 Murine ca	779	13	22.8	201	13	ADSA1331	Ads1331 Human aut	
707	14	24.6	259202	12	ADQ18492	Adq18492 Human sof	780	13	22.8	220	13	AAO98824	Aao98824 Tomato ge	
708	14	24.6	295644	14	AEBS3521	AEb3521 L. pneumo	781	13	22.8	220	6	ABL74424	AbL74424 Corn tass	
709	14	24.6	349980	5	AAH68531	C glutami	782	13	22.8	220	6	ABL74281	AbL74281 Corn tass	
710	14	24.6	349980	5	AAH41223	Pyrococcu	783	13	22.8	225	8	AAAD41344	AAa41344 5' parlia	
711	14	24.6	349980	5	AAH64631	Pyrococcu	784	13	22.8	227	2	AAH86238	Aah86238 Human bin	
712	14	24.6	349980	6	ABQ81846	Bifidobac	785	13	22.8	230	3	AAC09092	Aac09092 Human bec	
713	14	24.6	349980	6	ABQ81847	Bifidobac	786	13	22.8	230	6	ABN24490	Abn24490 Human ORF	
714	14	24.6	349980	6	ABQ81844	Bifidobac	787	13	22.8	231	11	ABD00875	Abd00875 Klebsiell	
715	14	24.6	349980	6	ABQ81842	Bifidobac	788	13	22.8	232	12	ADH00634	Adh00634 Kidney di	
716	13	22.8	349980	17	ACN09728	MNV minus	789	13	22.8	237	6	ABL71281	AbL71281 Corn tass	
717	13	22.8	349980	17	ACN07575	MNV minus	790	13	22.8	242	6	AAAD41344	AAa41344 5' parlia	
718	13	22.8	349980	17	ACN09727	MNV minus	791	13	22.8	249	12	ADP62676	Adp62676 Maize car	
719	13	22.8	349980	17	ACN07574	MNV minus	792	13	22.8	252	12	ADH00099	Adh00099 Kidney di	
720	13	22.8	349980	17	ACN07224	MNV Amber	793	13	22.8	260	7	ADS69387	Ads69387 Corn seed	
721	13	22.8	349980	17	ACN07225	MNV Amber	794	13	22.8	261	5	AAH68431	Aah68431 C glutami	
722	13	22.8	349980	17	ACN03299	MNV Inocy	795	13	22.8	263	9	ADA01916	Ada01916 Mouse car	
723	13	22.8	349980	17	ACN05396	MNV DNazy	796	13	22.8	263	10	ADB71655	Adb71655 Mouse car	
724	13	22.8	349980	19	AEBO4923	Human IL-	797	13	22.8	266	12	ADP62675	Adp62675 Maize car	
725	13	22.8	349980	19	AEBO4994	Human IL-	798	13	22.8	273	12	ADL12513	AdL12513 Human bre	
726	13	22.8	349980	19	AECL14831	Human IL-	799	13	22.8	278	5	ABA11699	Aba11699 Human ner	
727	13	22.8	349980	19	AECL14760	Human IL-	800	13	22.8	279	2	AAK27687	Aak27687 Synthetic	
728	13	22.8	349980	21	ABX75430	Human int	801	13	22.8	279	6	ABL51801	AbL51801 Hydroxyc	
729	13	22.8	349980	21	ABX29104	Euroclum	802	13	22.8	279	13	ADU09211	Adu09211 HGRP/GAGP	
730	13	22.8	349980	22	ABN99507	Fungl pro	803	13	22.8	294	4	ABK42386	Abk42386 Genomic s	
731	13	22.8	349980	22	ADL25779	Human can	804	13	22.8	294	4	ABK42384	Abk42384 Genomic s	
732	13	22.8	349980	24	ABBS56856	Human PDZ	805	13	22.8	294	4	ABK41769	Abk41769 CDNA enco	
733	13	22.8	349980	25	9	ACT92685	Human mic	806	13	22.8	294	4	ABK42385	Abk42385 Genomic s
734	13	22.8	349980	25	9	ACK06189	Human mic	807	13	22.8	294	9	ADB60542	Adb60542 Connectiv
735	13	22.8	349980	25	10	ADFA4805	Internal	808	13	22.8	294	9	ADB59436	Adb59436 Connectiv
736	13	22.8	349980	25	10	ADFA4805	Internal	809	13	22.8	294	9	ADB60540	Adb60540 Connectiv
737	13	22.8	349980	27	AAV98654	Human EGF	810	13	22.8	294	9	ADB60541	Adb60541 Connectiv	
738	13	22.8	349980	27	6	ABX22011	EPSP synz	811	13	22.8	295	3	AAK22390	Aak22390 Human sec
739	13	22.8	349980	27	6	ADAI4545	Staphyloc	812	13	22.8	298	10	ABX88802	Abx88802 Corn ear-
740	13	22.8	349980	27	10	ADP33240	Glyphosat	813	13	22.8	300	14	ADVA32529	Adv42529 Human pay
741	13	22.8	349980	27	14	ADW08992	PCR prime	814	13	22.8	301	14	ADVA33414	Adv43414 Human psy
742	13	22.8	349980	28	10	ABX95853	PCR prime	815	13	22.8	307	6	ABN18276	Abn18276 Human ORF
743	13	22.8	349980	28	14	ADZ87374	Cotcon ev	816	13	22.8	316	10	ADKS5925	Adk55925 Plant DNA
744	13	22.8	349980	29	2	AAQ94602	Upstream	817	13	22.8	324	5	AAK75155	Aak75155 DNA encod
745	13	22.8	349980	29	2	AAK2153	Integrin	818	13	22.8	324	5	AAK79736	Aak79736 DNA encod
746	13	22.8	349980	44	5	AAI16775	EPSP8 com	819	13	22.8	324	5	AAK79736	Aak79736 Streptoco
747	13	22.8	349980	44	5	AAI16775	S. typhimu	820	13	22.8	326	5	ADT77258	Adt77258 Human ova
748	13	22.8	349980	46	14	ADZ51339	PCR prime	821	13	22.8	326	5	ADT70945	Adt70945 Human ova
749	13	22.8	349980	47	9	ADA14554	Staphyloc	822	13	22.8	329	5	ABAI5904	Abai5904 Human ner



C 823	13	22.8	330	6	ABV78112	ABV78112 Hypoxia-r	896	13	22.8	451	4	AAI15867	AAI15867 Probe #58
C 824	13	22.8	330	13	ACNA0169	ACNA0169 Tumour-as	897	13	22.8	451	4	ABA58163	ABA58163 Human foe
C 825	13	22.8	336	2	AAQ28943	AAQ28943 Asp41-Cyt	898	13	22.8	451	4	AAI37770	AAI37770 Probe #64
C 826	13	22.8	336	2	AAQ28944	AAQ28944 Gly41-Cyt	899	13	22.8	451	4	ABA27353	ABA27353 Probe #58
C 827	13	22.8	336	6	ABN61515	ABN61515 Human can	900	13	22.8	451	4	AAK31903	AAK31903 Human bon
C 828	13	22.8	337	3	AAOC05074	AAOC05074 Human sec	901	13	22.8	451	4	AAK06243	AAK06243 Human bon
C 829	13	22.8	338	12	ADOO4828	ADOO4828 Maize leu	902	13	22.8	451	4	ABN31593	ABN31593 Human liv
C 830	13	22.8	339	4	AA537565	AA537565 Novel hum	903	13	22.8	451	6	AB506665	AB506665 Human gen
C 831	13	22.8	339	6	ABL66086	ABL66086 Lung can	904	13	22.8	451	11	ACN81388	ACN81388 Breast ca
C 832	13	22.8	342	3	ABK10766	ABK10766 Interleuk	905	13	22.8	454	6	ABL93817	ABL93817 Arabidops
C 833	13	22.8	351	9	ACH31695	ACH31695 Human bon	906	13	22.8	455	4	AAK61999	AAK61999 Human imm
C 834	13	22.8	353	6	ABL83078	ABL83078 Human ova	907	13	22.8	457	6	ABL01393	ABL01393 Murine ap
C 835	13	22.8	354	6	ABO91036	ABO91036 M. caperu	908	13	22.8	458	2	AAV18163	AAV18163 Polio vac
C 836	13	22.8	358	10	AD182022	AD182022 A. thalia	909	13	22.8	458	2	AAV18160	AAV18160 Polio vac
C 837	13	22.8	364	8	ABZ54387	ABZ54387 Aspergill	910	13	22.8	458	13	ACN57613	ACN57613 Cotton gy
C 838	13	22.8	371	3	AAFI5714	AAFI5714 Human pro	911	13	22.8	459	2	AAV18162	AAV18162 Polio vac
C 839	13	22.8	375	12	ADP93945	ADP93945 Cotton ex	912	13	22.8	459	2	AAV18161	AAV18161 Polio vac
C 840	13	22.8	376	2	AAI11187	AAI11187 Human bre	913	13	22.8	460	4	AAI09185	AAI09185 Human bre
C 841	13	22.8	378	2	AAT88830	AAT88830 Gamma-1 h	914	13	22.8	460	8	ABX39673	ABX39673 Bovine ES
C 842	13	22.8	378	6	ABO69645	ABO69645 Listeria	915	13	22.8	468	8	ACF73776	ACF73776 Staphyloc
C 843	13	22.8	378	13	ADK44264	ADK44264 Streptoco	916	13	22.8	471	4	AAI12494	AAI12494 Probe #24
C 844	13	22.8	379	3	AAOC04519	AAOC04519 Human sec	917	13	22.8	471	4	ABA54199	ABA54199 Human foe
C 845	13	22.8	386	4	ABA88822	ABA88822 Escherich	918	13	22.8	471	4	AAI33849	AAI33849 Probe #25
C 846	13	22.8	390	11	ACH95810	ACH95810 Klebsiell	919	13	22.8	471	4	ABA43746	ABA43746 Human bre
C 847	13	22.8	391	3	AAOC01117	AAOC01117 Human sec	920	13	22.8	471	4	ABA23950	ABA23950 Probe #24
C 848	13	22.8	391	8	ABL35175	ABL35175 Human mus	921	13	22.8	471	4	AAK27915	AAK27915 Human bon
C 849	13	22.8	391	8	ABX58163	ABX58163 cDNA enco	922	13	22.8	471	4	AAK02476	AAK02476 Human bra
C 850	13	22.8	391	12	ADU27890	ADJ27890 Human mus	923	13	22.8	471	4	ABS27498	ABS27498 Human liv
C 851	13	22.8	393	4	AAFI71941	AAFI71941 Corynebac	924	13	22.8	471	5	AAI02404	AAI02404 Probe #23
C 852	13	22.8	393	6	ABO67481	ABO67481 Listeria	925	13	22.8	471	6	ABS02370	ABS02370 Human gen
C 853	13	22.8	396	4	AAH28514	AAH28514 Human int	926	13	22.8	477	10	ADR79909	ADR79909 Leukemia
C 854	13	22.8	399	14	ABE21364	ABE21364 Monkey in	927	13	22.8	481	3	AAAC38789	AAAC38789 Arabidops
C 855	13	22.8	399	14	ABE31122	ABE31122 M. fascic	928	13	22.8	482	8	ABZ52897	ABZ52897 Aspergill
C 856	13	22.8	400	5	AAFI64369	AAFI64369 Novel hum	929	13	22.8	482	9	ACH41796	ACH41796 Human foe
C 857	13	22.8	400	14	ADM87914	ADM87914 Human Par	930	13	22.8	483	3	AAAC33358	AAAC33358 Arabidops
C 858	13	22.8	401	6	ABV72937	ABV72937 K. pneumo	931	13	22.8	483	3	ACH14010	ACH14010 Human adu
C 859	13	22.8	402	13	AD078731	ADG78731 Novel can	932	13	22.8	485	5	AA567700	AA567700 DNA encod
C 860	13	22.8	405	5	ADL42494	ADL42494 Human ova	933	13	22.8	487	2	AAK39575	AAK39575 Human sec
C 861	13	22.8	405	8	ABX62601	ABX62601 Arabidops	934	13	22.8	489	6	ABN91370	ABN91370 Staphyloc
C 862	13	22.8	406	3	AACT9193	AACT9193 Human lun	935	13	22.8	491	1	ACH36252	ACH36252 Human end
C 863	13	22.8	406	4	ADD23269	ADD23269 Human lun	936	13	22.8	492	12	ADJ44251	ADJ44251 Plant cDN
C 864	13	22.8	406	10	ADD66543	ADD66543 Human lun	937	13	22.8	495	4	ABK42087	ABK42087 cDNA enco
C 865	13	22.8	406	10	ADH87797	ADH87797 Human lun	938	13	22.8	495	9	ADH859754	ADH859754 Connectiv
C 866	13	22.8	407	8	AAK67683	AAK67683 Human imm	939	13	22.8	495	10	ADH81794	ADH81794 Arabidops
C 867	13	22.8	407	8	ABX37050	ABX37050 Bovine ES	940	13	22.8	495	11	ABDI0762	ABDI0762 Pseudomon
C 868	13	22.8	408	2	ABX46479	ABX46479 Bovine ES	941	13	22.8	495	14	ADV75757	ADV75757 Human col
C 869	13	22.8	411	2	AAT91023	AAT91023 Human bet	942	13	22.8	500	13	ACN45475	ACN45475 Cotton pr
C 870	13	22.8	413	3	AAOC08696	AAOC08696 Human sec	943	13	22.8	501	13	ADQ49953	ADQ49953 Arabidops
C 871	13	22.8	414	5	ABV10668	ABV10668 Human pro	944	13	22.8	504	8	ADA68462	ADA68462 Novel can
C 872	13	22.8	417	8	ACA37008	ACA37008 Prokaryot	945	13	22.8	504	10	ADD344616	ADD344616 Mouse mit
C 873	13	22.8	418	3	AAA68121	AAA68121 Eucalyptu	946	13	22.8	504	13	ADL36435	ADL36435 A Chalian
C 874	13	22.8	418	10	ADD41871	ADD41871 Diphenol	947	13	22.8	506	4	AAI36682	AAI36682 Human mus
C 875	13	22.8	419	10	ADK61249	ADK61249 Ovarian c	948	13	22.8	506	8	ABX59670	ABX59670 cDNA enco
C 876	13	22.8	436	2	AAO39826	AAQ39826 Expressed	949	13	22.8	506	10	ADH81518	ADH81518 Arabidops
C 877	13	22.8	436	10	ADH57737	ADH57737 Toxicity-	950	13	22.8	507	12	ADJ30420	ADJ30420 Human mus
C 878	13	22.8	437	6	ABN94877	ABN94877 Gene #137	951	13	22.8	507	12	ADQ92215	ADQ92215 Human aut
C 879	13	22.8	437	8	ABX48154	ABX48154 Bovine ES	952	13	22.8	509	9	ACH45209	ACH45209 Human foe
C 880	13	22.8	439	9	ACH46701	ACH46701 Human inf	953	13	22.8	510	6	ABL65697	ABL65697 Lung can
C 881	13	22.8	443	14	AE888977	AE888977 Isolated	954	13	22.8	510	6	ABL66407	ABL66407 Lung can
C 882	13	22.8	444	4	AAI20086	AAI20086 Human bre	955	13	22.8	510	6	ABL65285	ABL65285 lung can
C 883	13	22.8	444	4	AAI15157	AAI15157 Probe #50	956	13	22.8	512	4	AAI36683	AAI36683 Human mus
C 884	13	22.8	444	4	ABA56910	ABA56910 Human foe	957	13	22.8	512	4	AAH70260	AAH70260 Human cer
C 885	13	22.8	444	4	AAI36485	AAI36485 Probe #51	958	13	22.8	512	4	ABX59671	ABX59671 cDNA enco
C 886	13	22.8	444	4	ABA46345	ABA46345 Human bre	959	13	22.8	512	8	AAH70260	AAH70260 Human cer
C 887	13	22.8	444	4	ABA26525	ABA26525 Probe #49	960	13	22.8	512	12	ADJ30421	ADJ30421 Human mus
C 888	13	22.8	444	4	AAK30541	AAK30541 Human bon	961	13	22.8	525	11	ACN79387	ACN79387 Breast ca
C 889	13	22.8	444	4	AAK05007	AAK05007 Human bra	962	13	22.8	526	10	ADH51374	ADH51374 Primary r
C 890	13	22.8	444	4	AB530204	AB530204 Human liv	963	13	22.8	535	1	AAAN91125	AAAN91125 Promoter
C 891	13	22.8	444	5	AAI04900	AAI04900 Probe #48	964	13	22.8	540	13	ADU14606	ADU14606 Solid tum
C 892	13	22.8	444	4	AB505186	AB505186 Human gen	965	13	22.8	541	4	ABA59767	ABA59767 Human foe
C 893	13	22.8	444	13	ACN56632	ACN56632 Cotton gy	966	13	22.8	541	4	AAI39637	AAI39637 Probe #83
C 894	13	22.8	447	13	ACN56543	ACN56543 Cotton gy	967	13	22.8	541	4	AAK33911	AAK33911 Human bon
C 895	13	22.8	449	3	AAA53190	AAA53190 Raphanus	968	13	22.8	541	4	AAK08039	AAK08039 Human bra



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c 969 13 22.8 541 4 ABS33717 AdS33717 Human liv
c 970 13 22.8 544 14 AC156344 Ac156344 Human col
c 971 13 22.8 544 5 ABV57369 ABV57369 Human pro
c 972 13 22.8 549 4 ABA61686 ABA61686 Human foe
c 973 13 22.8 549 4 AA141598 AA141598 Probe #10
c 974 13 22.8 549 4 AAK35882 AAK35882 Human bra
c 975 13 22.8 549 4 AAK09988 AAK09988 Human bra
c 976 13 22.8 549 4 ABS35591 ABS35591 Human liv
c 977 13 22.8 549 6 ABS10108 ABS10108 Human gen
c 978 13 22.8 549 9 ACC73147 ACC73147 Cat flea
c 979 13 22.8 549 12 ADL07992 ADL07992 Cat flea
c 980 13 22.8 552 12 ACH70709 ACH70709 Human gen
c 981 13 22.8 555 10 ADC91108 ADC91108 E. faeciu
c 982 13 22.8 556 13 ACN56585 ACN56585 Cotton gy
c 983 13 22.8 560 8 ADA99008 ADA99008 Human sec
c 984 13 22.8 560 8 ADA44586 ADA44586 Human sec
c 985 13 22.8 560 10 ADC21040 ADC21040 Human sec
c 986 13 22.8 560 10 ADF11028 ADF11028 Human sec
c 987 13 22.8 563 12 ADOS7633 ADOS7633 Actinobac
c 988 13 22.8 563 12 ADQ92086 ADQ92086 Human aut
c 989 13 22.8 565 12 ADQ21501 ADQ21501 Human sof
c 990 13 22.8 568 12 ADN41938 ADN41938 Nucleotid
c 991 13 22.8 573 8 ACA27617 ACA27617 Prokaryot
c 992 13 22.8 573 12 ADH13015 ADH13015 Francisel
c 993 13 22.8 574 4 AA117086 AA117086 Probe #70
c 994 13 22.8 574 4 ABA61432 ABA61432 Human foe
c 995 13 22.8 574 4 AA141342 AA141342 Probe #10
c 996 13 22.8 574 4 ABA29187 ABA29187 Probe #76
c 997 13 22.8 574 4 AAK35625 AAK35625 Human bon
c 998 13 22.8 574 4 AAK09732 AAK09732 Human bra
c 999 13 22.8 574 4 ABS35348 ABS35348 Human liv
1000 13 22.8 574 6 ABS09919 ABS09919 Human gen

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## ALIGNMENTS

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RESULT 1
ADR48523
ID ADR48523 standard; DNA; 57 BP.
XX
AC ADR48523;
XX
DT 04-NOV-2004 (first entry)
XX
DE paga target sequence #1.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; paga; capB;
KW pXO1; pXO2; target sequence; ds.
XX
OS Bacillus anthracis.
XX
FN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PE 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX
PR 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX
DR WPI; 2004-604428/58.
XX
XX New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthracis
PT infections.
XX
PS Claim 1; SEQ ID NO 21; 61bp; English.
XX

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CC The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from paga and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXO1 and pXO2, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a paga
CC target sequence.
CC
SQ Sequence 57 BP; 14 A; 13 C; 16 G; 14 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 13; Length 57;
Best Local Similarity 100.0%; Pred. No. 3.1e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCAATGAGG 57
Db 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCAATGAGG 57
RESULT 2
AAD29116
ID AAD29116 standard; DNA; 774 BP.
XX
AC AAD29116;
XX
DT 07-MAY-2002 (first entry)
XX
DE Bacillus subtilis protective antigen (PA) domain 1 DNA.
XX
KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT 1..774 /*tag= a
FT /product= "Domain 1"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200204646-A1.
XX
PD 17-JAN-2002.
XX
PE 06-JUL-2001; 2001WO-GB003065.
XX
PF 06-JUL-2001; 2001WO-GB003065.
XX
PR 08-JUL-2000; 2000GB-00016702.
XX
PA (MINA ) UK SEC FOR DEFENCE.
XX
PI Williamson ED, Miller J, Walker ND, Baillie LMW, Holden PT;
PI Flick-Smith HC, Bullfeint HL, Tiddall RW, Topping AW;
XX
DR WPI; 2002-171720/22.
XX
DR P-PSDB; AAE18284.
XX
PT New immunogenic reagent having a polypeptide of the full length
PT Protective Antigen of Bacillus anthracis, useful for treating B.
PT anthracis infection or in preparing a medicament for the prophylaxis or
PT treatment of the infection.
XX
PS Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
CC an immune response that is protective against Bacillus anthracis. The
CC reagent comprises one or more polypeptides which together represent up to
CC three domains of the full length Protective Antigen (PA) of Bacillus
CC anthracis or variants of these, and at least one of the domains comprises

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CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
CC vaccine. The immunogenic reagent is useful in the preparation of a  
CC medicament for the prophylaxis or treatment of B. anthracis infection.  
CC The present sequence is Bacillus subtilis protective antigen domain 1 DNA  
XX  
SQ Sequence 774 BP; 288 A; 125 C; 146 G; 215 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 57; DB 6; Length 774;  
Best Local Similarity 100.0%; Pred. No. 3,4e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 565  
  
RESULT 3  
AAD29118  
ID AAD29118 standard; DNA; 954 BP.  
XX  
AC AAD29118;  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Bacillus subtilis protective antigen (PA) domain 1b+2 DNA.  
XX  
KM Immunogenic reagent; immune response; protective antigen; PA; vaccine;  
KM Bacillus anthracis infection; antibacterial; ds.  
XX  
OS Bacillus subtilis.  
XX  
FH Key Location/Qualifiers  
FT 1. .954  
FT CDS /tag= a  
FT /product= "Domain 1b+2"  
FT /note= "CDS does not include start and stop codon"  
FT /partial  
XX  
XX WO200204646-A1.  
XX  
XX 17-JAN-2002.  
XX  
XX PD  
XX PE 06-JUL-2001; 2001WO-GB003065.  
XX  
XX PR 08-JUL-2000; 2000GB-00016702.  
XX  
XX PA (MINA ) UK SEC FOR DEFENCE.  
XX  
XX PI Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;  
XX Flick-Smith HC, Bullifent HU, Tibball RW, Topping AW;  
XX  
XX WPI; 2002-171720/22.  
XX P-PSDB; AAE18286.  
XX  
PT New immunogenic reagent having a polypeptide of the full length  
PT Protective Antigen of Bacillus anthracis, useful for treating B.  
PT anthracis infection or in preparing a medicament for the prophylaxis or  
PT treatment of the infection.  
XX  
XX  
XX Example 5; Fig 3; 40pp; English.  
XX  
CC The present invention relates to an immunogenic reagent, which produces  
CC an immune response that is protective against Bacillus anthracis. The  
CC reagent comprises one or more polypeptides which together represent up to  
CC three domains of the full length Protective Antigen (PA) of Bacillus  
CC anthracis or variants of these, and at least one of the domains comprises  
CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
CC vaccine. The immunogenic reagent is useful in the preparation of a  
CC medicament for the prophylaxis or treatment of B. anthracis infection.  
CC The present sequence is Bacillus subtilis protective antigen domain 1b+2  
CC DNA  
XX  
SQ Sequence 954 BP; 351 A; 163 C; 192 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 6; Length 954;  
Best Local Similarity 100.0%; Pred. No. 3,4e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 57  
Db 2 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 58  
  
RESULT 4  
ADR48535  
ID ADR48535 standard; DNA; 1108 BP.  
XX  
AC ADR48535;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE pagA target sequence #5.  
XX  
KM Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
KM pX01; pX02; target sequence; ds.  
XX  
OS Bacillus anthracis.  
XX  
PN WO2004070001-A2.  
XX  
PD 19-AUG-2004.  
XX  
PE 12-NOV-2003; 2003WO-US036240.  
XX  
PR 15-NOV-2002; 2002US-0426552P.  
PR 16-MAY-2003; 2003US-0471082P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Norman SA, Bungo JI, Hogan JI, Weisburg WG;  
XX  
XX WPI; 2004-604428/58.  
XX  
XX DR  
XX PT New oligonucleotides that hybridize specifically to a Bacillus anthracis  
XX PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax  
XX PT infections.  
XX  
XX PS Claim 21; SEQ ID NO 33; 61pp; English.  
XX  
XX CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
XX CC that specifically hybridises to a sequence contained in a Bacillus  
XX CC anthracis target sequence. The methods and compositions of the present  
XX CC invention are useful for detecting the presence of Bacillus anthracis  
XX CC nucleic acid in a sample, in particular for detecting cutaneous and  
XX CC respiratory anthrax infections. Two synthetic genetic target sequences,  
XX CC derived from pagA and capB gene sequences, were synthesized to provide  
XX CC known standards for testing oligonucleotides for detection of the genes  
XX CC carried by the plasmids pX01 and pX02, without requiring handling of  
XX CC virulent Bacillus anthracis. The present sequence represents a pagA  
XX CC target sequence.  
XX  
SQ Sequence 1108 BP; 409 A; 188 C; 224 G; 287 T; 0 U; 0 Other;  
  
Query Match 100.0%; Score 57; DB 13; Length 1108;  
Best Local Similarity 100.0%; Pred. No. 3,4e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 57  
Db 7 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAGATCCCTGATTCAATTAGAGG 63  
  
RESULT 5  
AAD29119  
ID AAD29119 standard; DNA; 1278 BP.  
XX



KM	Antigen; Bacillus anthracis infection; antibacterial; vaccine;
KM	protective antigen; PA; de.
XX	
OS	Bacillus anthracis.
PN	M02005068493-AI.
XX	
PD	28-JUL-2005.
PF	17-JAN-2005; 2005MO-GB000170.
PR	17-JAN-2004; 2004GB-00001036.
PA	(UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.
PI	Cutting SW;
DR	WPI; 2005-563956/57.
XX	
PT	New non-pathogenic spore comprising an antigenic fragment of anthrax protective antigen, useful as an anthrax vaccine or for manufacturing an anthrax vaccine.
PS	Claim 5; SEQ ID NO 10; 90pp; English.
XX	
CC	The present invention relates to a non-pathogenic spore comprising an antigenic fragment of anthrax protective antigen. Also given is a pharmaceutical composition comprising a non-pathogenic spore comprising at least an antigenic fragment of anthrax protective antigen in association with a pharmaceutical carrier and/or excipient; and methods of inducing immunity to anthrax in a mammal susceptible to anthrax infection. The Bacillus species spore is a spore from many species such as Bacillus alvei; Bacillus pasteurii; Bacillus brevis and preferably a spore from Bacillus subtilis. The spore comprises an antigenic fragment of anthrax protective antigen in the form of a protein attached to the proteinaceous coat of the spore. It comprises an antigenic fragment of anthrax protective antigen encoded in the form of DNA which is adapted to be expressed when the spore germinates. The antigenic fragment is one or more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the protective antigen which has a sequence of SEQ ID NO: 4; and Domain DIB23 which is a sequence of SEQ ID NO: 10. The composition further comprises an adjuvant that potentiates an antigen-specific immune response. The composition (including the spore) is useful as an anthrax vaccine or for manufacturing an anthrax vaccine. The composition and method are used for inducing an immune response against anthrax. The present sequence is DNA encoding anthrax protective antigen domain DIB23.
SQ	Sequence 1281 BP; 492 A; 210 C; 244 G; 335 T; 0 U; 0 Other;
Query Match	100.0%; Score 57; DB 14; Length 1281;
Best Local Similarity	100.0%; Pred. No. 3.4e-23;
Matches	57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 GTGGCTGGAACCTACCGGTTCAGACCGTGATCATGTAATCCTGATTCTTAGAG 57
Dd	8 GTGCTGGAGCTTACGCTTCAGACCGTGATCATGTAATCCTGATTCTTAGAG 64
RESULT 7	
AAD29117	ID
AAID29117	standard; DNA; 1461 BP.
XX	
AC	AAID29117;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	Bacillus subtilis protective antigen (PA) domain 1+2 DNA.
XX	
KX	Immunogenic reagent; immune response; protective antigen; PA; Vaccine;



KM	Bacillus anthracis infection; antibacterial; ds.
OS	Bacillus subtilis.
XX	
FH	Key Location/Qualifiers
FT	1..1461
PT	/tag=a
FT	/product= "Domain 1+2"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	
PN	WO200204646-A1.
XX	
PD	17-JAN-2002.
XX	
PF	06-JUL-2001; 2001WO-GB003065.
XX	
PR	08-JUL-2000; 2000GB-00016702.
XX	
PA	(MINA ) UK SEC FOR DEFENCE.
XX	
PI	Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
PI	Flick-Smith HC, Bullifent HL, Tibball RW, Topping AM;
XX	
DR	WPI; 2002-171720/22.
DR	P-PSTD; AAE18285.
XX	
PT	New immunogenic reagent having a polypeptide of the full length
PT	Protective Antigen of Bacillus anthracis, useful for treating B.
PT	anthracis infection or in preparing a medicament for the prophylaxis or
PT	treatment of the infection.
XX	
PS	Example 5; Fig 3; 40pp; English.
XX	
CC	The present invention relates to an immunogenic reagent, which produces
CC	an immune response that is protective against Bacillus anthracis. The
CC	reagent comprises one or more polypeptides which together represent up to
CC	three domains of the full length Protective Antigen (PA) of Bacillus
CC	anthracis or variants of these, and at least one of the domains comprises
CC	domain 1 or domain 4 of PA or its variant. The invention is used as a
CC	vaccine. The immunogenic reagent is useful in the preparation of a
CC	medicament for the prophylaxis or treatment of B. anthracis infection.
CC	The present sequence is Bacillus subtilis protective antigen domain 1+2
CC	DNA
XX	
SQ	Sequence 1461 BP; 548 A; 238 C; 280 G; 395 T; 0 U; 0 Other;
	Query Match 100.0%; Score 57; DB 6; Length 1461;
	Best Local Similarity 100.0%; Pred. No. 3.4e-23;
	Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0
OY	1 GTGCTGCAGCCTTACGGTTCCAGACCCTGCACAATGAATGAAATCCCTGATTATTAGAAGG 57       
DB	509 GTGTGCAGCACTTACGGTTCCAGACCCTGCACAATGAATGAAATCCCTGATTATTAGAAGG 565
RESULT 8	
ADZ51325	
ID	ADZ51325 standard; DNA; 1704 BP.
XX	
AC	ADZ51325;
XX	
DT	30-JUN-2005 (first entry)
XX	
DE	Nucleotide sequence of a PA63 gene fragment.
XX	
KM	protective antigen protein; PA63; PA83; antibacterial; vaccine;
KM	prophylactic immunization; anthrax infection; gene; ds.
XX	
OS	Bacillus anthracis.
XX	
Key	Location/Qualifiers
FT	CDS 1..1704

```

FT      /*tag= a
FT      /partial
FT      /product= "PA63 fragment"
FT      /transl_except= (pos:475..477, aa:Xaa)
FT      /note= "Xaa represents Asn, Phe, Ile, Gly"
FT
XX
XX      WO2005034841-A2.
XX
XX      21-APR-2005.
XX
XX      13-MAY-2004; 2004WO-US014971.
XX
XX      14-MAY-2003; 2003US-0470563P.
XX
XX      (MERI ) MERCK & CO INC.
XX
XX      Hepler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L,
XX
XX      WPI; 2005-306231/31.
XX      P-PSDB; AD251326.
XX
XX      Producing recombinant Bacillus anthracis Protective Antigen protein
XX      encoded by an expression vector having a nucleotide sequence being codon-
XX      optimized for expression in yeast, useful for manufacturing anthrax
XX      vaccines.
XX
XX      Example 1; SEQ ID NO 47; 91pp; English.
XX
XX      The specification describes a method for producing recombinant Bacillus
XX      anthracis protective antigen protein. The method comprises providing an
XX      expression vector having a polynucleotide encoding a Bacillus anthracis
XX      protective antigen protein which is codon-optimized for expression in
XX      yeast, transforming a yeast with the vector, fermenting the transformed
XX      yeast for the expression of the protein, and isolating the protein. The
XX      protective antigen protein is PA63 or PA83. The method of the invention
XX      is useful for the produce of antigen protein, which is used for
XX      prophylactic immunization against anthrax infections. The present
XX      sequence encodes a PA63 fragment.
XX
XX      Sequence 1704 BP; 663 A; 248 C; 328 G; 465 T; 0 U; 0 Other;
XX
XX      Query Match      100.0%; Score 57; DB 14; Length 1704;
XX      Best Local Similarity 100.0%; Pred. No. 3,4e-23;
XX      Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX      1 GTGCTGGAACCTACCGTTCCAGACCGGTGACATATGTGAAATCCCTGATTCAATTAGAG 57
XX      |||||||
XX      8 GTGCTGGAACCTACCGTTCCAGACCGGTGACATATGTGAAATCCCTGATTCAATTAGAG 64
XX
XX
XX      RESULT 9
XX      ID ABB63720 standard; DNA; 1707 BP.
XX
XX      ABB63720;
XX      AC
XX      XX
XX      06-OCT-2005 (first entry)
XX
XX      DNA encoding anthrax protective antigen PA63.
XX
XX      Antigen; bacillus anthracis infection; antibacterial; vaccine;
XX      protective antigen; PA; de.
XX
XX      Bacillus anthracis.
XX      OS
XX      WO2005068493-A1.
XX      PV
XX      28-JUL-2005.
XX
XX      17-JAN-2005; 2005WO-GB000170.
XX      PF
XX      17-JAN-2004; 2004GB-00001036.
XX      PR

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PA (UNIL0 ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX  
XX Cutting SM;  
XX  
XX WPI: 2005-563956/57.  
XX  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
XX Disclosure; SEQ ID NO 8; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus badus; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain Db23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen PA63.  
XX  
XX Sequence 1707 BP; 665 A; 248 C; 327 G; 467 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 57; DB 14; Length 1707;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 57  
Db 8 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 64

RESULT 10  
AAZ56877  
ID AAZ56877 standard; DNA; 1710 BP.  
XX  
XX AAZ56877;  
XX  
XX 25-APR-2000 (first entry)  
XX  
XX B. anthracis PA63 protein encoding DNA.  
XX  
XX  
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
XX Bacillus anthracis.  
XX  
XX  
XX Key Location/Qualifiers  
FT 1. .1710  
FT /\*tag= a  
FT /product= "MAT-PA protein"  
XX  
XX MO200002522-A2.  
XX  
XX PD 20-JAN-2000.

PF 09-JUL-1999; 99MO-US015568.  
XX  
XX 10-JUL-1998; 98US-0092416P.  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
XX Lee US, Pushko P, Parker MD, Smith JF, Welkoe SL;  
PI  
XX WPI: 2000-182165/16.  
XX  
XX P-PSDB; AAY56961.  
XX  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
PT host cells for analyzing the drugs and agents inhibiting anthrax.  
XX  
XX Disclosure; Page 35; 35pp; English.  
XX  
XX The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis PA63 protein encoding DNA  
XX  
XX Sequence 1710 BP; 666 A; 248 C; 329 G; 467 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 57; DB 3; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 3.4e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 57  
Db 11 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 67

RESULT 11  
ADL16356  
ID ADL16356 standard; DNA; 1722 BP.  
XX  
XX ADL16356;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX pBP111 vector DNA for expression of 64kDa PA deletion mutant (PA64).  
XX  
XX  
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;  
KW lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.  
XX  
XX Bacillus anthracis.  
XX  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FT 1. .1722  
FT /\*tag= a  
FT /product= "PA deletion mutant protein (PA64)"  
FT /partial  
FT /note= "No start codon"  
XX  
XX US2004028695-A1.  
XX  
XX 12-FEB-2004.  
XX  
XX 28-MAR-2003; 2003US-00402466.  
XX  
XX 12-APR-2002; 2002US-0372152P.  
XX  
XX (PARK/) PARK S.  
XX (GIRI/) GIRI L.  
XX  
XX PA



```

XX XX Park S, Gari L,
PI XX
XX XX WPI, 2004-16865/16.
DR XX
XX XX P-PSDB; ADL16357.
PT XX
XX XX Immunogenic composition for preparing a vaccine against a lethal
PT infection of Bacillus anthracis in an animal, comprises an immunizing
PT amount of a recombinant B. anthracis protective antigen protein and/or
PT lethal factor protein.
XX XX
XX XX Disclosure; SEQ ID NO 21; 143pp; English.
XX XX
XX XX The present invention relates to immunogenic compositions useful for
CC preparing a vaccine against a lethal infection of Bacillus anthracis in
CC an animal. The compositions comprise an immunizing amount of a
CC recombinant B. anthracis protective antigen (rPA) protein and a
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and
CC methods are useful in protecting against anthrax or lethal infections
CC caused by B. anthracis. The present sequence is pBR11 vector DNA for the
CC expression of Bacillus anthracis 64kDa N-terminal PA deletion mutant
CC (PA64). This sequence is used in the invention.
XX XX
SQ Sequence 1722 BP; 673 A; 251 C; 330 G; 468 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 12; Length 1722;
Best Local Similarity 100.0%; Pred. No. 3.4e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGACCTACGCTTCAGACCGGACAAATGATGGAATCCCTGATTCATTAGAG 57
Db 23 GTGCTGACCTACGCTTCAGACCGGACAAATGATGGAATCCCTGATTCATTAGAG 79

RESULT 12
AAD29120
ID AAD29120 standard; DNA; 1785 BP.
XX XX
AC AAD29120;
XX XX
DT 07-MAY-2002 (first entry)
XX XX
DE Bacillus subtilis protective antigen (PA) domain 1+2+3 DNA.
XX XX
KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX XX
OS Bacillus subtilis.
XX XX
FH Key Location/Qualifiers
FT CDS 1..1785
FT /tag= a
FT /product= "Domain 1+2+3"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX XX
XX XX WO200204646-A1.
XX XX
XX XX 17-JAN-2002.
XX XX
XX XX 06-JUL-2001; 2001WO-GB003065.
XX XX
XX XX 08-JUL-2000; 2000GB-00016702.
XX XX
XX XX (MINA ) UK SEC FOR DEFENCE.
XX XX
XX XX Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
PI Flick-Smith HC, Bullifent HL, Titchell RW, Topping AW;
XX XX
XX XX WPI, 2002-171720/22.
DR XX
XX XX P-PSDB; AAE18288.
PT XX
XX XX New immunogenic reagent having a polypeptide of the full length

```

```

PT Protective Antigen of Bacillus anthracis, useful for treating B.
PT anthracis infection or in preparing a medicament for the prophylaxis or
PT treatment of the infection.
XX XX
XX XX Example 5; Fig 3; 40pp; English.
XX XX
XX XX The present invention relates to an immunogenic reagent, which produces
CC an immune response that is protective against Bacillus anthracis. The
CC reagent comprises one or more polypeptides which together represent up to
CC three domains of the full length Protective Antigen (PA) of Bacillus
CC anthracis or variants of these, and at least one of the domains comprises
CC domain 1 or domain 4 of PA or its variant. The invention is used as a
CC vaccine. The immunogenic reagent is useful in the preparation of a
CC medicament for the prophylaxis or treatment of B. anthracis infection.
CC The present sequence is Bacillus subtilis protective antigen domain 1+2+3
CC DNA
XX XX
SQ Sequence 1785 BP; 686 A; 285 C; 333 G; 481 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GTGCTGACCTACGCTTCAGACCGGACAAATGATGGAATCCCTGATTCATTAGAG 57
Db 509 GTGCTGACCTACGCTTCAGACCGGACAAATGATGGAATCCCTGATTCATTAGAG 565

RESULT 13
ADZ51331
ID ADZ51331 standard; DNA; 2205 BP.
XX XX
AC ADZ51331;
XX XX
XX XX 30-JUN-2005 (first entry)
XX XX
DE Nucleotide sequence of a PA83 gene fragment.
XX XX
KW protective antigen protein; PA63; PA83; antibacterial; vaccine;
KW prophylactic immunization; anthrax infection; ss.
XX XX
OS Bacillus anthracis.
XX XX
XX XX WO2005034841-A2.
XX XX
XX XX 21-APR-2005.
XX XX
XX XX 13-MAY-2004; 2004WO-US014971.
XX XX
XX XX 14-MAY-2003; 2003US-0470563P.
XX XX
XX XX (MERI ) MERCK & CO INC.
XX XX
XX XX Hepler R, Jansen K, Kelly R, Kurtz W, Lozada MC, Schultz L;
PI WPI, 2005-306231/31.
XX XX
XX XX P-PSDB; ADZ51332.
XX XX
XX XX Producing recombinant Bacillus anthracis Protective Antigen protein
PT encoded by an expression vector having a nucleotide sequence being codon-
PT optimized for expression in yeast, useful for manufacturing anthrax
PT vaccines.
XX XX
XX XX Example 6; SEQ ID NO 53; 91pp; English.
XX XX
XX XX The specification describes a method for producing recombinant Bacillus
CC anthracis protective antigen protein. The method comprises providing an
CC expression vector having a polynucleotide encoding a Bacillus anthracis
CC protective antigen protein which is codon-optimized for expression in
CC yeast, transforming a yeast with the vector, fermenting the transformed
CC yeast for the expression of the protein, and isolating the protein. The
CC protective antigen protein is PA63 or PA83. The method of the invention
CC is useful for the produce of antigen protein, which is used for

```



CC Prophylactic immunization against anthrax infections. The present  
 CC sequence encodes a PA83 fragment.  
 XX  
 SQ Sequence 2205 BP; 857 A; 322 C; 415 G; 611 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 57; DB 14; Length 2205;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 57  
 DB 509 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 565  
 RESULT 14  
 AAD29121  
 ID AAD29121 standard; DNA; 2208 BP.  
 XX  
 AC AAD29121;  
 XX  
 DT 07-MAY-2002 (first entry)  
 XX  
 DE Bacillus subtilis protective antigen (PA) domain 1+2+3+4 DNA.  
 XX  
 KM Immunogenic reagent; immune response; protective antigen; PA; vaccine;  
 KM Bacillus anthracis infection; antibacterial; ds.  
 XX  
 OS Bacillus subtilis.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..2208  
 FT CDS /tag= a  
 FT /product= "Domain 1+2+3+4"  
 FT /transl\_except= (pos:853..855, aa:Gln)  
 FT /note= "CDS does not include start codon"  
 FT /partial  
 XX  
 PN WO200204646-A1.  
 PD 17-JAN-2002.  
 XX  
 PF 06-JUL-2001; 2001WO-GB003065.  
 XX  
 PR 08-JUL-2000; 2000GB-00016702.  
 XX  
 PA (MUNA ) UK SEC FOR DEFENCE.  
 XX  
 PI Williamsen BD, Miller J, Walker NU, Baillie LMJ, Holden PT;  
 PI Flick-Smith HC, Bullfeint HL, Tidball RW, Topping AW;  
 XX  
 XX WPI: 2002-171720/22.  
 DR P-PSDB; AAE18289.  
 XX  
 XX New immunogenic reagent having a polypeptide of the full length  
 PT Protective Antigen of Bacillus anthracis, useful for treating B.  
 PT anthracis infection or in preparing a medicament for the prophylaxis or  
 PT treatment of the infection.  
 XX  
 PS Example 5; Fig 3; 40pp; English.  
 XX  
 XX The present invention relates to an immunogenic reagent, which produces  
 CC an immune response that is protective against Bacillus anthracis. The  
 CC reagent comprises one or more polypeptides which together represent up to  
 CC three domains of the full length Protective Antigen (PA) of Bacillus  
 CC anthracis or variants of these, and at least one of the domains comprises  
 CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
 CC vaccine. The immunogenic reagent is useful in the preparation of a  
 CC medicament for the prophylaxis or treatment of B. anthracis infection.  
 CC The present sequence is Bacillus subtilis protective antigen domain  
 CC 1+2+3+4 DNA  
 XX  
 SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 6; Length 2208;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 57  
 DB 509 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 565  
 RESULT 15  
 AAI99904  
 ID AAI99904 standard; DNA; 2208 BP.  
 XX  
 AC AAI99904;  
 XX  
 DT 01-FEB-2002 (first entry)  
 XX  
 DE Anthrax PA encoding polynucleotide.  
 XX  
 KM Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;  
 KM B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; ds.  
 XX  
 OS Bacillus anthracis.  
 XX  
 XX Key Location/Qualifiers  
 FH 1..2211  
 FT CDS /tag= a  
 FT /product= "PA"  
 FT  
 XX  
 PN WO200182788-A2.  
 PD 08-NOV-2001.  
 XX  
 PF 04-MAY-2001; 2001WO-US014372.  
 XX  
 PR 04-MAY-2000; 2000US-0201800P.  
 XX  
 PA (HARD ) HARVARD COLLEGE.  
 XX  
 PI Collier RJ, Selman BR;  
 XX  
 DR WPI: 2002-017725/02.  
 DR P-PSDB; AAM51483.  
 XX  
 XX Protecting humans against anthrax using mutant B groups (anthrax  
 PT protective antigens) of the pore-forming binary A-B toxin of Bacillus  
 PT anthracis.  
 XX  
 PS Disclosure; Fig 14; 77pp; English.  
 XX  
 XX The invention relates to antibacterial agents comprising mutant forms of  
 CC pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants  
 CC in the B moiety of the pore-forming binary A-B anthrax toxin, where the B  
 CC moiety is anthrax protective antigen (PA) and using these mutants or  
 CC compositions of them for protecting against Bacillus anthracis infections  
 CC in humans, especially as vaccines. The present sequence is that of the  
 CC anthrax PA encoding DNA  
 XX  
 SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 57; DB 6; Length 2208;  
 Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 57  
 DB 509 GTGCTGACCTACGCTTCAGACCGGTGACATGATGGAATCCCTGATTCTTAGAG 565  
 RESULT 16  
 ADL16343  
 ID ADL16343 standard; DNA; 2208 BP.  
 XX



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AC ADL16343;
XX
XX
DT 06-MAY-2004 (first entry)
XX
XX Bacillus anthracis wild-type rPA DNA #1.
DE
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
XX Bacillus anthracis.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..2208
FT /*tag= a
FT /product= "rPA protein"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX PD 12-FEB-2004.
XX
XX PF 28-MAR-2003; 2003US-00402466.
XX
XX PR 12-APR-2002; 2002US-0372152P.
XX
XX PA (PARK/) PARK S.
XX PA (GIRI/) GIRI L.
XX
XX PI Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16344.
XX
XX PT Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX PS Disclosure; SEQ ID NO 8; 143bp; English.
XX
XX CC The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunising amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis wild-
XX type rPA DNA used in the invention.
XX
XX SQ Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 57; DB 12; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-23;
XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57
XX 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 565
XX
XX RESULT 17
XX ADL16346
XX ID ADL16346 standard; DNA; 2208 BP.
XX
XX AC ADL16346;
XX
XX XX 06-MAY-2004 (first entry)
XX
XX DE Bacillus anthracis PA DNA from PBPI05 vector.
XX
XX KM Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX lethal factor; LF; anthrax; antibacterial; gene; ds.
XX

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XX
XX OS Bacillus anthracis.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2208
XX FT /*tag= a
XX FT /product= "PA protein"
XX FT /partial
XX FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX PD 12-FEB-2004.
XX
XX PF 28-MAR-2003; 2003US-00402466.
XX
XX PR 12-APR-2002; 2002US-0372152P.
XX
XX PA (PARK/) PARK S.
XX PA (GIRI/) GIRI L.
XX
XX PI Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16348.
XX
XX PT Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX PS Disclosure; SEQ ID NO 11; 143bp; English.
XX
XX CC The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunising amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis PA DNA
XX from PBPI05 vector used in the invention.
XX
XX SQ Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 57; DB 12; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 3.5e-23;
XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57
XX 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 565
XX
XX RESULT 18
XX ADM05484
XX ID ADM05484 standard; DNA; 2208 BP.
XX
XX AC ADM05484;
XX
XX DT 07-APR-2005 (first entry)
XX
XX DE B. anthracis wild-type protective antigen, DNA.
XX
XX KM Protein engineering; Bacillus anthracis infection; protective antigen;
XX toxin; bacterial infection; vaccine; antibacterial; ds; gene.
XX
XX OS Bacillus anthracis.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2208
XX FT /*tag= a
XX FT /product= "Protective antigen"
XX FT /partial
XX

```



/note= "No start codon shown"

FT XX MO2005004791-A2.  
PN XX  
XX 20-JAN-2005.  
PD XX  
XX 10-NOV-2003; 2003WO-US035733.  
PF XX  
XX 08-NOV-2002; 2002US-0424987P.  
PR XX  
XX (HARD ) HARVARD COLLEGE.  
PA (UTOK-) UNIV OKLAHOMA.  
XX  
XX  
PI Collier RJ, Ballard JD, Tweten R, Mourez M;  
PI WPI: 2005-091963/10.  
DR P-PSDB; ADM05483.  
XX  
XX New B moiety of pore-forming binary A-B toxin or its fragment, where the  
PT moiety has a mutation that inhibits its pore-forming ability, useful for  
PT preventing or treating bacterial infection, e.g. anthrax.  
XX  
XX Disclosure; SEQ ID NO 22; 129pp; English.  
XX  
XX The invention relates to a B moiety of pore-forming binary A-B toxin or  
CC its fragment, where the moiety has a mutation that inhibits its pore-  
CC forming ability and is selected from S382, N399, and N422 of the Bacillus  
CC anthracis protective antigen (PA) appearing as ADM05483. Also included  
CC are a vaccine composition comprising the mutant B moiety or its fragment  
CC (and a carrier), preventing or treating a bacterial infection in a mammal  
CC by administering the vaccine to the mammal, a nucleic acid encoding the  
CC mutant B moiety, a vector comprising the nucleic acid and a purified  
CC antibody that specifically binds a B moiety, but fails to bind a  
CC naturally occurring B moiety. The B moiety is selected from Clostridium  
CC difficile, C. perfringens, C. spiroforme, C. botulinum, and Bacillus  
CC cereus. The mutation inhibits the pore-forming ability of the toxin in  
CC vivo. The B moiety and vaccine composition are useful for preventing or  
CC treating a bacterial infection, e.g. anthrax. The present sequence  
CC encodes the wild-type PA protein.  
XX  
XX Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 57; DB 14; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 57  
DB 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 565

RESULT 19  
AEB63729  
ID AEB63729 standard; DNA; 2208 BP.  
XX  
XX AEB63729;  
AC  
XX  
XX 06-OCT-2005 (first entry)  
DT  
XX  
XX DNA encoding anthrax protective antigen, PA83.  
DB  
XX  
XX Antigen; bacillus anthracis infection; antibacterial; vaccine;  
KW protective antigen; PA; ds; gene.  
XX  
XX Bacillus anthracis.  
OS  
XX  
XX MO2005068493-A1.  
PN  
XX  
XX 28-JUL-2005.  
PD  
XX  
XX 17-JAN-2005; 2005WO-GB000170.  
PF  
XX  
XX 17-JAN-2004; 2004GB-00001036.  
PR

XX  
XX (UNIO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
PA  
XX  
XX Cutting SM;  
PI  
XX  
XX WPI: 2005-563956/57.  
DR  
XX  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
XX Disclosure; SEQ ID NO 17; 90pp; English.  
XX  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus badus; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain 1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen, PA83.  
XX  
XX Sequence 2208 BP; 859 A; 321 C; 414 G; 614 T; 0 U; 0 Other;  
SQ  
Query Match 100.0%; Score 57; DB 14; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 57  
DB 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCATTAGAG 565

RESULT 20  
AAZ56875  
ID AAZ56875 standard; DNA; 2211 BP.  
XX  
XX AAZ56875;  
AC  
XX  
XX 25-APR-2000 (first entry)  
DT  
XX  
XX B. anthracis MAT-PA protein encoding DNA.  
DB  
XX  
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
XX Bacillus anthracis.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1. .2211  
FT CDS /\*cag= a  
FT /product= "MAT-PA protein"  
XX  
XX MO200002522-A2.  
PN  
XX  
XX 20-JAN-2000.  
PD



XX 09-JUL-1999; 99WO-US015568.  
XX 10-JUL-1998; 98US-0092416P.  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX WPI; 2000-182165/16.  
XX P-PSDB; AAY56959.  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX Disclosure; Page 34; 35pp; English.  
XX The invention provides a recombinant DNA construct that comprises a  
XX vector and at least one nucleic acid (or its fragment) encoding a  
XX combination of Bacillus anthracis proteins, selected from protective  
XX antigen (PA), Maf-PA (PA with its secretory signals removed), TPA-PA (PA  
XX with its secretory signals replaced with those of tissue plasminogen  
XX activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
XX for anthrax and in producing infectious alpha virus particles. These  
XX particles, expressing the B. anthracis proteins are useful also as  
XX vaccines for anthrax. Host cells transformed with the construct are  
XX useful for analyzing the effectiveness of drugs and agents that inhibit  
XX anthrax or B. anthracis proteins. The present sequence represents a B.  
XX anthracis Maf-PA protein encoding DNA  
SQ Sequence 2211 BP; 860 A; 322 C; 416 G; 613 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 3; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTGACCTTAACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 57  
DB 512 GTGCTGACCTTAACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 568

RESULT 21  
ADY84835  
ID ADY84835 standard; DNA; 2211 BP.  
AC ADY84835;  
XX 02-JUN-2005 (first entry)  
DT Bacillus anthracis protective antigen coding sequence.  
XX Bacillus anthracis infection; vaccine; antibacterial; protective antigen;  
XX gene; ds.  
XX Bacillus anthracis.  
OS  
XX Key Location/Qualifiers  
XX CDS 1..2211  
XX /\*tag= a  
XX /product= "Protective antigen"  
XX WO2005026203-A2.  
XX 24-MAR-2005.  
XX 20-SEP-2004; 2004WO-US030616.  
XX 18-SEP-2003; 2003US-0504504P.  
XX 18-SEP-2003; 2003US-0504505P.  
XX (USNA ) US SEC OF NAVY.  
XX Kopecko DJ, Osorio M, Bhattacharya S, Giri CP, Blake M;

XX WPI; 2005-233481/24.  
XX New attenuated bacterium capable of expressing a heterologous protein,  
XX which is under the control of a promoter, useful as a vaccine against  
XX Bacillus anthracis infection, or for treating Bacillus anthracis  
XX infection.  
XX Claim 10; SEQ ID NO 9; 83pp; English.  
XX The invention provides an attenuated bacterium which is capable of  
XX expressing a heterologous protein. The expression of the heterologous  
XX protein is under the control of a promoter selected from 8 fully defined  
XX sequences ADY84827-ADY84834. The attenuated bacterium is preferably  
XX Salmonella typhi or Salmonella typhimurium. The heterologous protein  
XX comprises an antigenic sequence derived from a virus, bacterium, fungus,  
XX yeast or parasite, and is especially a protective antigen (PA) of  
XX Bacillus anthracis. A claimed live attenuated vaccine for immunization  
XX against anthrax comprises an attenuated galactose epimerase-less mutant  
XX strain of S. typhi (e.g. strain Ty21a) carrying a Bacillus anthracis PA,  
XX especially a wild-type PA or its immunogenic fragment. The PA is  
XX preferably encoded by a low-copy plasmid such as pG82. The plasmid  
XX promotes expression of the PA by a n1rb promoter or by a Sec signal  
XX sequence. The vaccine is used in a claimed method of immunizing a  
XX susceptible host against B. anthracis disease. The present sequence is  
XX the B. anthracis PA coding sequence (wild-type).  
SQ Sequence 2211 BP; 860 A; 323 C; 415 G; 613 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 14; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GTGCTGACCTTAACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 57  
DB 512 GTGCTGACCTTAACGGTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 568

RESULT 22  
ADY96726  
ID ADY96726 standard; DNA; 2220 BP.  
AC ADY96726;  
XX 24-FEB-2005 (first entry)  
DT Gene of the invention SEQ ID NO:12.  
XX antineoplastic; chemotherapy; toxin; tumor; cytostatic; ds; gene.  
XX unidentified.  
OS  
XX Key Location/Qualifiers  
XX CDS 1..2220  
XX /\*tag= a  
XX CN1513878-A.  
XX 21-JUL-2004.  
XX 13-JUN-2003; 2003CN-00143142.  
XX 13-JUN-2003; 2003CN-00143142.  
XX (MIJY/) MI J.  
XX Mi J;  
XX WPI; 2004-710658/70.  
XX P-PSDB; ADY96725.  
XX Antitumour medicine containing recombinant bacterial toxin protein  
XX complex substance.



XX PS Claim 2; SEQ ID NO 12; 29pp; Chinese.  
XX CC The invention relates to a novel antineoplastic medicine containing the  
CC recombinant bacteriotoxin protein composition TPCB whose key components  
CC are recombinant proteins I93 and LPI4. Under the action of a particular  
CC enzyme generated by tumor cells, the non-toxic protein can be changed  
CC into toxic protein to directly kill tumor cells specifically. The present  
CC sequence encodes a protein of the invention.  
XX SQ Sequence 2220 BP; 860 A; 326 C; 419 G; 615 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 13; Length 2220;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 57  
DB 521 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 577  
RESULT 23  
AAZ56876 ID AAZ56876 standard; DNA; 2292 BP.  
XX AC AAZ56876;  
XX AC AAZ56876;  
XX DT 25-APR-2000 (first entry)  
XX DB B. anthracis TPA-PA protein encoding DNA.  
XX KM Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
XX KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX OS Bacillus anthracis.  
XX FH Key Location/Qualifiers  
FT CDS 1..2292  
FT /\*tag= a  
FT /product= "TPA-PA protein"  
XX PN WO200002522-A2.  
XX PD 20-JAN-2000.  
XX PF 09-JUL-1999; 99WO-US015568.  
XX PR 10-JUL-1998; 98US-0092416P.  
XX PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX PI Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX DR WPI: 2000-182165/16.  
XX DR P-PSDB; AAY56960.  
XX PT Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX PS Disclosure; Page 32; 35pp; English.  
XX CC The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis TPA-PA protein encoding DNA

XX SQ Sequence 2292 BP; 874 A; 337 C; 446 G; 635 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 3; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 57  
DB 593 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 649  
RESULT 24  
AAZ56874 ID AAZ56874 standard; DNA; 2295 BP.  
XX AC AAZ56874;  
XX AC AAZ56874;  
XX DT 25-APR-2000 (first entry)  
XX DB B. anthracis protective antigen (PA) protein encoding DNA.  
XX KM Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
XX KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX OS Bacillus anthracis.  
XX FH Key Location/Qualifiers  
FT CDS 1..2295  
FT /\*tag= a  
FT /product= "PA protein"  
XX PN WO200002522-A2.  
XX PD 20-JAN-2000.  
XX PF 09-JUL-1999; 99WO-US015568.  
XX PR 10-JUL-1998; 98US-0092416P.  
XX PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX PI Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX DR WPI: 2000-182165/16.  
XX DR P-PSDB; AAY56958.  
XX PT Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX PS Disclosure; Page 33; 35pp; English.  
XX CC The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis PA protein encoding DNA  
XX SQ Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 3; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 3.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCAATTAGAG 57  
|||||



Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 25

AAC6016  
ID AAC6016 standard; CDNA; 2295 BP.

AC AAC6016;

DT 29-AUG-2001 (first entry)

XX Wild type B. anthracis protective antigen coding sequence.

XX Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine;

KM humoral; cell-mediated; immune memory response; ss.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT sig\_peptide

FT

FT mat\_peptide

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FT misc\_RNA

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Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 26

ADW29247  
ID ADW29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

XX B. anthracis DNA encoding protective antigen, PA.

XX Protective antigen; bacillus anthracis infection; vaccine; infection; ds;

KM antibacterial.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT CDS

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Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 26

ADW29247  
ID ADW29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

XX B. anthracis DNA encoding protective antigen, PA.

XX Protective antigen; bacillus anthracis infection; vaccine; infection; ds;

KM antibacterial.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT CDS

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Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 26

ADW29247  
ID ADW29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

XX B. anthracis DNA encoding protective antigen, PA.

XX Protective antigen; bacillus anthracis infection; vaccine; infection; ds;

KM antibacterial.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT CDS

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Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 26

ADW29247  
ID ADW29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

XX B. anthracis DNA encoding protective antigen, PA.

XX Protective antigen; bacillus anthracis infection; vaccine; infection; ds;

KM antibacterial.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT CDS

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Db 596 GTGCTGACCTACGGTTCCAGACCGTGACATGATGAATCCCTGATTATTAGAGG 652

## RESULT 26

ADW29247  
ID ADW29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

XX B. anthracis DNA encoding protective antigen, PA.

XX Protective antigen; bacillus anthracis infection; vaccine; infection; ds;

KM antibacterial.

XX Bacillus anthracis.

OS Key Location/Qualifiers

FT CDS

FT



Db 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 652

## RESULT 27

AE63728 ID AEB63728 standard; DNA; 2295 BP.

AC AEB63728;

DT 06-OCT-2005 (first entry)

DE DNA encoding full length anthrax protective antigen, PA83.

KW Antigen; bacillus anthracis infection; antibacterial; vaccine;

OS Bacillus anthracis.

PN WO2005068493-A1.

PD 28-JUL-2005.

PE 17-JAN-2005; 2005WO-GB000170.

PR 17-JAN-2004; 2004GB-00001036.

PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.

PI Cutting SM;

DR WPI, 2005-563956/57.

PT New non-pathogenic spore comprising an antigenic fragment of anthrax protective antigen, useful as an anthrax vaccine or for manufacturing an anthrax vaccine.

PS Claim 5; SEQ ID NO 16; 90pp; English.

CC The present invention relates to a non-pathogenic spore comprising an antigenic fragment of anthrax protective antigen. Also given is a pharmaceutical composition comprising a non-pathogenic spore comprising at least an antigenic fragment of anthrax protective antigen in association with a pharmaceutical carrier and/or excipient; and methods of inducing immunity to anthrax in a mammal susceptible to anthrax infection. The Bacillus species spore is a spore from many species such as Bacillus alvei; Bacillus badu; Bacillus brevis and preferably a spore from Bacillus subtilis. The spore comprises an antigenic fragment of anthrax protective antigen in the form of a protein attached to the proteinaceous coat of the spore. It comprises an antigenic fragment of anthrax protective antigen encoded in the form of DNA which is adapted to be expressed when the spore germinates. The antigenic fragment is one or more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1B23 which is a sequence of SEQ ID NO: 10. The composition further comprises an adjuvant that potentiates an antigen-specific immune response. The composition (including the spore) is useful as an anthrax vaccine or for manufacturing an anthrax vaccine. The composition and method are used for inducing an immune response against anthrax. The present sequence is DNA encoding full length anthrax protective antigen, PA83.

SO Sequence 2295 BP; 892 A; 332 C; 432 G; 639 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 14; Length 2295;

Best Local Similarity 100.0%; Pred. No. 3.5e-23; Mismatches 0; Indels 0; Gaps 0;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57

Db 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 652

## RESULT 28

ADE65871 ID ADE65871 standard; DNA; 2605 BP.

AC ADE65871;

DT 29-JAN-2004 (first entry)

DE Bacillus anthracis PA antigen encoding sequence.

KW Antibacterial; Vaccine; immune response; Bacillus anthracis; ds.

OS Bacillus anthracis.

FN Key Location/Qualifiers

FT CDS 3..2600

PN WO2003087378-A1.

PD 23-OCT-2003.

PE 11-APR-2003; 2003WO-GB001553.

PR 11-APR-2002; 2002US-0371416P.

PA (POMD-) POWDERJECT RES LTD.

PI Schmaljohn C, Fuller J;

DR WPI; 2003-877105/81.

DR P-PSDB; ADE65872.

PT New polynucleotide vaccine composition comprising a nucleic acid sequence that encodes a Bacillus anthracis antigen, useful for eliciting a protective immune response against Bacillus anthracis.

PS Example 1; SEQ ID NO 3; 65pp; English.

CC The present invention relates to a new polynucleotide vaccine composition comprising a nucleic acid sequence that encodes a Bacillus anthracis antigen and that is operatively linked to a promoter suitable for expression of the antigen in a mammalian cell. The polynucleotide vaccine composition is useful for eliciting a protective immune response against Bacillus anthracis. The present sequence represents Bacillus anthracis PA antigen encoding sequence.

SO Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 10; Length 2605;

Best Local Similarity 100.0%; Pred. No. 3.5e-23; Mismatches 0; Indels 0; Gaps 0;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57

769 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 825

## RESULT 29

AEB20797 ID AEB20797 standard; DNA; 2605 BP.

AC AEB20797;

DT 08-SEP-2005 (first entry)

DE Bacillus anthracis Protective Antigen (PA) gene, SEQ ID NO:3.

KW Nucleic acid vaccine; Bacillus anthracis infection; Protective Antigen; gene; ds.



```
XX OS Bacillus anthracis.
XX FH Location/Qualifiers
XX Key 3..2603
XX CDS
FT /tag= a
FT /partial
FT /product= "Translated sequence shown in Fig 1A-O"
FT /note= "No start or stop codon given. Xaa corresponds to
FT in-frame stop codon"
FT /transl_except= (pos:15..17,aa:Xaa)
FT /transl_except= (pos:63..65,aa:Xaa)
FT /transl_except= (pos:81..83,aa:Xaa)
FT /transl_except= (pos:141..143,aa:Xaa)
FT /transl_except= (pos:147..149,aa:Xaa)
FT /transl_except= (pos:246..248,aa:Xaa)
FT /transl_except= (pos:2481..2483,aa:Xaa)
FT /transl_except= (pos:2556..2558,aa:Xaa)
FT /transl_except= (pos:2568..2570,aa:Xaa)
FT /transl_except= (pos:2586..2588,aa:Xaa)
FT /transl_except= (pos:2598..2600,aa:Xaa)
FT /transl_except= (pos:2604..2605,aa:Pro)
FT CDS
FT /tag= c
FT /product= "Bacillus anthracis Protective Antigen"
FT sig_peptide
FT 174..245
FT /tag= b
FT mat_peptide
FT 246..2465
FT /tag= d
FT /product= "Mature Protective Antigen"
XX
XX US2005148529-A1.
XX
XX 07-JUN-2005.
XX
XX 05-JAN-2004; 2004US-00751103.
XX
XX 05-JAN-2004; 2004US-00751103.
XX
XX (POMD-) POWDERJECT VACCINES INC.
XX
XX Schmaljohn CS, Fuller JT;
XX
XX WPI; 2005-478100/48.
XX
XX P-PSDB; AEB20798; AEB20803.
XX
XX New polynucleotide vaccine composition comprising a nucleic acid sequence
XX that encodes a Bacillus anthracis antigen, useful for eliciting an immune
XX response against B. anthracis in a subject.
XX
XX Example 1; SEQ ID NO 3; 40pp; English.
XX
XX The invention relates to a polynucleotide vaccine composition comprising
XX a Bacillus anthracis antigen-encoding nucleic acid which is operatively
XX linked to a promoter for expression of the antigen in a mammalian cell.
XX The invention also relates to use of the vaccine composition of the
XX invention for eliciting an immune response in an individual. Preferably,
XX the antigen encoded by the polynucleotide vaccine is obtained or derived
XX from the Bacillus anthracis Protective Antigen (PA), a non-toxic factor
XX responsible for binding to cell membranes which is known to confer active
XX protection against anthrax. The encoded Bacillus anthracis antigen may
XX also be linked to a leader signal peptide (such as the tissue plasminogen
XX activator (TPA) signal peptide) which permits its secretion. The vaccine
XX composition may additionally comprise an adjuvant component such as a CpG
XX sequence, a nucleic acid encoding a polypeptide adjuvant, a lipid, a non-
XX protein hormone or a vitamin. The polynucleotide vaccine composition of
XX the invention can be administered directly into skin or muscle tissue,
XX preferably in particulate form, and is useful for inducing a protective
XX immune response against Bacillus anthracis infection. The present
XX sequence represents the complete nucleotide sequence encoding the
XX Bacillus anthracis Protective Antigen, used in the construction of a
XX Bacillus anthracis polynucleotide vaccine in an example of the invention.
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SQ Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 14; Length 2605;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Cy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCGATTCATTAGAG 57
Db 769 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCGATTCATTAGAG 825
RESULT 30
ID AAQ70184 standard; DNA; 2709 BP.
XX AAQ70184;
AC
XX AAQ70184;
AC
XX 25-MAR-2003 (revised)
DT 04-APR-1995 (first entry)
XX
XX PA(1-725)----Human CD4 fusion protein coding sequence.
DE
XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;
XX protective antigen; cell killing; targeting; targeting; pathogen;
XX intracellular; HIV; human immunodeficiency virus; toxin; pseudomonas;
XX exotoxin; ss.
XX Bacillus anthracis.
OS Homo sapiens.
XX
XX Key Location/Qualifiers
FT CDS
FT 1..2709
FT /tag= a
FT /product= "Anthrax fusion protein."
XX
XX W09418332-A2.
XX
XX 18-AUG-1994.
XX
XX 14-FEB-1994; 94MO-US001624.
XX
XX 12-FEB-1993; 93US-00021601.
XX 25-JUN-1993; 93US-00082849.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Leppla SH, Klimpel K, Arora N, Singh Y, Nichols PJ;
XX
XX WPI; 1994-279753/34.
XX P-PSDB; AAR60183.
XX
XX Nucleic acid encoding anthrax toxin fusion protein - useful for
XX targeting toxin to specific cells, eg for killing tumour cells or HIV-
XX infected cells.
XX
XX Disclosure; Page 97-100; 124pp; English.
XX
XX This sequence encodes a fusion protein comprising amino acid residues 1-
XX 725 of the anthrax protective antigen protein and a sequence encoding
XX residues 1-178 of human CD4, the portion which binds to gp120 on HIV
XX infected cells. Such fusion proteins may be useful for the specific
XX killing of tumour cells or the killing of cells infected with
XX intracellular pathogens, especially HIV, depending on their components.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2709 BP; 1006 A; 444 C; 551 G; 708 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 57; DB 2; Length 2709;
Best Local Similarity 100.0%; Pred. No. 3.5e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCGATTCATTAGAG 57
|||||
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OS	Bacillus anthracis.
XX	
XX	WO2004024067-A2.
XX	
PD	25-MAR-2004.
XX	
PF	10-SEP-2003; 2003WO-US028199.
XX	
PR	10-SEP-2002; 2002US-0409307P.
XX	
PR	18-OCT-2002; 2002US-0419089P.
XX	
PA	(VICA-) VICAL INC.
XX	
PI	Hermanson GG;
XX	
DR	WPI; 2004-269870/25.
DR	P-PSDB; ADL72869.
PT	Novel isolated codon-optimized polynucleotide encoding Bacillus anthracis protective antigen, useful for treating anthrax infections in vertebrate.
XX	
PS	Example 1; Page 205-209; 288bp; English.
XX	
CC	The present invention relates to codon-optimised versions of the Bacillus anthracis protective antigen coding sequence, and vectors containing such sequences. These can be used in vaccines to protect vertebrates against anthrax infection. The present sequence is a polynucleotide of the invention.
CC	
XX	
SQ	Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;
	Query Match 100.0%; Score 57; DB 12; Length 4235;
	Best Local Similarity 100.0%; Pred. No. 3.5e-23;
	Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GTGCTGACCTACGGTTCCAGACCGGTGACATGATGAAATCCCTGATTCAATGAGG 57
DB	2399 GTGCTGACCTACGGTTCCAGACCGGTGACATGATGAAATCCCTGATTCAATGAGG 2455
RESULT 34	
ADL16342	
ID	ADL16342 standard; DNA; 8198 BP.
XX	
AC	ADL16342;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	pBP103 expression vector DNA for expression of rPA.
XX	
KW	Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX	
KW	lethal factor; LF; anthrax; antibacterial; ds.
XX	
OS	Unidentified.
XX	
PN	US2004028695-A1.
XX	
PD	12-FEB-2004.
XX	
PF	28-MAR-2003; 2003US-00402466.
XX	
PR	12-APR-2002; 2002US-0372152P.
XX	
PA	(PARK/) PARK S.
XX	
PA	(GIRI/) GIRI L.
XX	
PI	Park S, Giri L;
XX	
DR	WPI; 2004-168865/16.
XX	

Immunogenic composition for preparing a vaccine against a lethal infection of Bacillus anthracis in an animal, comprises an immunizing amount of a recombinant B. anthracis protective antigen protein and/or

PT	lethal factor protein.
XX	
PS	Disclosure; SEQ ID NO 7; 143pp; English.
XX	
CC	The present invention relates to immunogenic compositions useful for
CC	preparing a vaccine against a lethal infection of <i>Bacillus anthracis</i> in
CC	an animal. The compositions comprise an immunizing amount of a
CC	recombinant <i>B. anthracis</i> protective antigen (rPA) protein and a
CC	recombinant <i>B. anthracis</i> lethal factor (rLF) protein. The composition and
CC	methods are useful in protecting against anthrax or lethal infections
CC	caused by <i>B. anthracis</i> . The present sequence is pBP103 expression vector
CC	DNA for the expression of rPA used in the invention.
XX	
SQ	Sequence 8198 BP; 2786 A; 1349 C; 1776 G; 2287 T; 0 U; 0 Other;
XX	
Query Match	100.0%; Score 57; DB 12; Length 8198;
Best Local Similarity	100.0%; Pred. No. 3.6e-23;
Matches	57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy	1 GTGCTGACCTCAGCGTTCAGACCGTGACATGATGCGTGCATTGAGG 57
Db	4243 GTGCTGACCTCAGCGTTCAGACCGTGACATGATGCGTGCATTGAGG 4299
XX	
RESULT 35	
ID	ADL16345
XX	ADL16345 standard; DNA; 9286 BP.
AC	ADL16345;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	pBP105 expression vector DNA for expression of rPA and LF30.
XX	
KM	Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX	lethal factor; LF; anthrax; antibacterial; gene; ds.
OS	<i>Bacillus anthracis</i> .
XX	Unidentified.
XX	
PH	Key
FT	CDS
XX	
FT	Location/Qualifiers
FT	3735..5942
FT	/*tag= a
FT	/product= "LF30 protein"
FT	/partial
FT	/note= "No start codon"
FT	6391..7161
FT	/*tag= b
FT	/product= "rPA protein"
FT	/partial
FT	/note= "No start codon"
XX	
PN	US2004028695-A1.
XX	
PD	12-FEB-2004.
XX	
PE	28-MAR-2003; 2003US-00402466.
XX	
PR	12-APR-2002; 2002US-0372152P.
XX	
PA	(PARK/) PARK S.
XX	(GIRI/) GIRI L.
XX	
PI	Park S, Giri L;
XX	
WI	WPI; 2004-168865/16.
XX	
DR	P-PSDB; ADL16339, ADL16344.
XX	
PT	Immunogenic composition for preparing a vaccine against a lethal
XX	infection of <i>Bacillus anthracis</i> in an animal, comprises an immunizing
XX	amount of a recombinant <i>B. anthracis</i> protective antigen protein and/or
XX	lethal factor protein.



PS Disclosure; SEQ ID NO 10; 143bp; English.

CC The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunising amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is pBR105 expression vector  
CC DNA for the expression of *Bacillus anthracis* rPA and LF30 used in the  
CC invention.

XX Sequence 9286 BP; 3228 A; 1474 C; 1973 G; 2611 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 57; DB 12; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 3.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GTGCTGACCTACGCTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 57  
DB 4243 GTGCTGACCTACGCTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 4239

RESULT 36  
AAQ70189  
ID AAQ70189 standard; DNA; 2160 BP.  
XX  
AC AAQ70189;  
XX  
DT 25-MAR-2003 (revised)  
DT 04-APR-1995 (first entry)  
XX  
DE Sequence encoding modified protective antigen of *Bacillus anthracis*.  
XX  
KW Anthrax; *Bacillus anthracis*; fusion protein; lethal factor;  
KW protective antigen; cell killing; targeting; pathogen;  
KW intracellular; HIV; human immunodeficiency virus; toxin; ss.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT 1..2160  
FT /\*tag= a  
FT /product= "Modified anthrax protective antigen."  
XX  
PN WO9418332-A2.  
XX  
PD 18-AUG-1994.  
XX  
PF 14-FEB-1994; 94WO-US001624.  
XX  
PR 12-FEB-1993; 93US-00021601.  
PR 25-JUN-1993; 93US-00082849.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
PI Leppia SH, Kimpel K, Arora N, Singh Y, Nichols PJ,  
XX WPI; 1994-279753/34.  
DR P-PSDB; AAR60193.  
XX  
XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
PT infected cells.  
XX  
XX Example 6; Page 111-113; 124pp; English.  
XX  
CC The sequence encoding the protective antigen of *Bacillus anthracis* may be  
CC used in the construction of a nucleic acid which encodes a fusion protein  
CC comprising the anthrax protective antigen binding domain of the native  
CC anthrax lethal factor and a sequence encoding an actively inducing domain  
CC of a second protein. Such fusion proteins are useful for the specific  
CC killing of tumour cells or the killing of cells infected with

CC intracellular pathogens, especially HIV, depending on the second  
CC component. The protective antigen and other toxins require proteolytic  
CC cleavage to acquire activity. Since some cells infected with an  
CC intracellular pathogen possess an active protease with quite a narrow  
CC substrate specificity e.g. HIV, the protease cleavage site found in the  
CC native toxin is replaced with an intracellular pathogen specific protease  
CC site (See AAR60184-88). The protease in cells that are infected with an  
CC intracellular pathogen cleaves the modified toxin which is then rendered  
CC active and kills the cell. This sequence encodes the *Bacillus anthracis*  
CC protective antigen but the nucleotide originally at positions 482-523  
CC have been replaced with the cassette described in AAQ70186, resulting in  
CC replacement in the corresponding protein of amino acids 162-171 with the  
CC HIV protease cleavable sequence described in AAR60186. (Updated on 25-MAR  
CC -2003 to correct PN field.)  
XX  
SQ Sequence 2160 BP; 828 A; 321 C; 408 G; 603 T; 0 U; 0 Other;  
XX

Query Match 91.2%; Score 52; DB 2; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 3e-20;  
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 GGACCTACGCTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 57  
DB 526 GGACCTACGCTTCAGACCGTGACATGATGATCCCTGATTCATTAGAG 577

RESULT 37  
ADR40459  
ID ADR40459 standard; DNA; 2235 BP.  
XX  
AC ADR40459;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE *Bacillus anthracis* protective antigen double mutant DNA seqid 3.  
XX  
KW antibacterial; vaccine; protective antigen; PA; proteolytic degradation;  
KW B. anthracis toxin; B. anthracis infection; passive immunisation;  
KW inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;  
KW gene; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT 88..2235  
FT /\*tag= a  
FT /product= "Bacillus anthracis protective antigen double  
FT mutant"  
XX  
PN US2004171121-A1.  
XX  
PD 02-SEP-2004.  
XX  
PF 08-AUG-2003; 2003US-00638006.  
XX  
PR 09-AUG-2002; 2002US-0402285P.  
XX  
PA (LEPP/) LEPPIA S H.  
PA (ROSO/) ROSOVITZ M J.  
PA (HSUS/) HSU S D.  
XX  
PI Leppia SH, Rosovitz MJ, Hsu SD;  
XX WPI; 2004-625107/60.  
DR P-PSDB; ADR40457.  
XX  
XX Novel *Bacillus anthracis* protective antigen having mutations conferring  
PT enhanced resistance to proteolytic degradation compared to wild type  
PT antigen, useful for inducing antibodies having neutralizing activity  
PT anthrax toxin.  
XX  
PS Example 5; SEQ ID NO 3; 30pp; English.



CC The present invention describes an isolated nucleic acid molecule (1)  
CC comprising the 548 base pair (bp) sequence of ADP44842, which is an  
CC internal positive control (IPC) nucleic acid molecule. Also described:  
CC, (1) a probe comprising (1) and a label; (2) an assay using the probe; (3)

Dy 15 GTTCGAGCCGTGACATGATGAATGCCATTCATTAGAG 57  
|||  
Db 28 GTTCCAGACCCTGACATGATGAATCCCATTCAATAGAG 70



```

RESULT 40
ADFA4815
ID   ADFA4815 standard; DNA; 348 BP.
XX
XX   ADFA4815;
XX
DT   12-FEB-2004 (first entry)
XX
DE   Internal positive control related fragment 5 SEQ ID NO:22.
XX
XX   Internal positive control; IPC; probe; probe-based nucleic acid; gene;
XX   ds.
XX
XX   Synthetic.
XX
XX   WO2003075837-A2.
XX
XX   18-SEP-2003.
XX
XX   03-MAR-2003; 2003WO-US006347.
XX
XX   04-MAR-2002; 2002US-0361455P.
XX
XX   (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
XX
XX   Hartman LJ, Norwood DA;
XX
XX   WPI; 2003-756781/71.
XX
XX   New nucleic acid molecule, useful as internal positive control in probe-
XX   based nucleic acid assay such as TaqMan based assay.
XX
XX   Disclosure; SEQ ID NO 22; 56bp; English.
XX
XX   The present invention describes an isolated nucleic acid molecule (1)
XX   comprising the 548 base pair (bp) sequence of ADFA4815, which is an
XX   internal positive control (IPC) nucleic acid molecule. Also described:
XX   (1) a probe comprising (1) and a label; (2) an assay using the probe; (3)
XX   a kit for a probe-based nucleic acid assay comprising the isolated
XX   nucleic acid molecule (1) packaged with instructions for use; and (4)
XX   making an IPC nucleic acid molecule for a probe-based nucleic acid
XX   molecule assay. The nucleic acid molecule (1) is useful as an IPC in
XX   probe-based nucleic acid assay such as TaqMan (RTM) based assay. The
XX   present sequence is used in the exemplification of the present invention.
XX
SQ   Sequence 348 BP; 135 A; 59 C; 64 G; 90 T; 0 U; 0 Other;
Query Match          75.4%; Score 43; DB 10; Length 348;
Best Local Similarity 100.0%; Pred. No. 5.3e-15;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY   15 GTTCGAGACCGTGACATGATGATCCCTGATTCATTAGAG 57
    |||||||
DB   163 GTTCGAGACCGTGACATGATGATCCCTGATTCATTAGAG 205

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Search completed: April 11, 2006, 16:26:05  
 Job time : 100.416 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 04:34:31 ; Search time 154.397 Seconds  
(without alignments)  
3052.864 Million cell updates/sec

Title: US-10-712-654-21

Perfect score: 57

Sequence: 1 gtctcgagactacggtccca.....aatccctgattcatagagg 57

Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 1

Total number of hits satisfying chosen parameters: 19584538

Minimum DB seq length: 0

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	57	100.0	774	6 US-10-332-282-4	Sequence 4, Appli
3	57	100.0	954	6 US-10-332-282-8	Sequence 2, Appli
4	57	100.0	1278	6 US-10-332-282-10	Sequence 10, Appli
5	57	100.0	1461	6 US-10-332-282-6	Sequence 6, Appli
6	57	100.0	1710	6 US-10-442-502-4	Sequence 4, Appli
7	57	100.0	1722	6 US-10-402-466A-21	Sequence 21, Appli
8	57	100.0	1785	6 US-10-332-282-12	Sequence 12, Appli
9	57	100.0	2208	6 US-09-848-909-22	Sequence 22, Appli
10	57	100.0	2208	6 US-10-332-282-14	Sequence 14, Appli
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C 143	15	26.3	600	9	US-10-972-079-517	Sequence 517, App	C 216	15	26.3	3107	8	US-10-800-023-35	Sequence 35, App1
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C 149	15	26.3	600	9	US-10-972-079-523	Sequence 523, App	C 222	15	26.3	5076	6	US-10-368-433-26235	Sequence 26235, App
C 150	15	26.3	601	4	US-09-925-065A-836853	Sequence 836853, App	C 223	15	26.3	5169	6	US-10-073-317-22	Sequence 22, App1
C 151	15	26.3	601	4	US-09-925-065A-836854	Sequence 836854, App	C 224	15	26.3	5169	5	US-10-073-317-28	Sequence 28, App1
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C 153	15	26.3	610	4	US-09-925-065A-800702	Sequence 800702, App	C 226	15	26.3	6204	7	US-10-381-556A-1	Sequence 1, App1
C 154	15	26.3	610	4	US-09-925-065A-800702	Sequence 800702, App	C 227	15	26.3	6420	10	US-11-097-143-10490	Sequence 10490, App
C 155	15	26.3	612	4	US-09-925-065A-672937	Sequence 672937, App	C 228	15	26.3	11439	10	US-11-097-143-18628	Sequence 18628, App
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C 157	15	26.3	616	4	US-09-925-065A-239736	Sequence 239736, App	C 230	15	26.3	34541	8	US-10-859-739-15	Sequence 15, App1
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C 159	15	26.3	622	4	US-09-925-065A-331015	Sequence 331015, App	C 232	15	26.3	35712	9	US-10-860-630-1	Sequence 1, App1
C 160	15	26.3	632	8	US-10-653-047-266	Sequence 266, App	C 233	15	26.3	35871	3	US-09-956-335-2	Sequence 2, App1
C 161	15	26.3	637	5	US-10-027-632-245916	Sequence 245916, App	C 234	15	26.3	35935	9	US-10-860-630-2	Sequence 2, App1
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C 163	15	26.3	662	4	US-09-925-065A-737928	Sequence 737928, App	C 236	15	26.3	35935	3	US-09-782-378A-5	Sequence 4, App1
C 164	15	26.3	662	4	US-09-925-065A-814582	Sequence 814582, App	C 237	15	26.3	35935	3	US-09-782-378A-5	Sequence 4, App1
C 165	15	26.3	670	4	US-09-925-065A-824827	Sequence 824827, App	C 238	15	26.3	35935	3	US-09-739-807-13	Sequence 13, App1
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C 167	15	26.3	722	8	US-10-425-115-110531	Sequence 130531, App	C 240	15	26.3	35935	7	US-10-432-989-1	Sequence 1, App1
C 168	15	26.3	744	5	US-10-027-632-24587	Sequence 24587, App	C 241	15	26.3	35935	7	US-10-433-661-1	Sequence 1, App1
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247	15	26.3	35978	3	US-09-956-335-1	Sequence 1, Appl1	320	14	24.6	383	7	US-10-424-599-127343	Sequence 127343, A
248	15	26.3	36083	9	US-10-944-496-21	Sequence 21, Appl1	321	14	24.6	393	3	US-09-880-107-1997	Sequence 1997, Ap
249	15	26.3	36620	3	US-09-952-060-30	Sequence 30, Appl1	322	14	24.6	400	3	US-09-918-595-6011	Sequence 6011, Ap
250	15	26.3	36620	7	US-10-380-641-30	Sequence 30, Appl1	323	14	24.6	415	7	US-10-424-535A-23735	Sequence 23735, A
251	15	26.3	36620	9	US-10-636-730-30	Sequence 30, Appl1	324	14	24.6	415	7	US-10-085-783A-23735	Sequence 23735, A
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253	15	26.3	37474	7	US-10-380-641-25	Sequence 25, Appl1	326	14	24.6	420	3	US-09-918-995-9565	Sequence 9565, Ap
254	15	26.3	37474	8	US-10-645-883A-7	Sequence 7, Appl1	327	14	24.6	425	3	US-09-983-965-2837	Sequence 2837, Ap
255	15	26.3	37474	8	US-10-645-187-6	Sequence 6, Appl1	328	14	24.6	426	5	US-10-027-632-286372	Sequence 286372, A
256	15	26.3	37474	9	US-10-636-730-25	Sequence 25, Appl1	329	14	24.6	426	5	US-10-027-632-286373	Sequence 286373, A
257	15	26.3	37474	9	US-10-507-098-2	Sequence 2, Appl1	330	14	24.6	426	6	US-10-027-632-286374	Sequence 286374, A
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262	15	26.3	80393	8	US-10-806-038-4	Sequence 4, Appl1	335	14	24.6	433	4	US-09-925-0658-528793	Sequence 528793, A
263	15	26.3	81098	5	US-10-087-192-2032	Sequence 2032, Ap	336	14	24.6	434	9	US-10-450-763-218	Sequence 218, App
264	15	26.3	92292	8	US-10-719-993-6838	Sequence 6838, Ap	337	14	24.6	442	3	US-09-918-995-11224	Sequence 11224, A
265	15	26.3	92563	8	US-09-997-722-70	Sequence 70, Appl1	338	14	24.6	444	8	US-10-357-930-37952	Sequence 37952, A
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268	15	26.3	158980	8	US-10-422-522-32	Sequence 32, Appl1	341	14	24.6	466	5	US-10-027-632-104060	Sequence 104060, A
269	15	26.3	160361	7	US-10-235-192A-35	Sequence 35, Appl1	342	14	24.6	466	5	US-10-027-632-323967	Sequence 323967, A
270	15	26.3	206739	9	US-10-981-277-49	Sequence 49, Appl1	343	14	24.6	466	6	US-10-027-632-104060	Sequence 104060, A
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294	14	24.6	177	3	US-09-902-941-248	Sequence 248, App	367	14	24.6	518	4	US-09-925-0658-415834	Sequence 415834, A
295	14	24.6	177	3	US-09-949-626-248	Sequence 248, App	368	14	24.6	521	4	US-09-925-0658-200411	Sequence 200411, A
296	14	24.6	177	3	US-09-476-300-248	Sequence 248, App	369	14	24.6	522	4	US-09-925-0658-195110	Sequence 195110, A
297	14	24.6	177	5	US-10-017-754-248	Sequence 248, App	370	14	24.6	522	4	US-09-925-0658-195111	Sequence 195111, A
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311	14	24.6	332	5	US-10-091-504-148	Sequence 148, App	384	14	24.6	545	4	US-09-925-0658-136677	Sequence 136677, A
312	14	24.6	332	6	US-10-227-577-148	Sequence 148, App	385	14	24.6	545	4	US-09-925-0658-346678	Sequence 346678, A
313	14	24.6	353	7	US-10-424-599-132705	Sequence 132705, A	386	14	24.6	545	4	US-09-925-0658-737102	Sequence 737102, A
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315	14	24.6	365	8	US-10-357-930-8003	Sequence 8003, Ap	388	14	24.6	549	3	US-09-991-936-1440	Sequence 1440, Ap



C 389	14	24.6	549	9	US-10-978-245-1420	Sequence 1420, App	462	14	24.6	633	4	US-09-925-065A-761829	Sequence 761829, A
C 390	14	24.6	550	3	US-09-991-936-136	Sequence 136, App	C 463	14	24.6	645	6	US-10-369-493-42779	Sequence 42779, A
C 391	14	24.6	550	4	US-09-925-065A-393261	Sequence 393261, App	464	14	24.6	649	7	US-10-437-863-79081	Sequence 79081, A
C 392	14	24.6	550	9	US-10-978-245-136	Sequence 136, App	465	14	24.6	650	5	US-10-027-632-117090	Sequence 117090, A
C 393	14	24.6	552	4	US-09-925-065A-357681	Sequence 357681, App	466	14	24.6	650	6	US-10-027-632-117090	Sequence 117090, A
C 394	14	24.6	553	4	US-09-925-065A-934707	Sequence 934707, App	467	14	24.6	656	4	US-09-925-065A-510060	Sequence 510060, A
C 395	14	24.6	556	6	US-10-029-386-1429	Sequence 1429, App	468	14	24.6	656	4	US-09-925-065A-735724	Sequence 735724, A
C 396	14	24.6	558	4	US-09-925-065A-206275	Sequence 206275, App	469	14	24.6	657	5	US-10-027-632-130334	Sequence 130334, A
C 397	14	24.6	558	7	US-10-424-599-122527	Sequence 122527, App	470	14	24.6	657	6	US-10-027-632-130334	Sequence 130334, A
C 398	14	24.6	570	4	US-09-925-065A-560657	Sequence 560657, App	C 471	14	24.6	658	4	US-09-925-065A-666653	Sequence 666653, A
C 399	14	24.6	571	4	US-09-925-065A-424618	Sequence 424618, App	C 472	14	24.6	658	5	US-10-027-632-199192	Sequence 199192, A
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C 401	14	24.6	575	5	US-10-027-632-264255	Sequence 264255, App	C 474	14	24.6	678	6	US-10-027-632-164083	Sequence 164083, A
C 402	14	24.6	575	6	US-10-027-632-264255	Sequence 264255, App	C 475	14	24.6	680	4	US-09-925-065A-895130	Sequence 895130, A
C 403	14	24.6	575	4	US-09-925-065A-415660	Sequence 415660, App	476	14	24.6	688	8	US-10-425-115-173489	Sequence 173489, A
C 404	14	24.6	577	6	US-10-029-386-1756	Sequence 4756, App	477	14	24.6	676	5	US-10-027-632-272944	Sequence 272944, A
C 405	14	24.6	580	4	US-09-925-065A-260968	Sequence 260968, App	478	14	24.6	676	6	US-10-027-632-272944	Sequence 272944, A
C 406	14	24.6	580	4	US-09-925-065A-260969	Sequence 260969, App	C 479	14	24.6	678	5	US-10-027-632-164083	Sequence 164083, A
C 407	14	24.6	582	7	US-10-021-323-947	Sequence 947, App	C 480	14	24.6	680	6	US-10-027-632-164083	Sequence 164083, A
C 408	14	24.6	584	3	US-09-864-761-8534	Sequence 8534, App	C 481	14	24.6	680	4	US-09-925-065A-895130	Sequence 895130, A
C 409	14	24.6	584	4	US-09-925-065A-248128	Sequence 248128, App	C 482	14	24.6	680	4	US-09-925-065A-916389	Sequence 916389, A
C 410	14	24.6	587	5	US-10-027-632-262329	Sequence 262329, App	C 483	14	24.6	680	4	US-10-027-632-102018	Sequence 102018, A
C 411	14	24.6	587	6	US-10-027-632-262329	Sequence 262329, App	484	14	24.6	681	5	US-10-027-632-102018	Sequence 102018, A
C 412	14	24.6	588	8	US-10-425-115-49294	Sequence 49294, A	485	14	24.6	681	5	US-10-027-632-102019	Sequence 102019, A
C 413	14	24.6	589	4	US-09-925-065A-812591	Sequence 812591, App	486	14	24.6	681	6	US-10-027-632-102018	Sequence 102018, A
C 414	14	24.6	593	5	US-10-060-036-1469	Sequence 1469, App	487	14	24.6	685	8	US-10-027-632-102019	Sequence 102019, A
C 415	14	24.6	594	4	US-09-925-065A-403092	Sequence 403092, App	488	14	24.6	685	8	US-10-027-632-102019	Sequence 102019, A
C 416	14	24.6	594	7	US-10-021-323-8169	Sequence 8169, App	C 489	14	24.6	705	8	US-10-767-795-2679	Sequence 2679, App
C 417	14	24.6	596	4	US-09-925-065A-169031	Sequence 169031, App	C 490	14	24.6	709	7	US-10-424-599-69223	Sequence 69223, A
C 418	14	24.6	596	4	US-09-925-065A-169032	Sequence 169032, App	491	14	24.6	728	9	US-10-450-763-22458	Sequence 22458, A
C 419	14	24.6	598	5	US-10-027-632-199905	Sequence 199905, App	492	14	24.6	728	9	US-10-027-632-22458	Sequence 22458, A
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C 425	14	24.6	598	6	US-10-027-632-199906	Sequence 199906, App	498	14	24.6	756	7	US-10-437-963-90193	Sequence 90193, A
C 426	14	24.6	598	6	US-10-027-632-199907	Sequence 199907, App	C 499	14	24.6	770	9	US-10-450-763-12681	Sequence 12681, A
C 427	14	24.6	598	6	US-10-027-632-199908	Sequence 199908, App	C 500	14	24.6	770	9	US-10-027-632-119500	Sequence 119500, A
C 428	14	24.6	598	6	US-10-027-632-225425	Sequence 225425, App	C 501	14	24.6	822	3	US-10-027-632-119500	Sequence 119500, A
C 429	14	24.6	600	9	US-10-972-079-5052	Sequence 5052, App	C 502	14	24.6	822	3	US-10-027-632-12006	Sequence 12006, A
C 430	14	24.6	600	9	US-10-972-079-54484	Sequence 54484, A	C 503	14	24.6	891	5	US-10-156-761-1251	Sequence 1251, A
C 431	14	24.6	600	9	US-10-972-079-76913	Sequence 76913, A	C 504	14	24.6	891	6	US-10-027-632-10918	Sequence 10918, A
C 432	14	24.6	600	9	US-10-972-079-76914	Sequence 76914, A	C 505	14	24.6	891	6	US-10-027-632-10918	Sequence 10918, A
C 433	14	24.6	600	9	US-10-972-079-77495	Sequence 77495, A	C 506	14	24.6	912	9	US-10-450-763-25071	Sequence 25071, A
C 434	14	24.6	601	4	US-09-925-065A-836335	Sequence 836335, App	C 507	14	24.6	912	9	US-10-450-763-25614	Sequence 25614, A
C 435	14	24.6	601	9	US-10-893-315-1981	Sequence 1981, App	C 508	14	24.6	912	9	US-10-450-763-25979	Sequence 25979, A
C 436	14	24.6	603	5	US-10-027-632-274038	Sequence 274038, App	C 509	14	24.6	921	7	US-10-437-963-68609	Sequence 68609, A
C 437	14	24.6	603	6	US-10-027-632-274038	Sequence 274038, App	C 510	14	24.6	948	7	US-10-282-122A-16776	Sequence 16776, A
C 438	14	24.6	607	6	US-10-027-632-197346	Sequence 197346, App	C 511	14	24.6	957	5	US-10-027-632-120131	Sequence 120131, A
C 439	14	24.6	607	6	US-10-027-632-197346	Sequence 197346, App	C 512	14	24.6	957	5	US-10-027-632-120132	Sequence 120132, A
C 440	14	24.6	608	4	US-09-925-065A-836336	Sequence 836336, App	C 513	14	24.6	957	6	US-10-027-632-120131	Sequence 120131, A
C 441	14	24.6	612	4	US-09-925-065A-530596	Sequence 530596, App	C 514	14	24.6	957	6	US-10-027-632-120132	Sequence 120132, A
C 442	14	24.6	613	4	US-09-925-065A-267245	Sequence 267245, App	C 515	14	24.6	963	3	US-09-738-626-1263	Sequence 1263, App
C 443	14	24.6	613	4	US-09-925-065A-833188	Sequence 833188, App	C 516	14	24.6	990	4	US-09-925-065A-727916	Sequence 727916, A
C 444	14	24.6	615	5	US-10-027-632-14023	Sequence 14023, A	C 517	14	24.6	993	7	US-10-282-122A-40559	Sequence 40559, A
C 445	14	24.6	615	6	US-10-027-632-14023	Sequence 14023, A	C 518	14	24.6	1003	4	US-09-925-065A-287772	Sequence 287772, A
C 446	14	24.6	619	5	US-10-027-632-86777	Sequence 86777, A	C 519	14	24.6	1008	7	US-10-437-963-67695	Sequence 67695, A
C 447	14	24.6	619	5	US-10-027-632-306501	Sequence 306501, App	C 520	14	24.6	1025	6	US-10-369-493-29619	Sequence 29619, A
C 448	14	24.6	619	6	US-10-027-632-86777	Sequence 86777, A	C 521	14	24.6	1025	6	US-10-369-493-29620	Sequence 29620, A
C 449	14	24.6	619	6	US-10-027-632-106501	Sequence 106501, App	C 522	14	24.6	1025	6	US-10-369-493-29621	Sequence 29621, A
C 450	14	24.6	624	5	US-10-027-632-210165	Sequence 210165, App	C 523	14	24.6	1028	8	US-09-814-353-130330	Sequence 130330, A
C 451	14	24.6	624	5	US-10-027-632-215972	Sequence 215972, App	C 524	14	24.6	1028	8	US-10-357-930-24830	Sequence 24830, A
C 452	14	24.6	624	5	US-10-027-632-215973	Sequence 215973, App	C 525	14	24.6	1083	3	US-09-815-242-6493	Sequence 6493, App
C 453	14	24.6	624	6	US-10-027-632-215972	Sequence 215972, App	C 526	14	24.6	1097	7	US-09-925-065A-48580	Sequence 48580, A
C 454	14	24.6	624	6	US-10-027-632-215972	Sequence 215972, App	C 527	14	24.6	1149	7	US-10-424-599-16045	Sequence 16045, A
C 455	14	24.6	625	4	US-09-925-065A-745671	Sequence 745671, App	C 528	14	24.6	1235	5	US-10-425-114-8624	Sequence 8624, App
C 456	14	24.6	625	4	US-09-925-065A-633364	Sequence 633364, App	C 529	14	24.6	1241	8	US-10-425-821-55	Sequence 821, App
C 457	14	24.6	631	4	US-09-925-065A-842003	Sequence 842003, App	C 530	14	24.6	1241	8	US-10-425-821-55	Sequence 821, App
C 458	14	24.6	631	5	US-10-027-632-265274	Sequence 265274, App	C 531	14	24.6	1260	7	US-10-469-204-84	Sequence 204, App
C 459	14	24.6	631	5	US-10-027-632-265274	Sequence 265274, App	C 532	14	24.6	1260	7	US-10-320-797-2176	Sequence 2176, App
C 460	14	24.6	631	6	US-10-027-632-265274	Sequence 265274, App	C 533	14	24.6	1291	5	US-10-027-632-151164	Sequence 151164, App
C 461	14	24.6	632	4	US-09-925-065A-415661	Sequence 415661, App	C 534	14	24.6	1291	6	US-10-027-632-151164	Sequence 151164, App



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C 536	14	24.6	1314	9	US-10-501-282-6129	Sequence 6219, Ap
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538	14	24.6	1389	7	US-10-282-122A-34580	Sequence 34580, A
539	14	24.6	1404	7	US-10-724-972A-242	Sequence 242, App
540	14	24.6	1419	7	US-10-437-963-47580	Sequence 47580, A
541	14	24.6	1440	7	US-10-424-559-18049	Sequence 18049, A
C 542	14	24.6	1454	3	US-09-965-529-59	Sequence 59, Appl
C 543	14	24.6	1454	3	US-09-969-680A-59	Sequence 59, Appl
C 544	14	24.6	1454	10	US-11-048-692-59	Sequence 59, Appl
C 545	14	24.6	1505	4	US-09-925-065A-666960	Sequence 666960, A
C 546	14	24.6	1505	4	US-09-925-065A-666961	Sequence 666961, A
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C 548	14	24.6	1552	8	US-10-425-115-11673	Sequence 11673, A
549	14	24.6	1590	7	US-10-320-797-1176	Sequence 1176, Ap
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551	14	24.6	1605	7	US-10-437-963-51039	Sequence 51039, A
552	14	24.6	1640	7	US-10-424-559-140551	Sequence 140551, A
C 553	14	24.6	1689	7	US-10-437-963-64033	Sequence 64033, A
554	14	24.6	1740	7	US-10-282-122A-16510	Sequence 16510, A
C 555	14	24.6	1780	7	US-10-424-559-56504	Sequence 56504, A
556	14	24.6	1824	6	US-10-156-761-6324	Sequence 6324, Ap
C 557	14	24.6	1825	4	US-09-925-065A-719286	Sequence 719286, A
558	14	24.6	1869	7	US-10-437-963-79325	Sequence 79325, A
559	14	24.6	1944	5	US-10-044-090-782	Sequence 782, App
C 560	14	24.6	1949	5	US-10-153-668-307	Sequence 307, App
561	14	24.6	1968	4	US-09-925-065A-48764	Sequence 48764, A
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564	14	24.6	2020	4	US-09-925-065A-707341	Sequence 707341, A
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568	14	24.6	2146	9	US-10-450-763-6819	Sequence 6819, Ap
C 569	14	24.6	2146	9	US-10-450-763-19088	Sequence 19088, A
570	14	24.6	2146	9	US-10-450-763-26764	Sequence 26764, A
571	14	24.6	2193	7	US-10-437-963-47568	Sequence 47568, A
572	14	24.6	2194	9	US-10-287-436A-1281	Sequence 1281, Ap
573	14	24.6	2194	9	US-10-287-436A-1282	Sequence 1282, Ap
C 574	14	24.6	2215	3	US-09-764-891-7534	Sequence 7534, Ap
C 575	14	24.6	2253	9	US-10-450-763-28864	Sequence 28864, A
C 576	14	24.6	2287	9	US-10-469-204-37	Sequence 37, Appl
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578	14	24.6	2288	6	US-10-117-722-836	Sequence 836, App
579	14	24.6	2288	6	US-10-122-851-836	Sequence 836, App
C 580	14	24.6	2298	8	US-10-357-930-23169	Sequence 23169, A
C 581	14	24.6	2298	8	US-10-357-930-29038	Sequence 29038, A
C 582	14	24.6	2341	4	US-09-925-065A-2567	Sequence 2567, Ap
C 583	14	24.6	2341	4	US-09-925-065A-2568	Sequence 2568, Ap
C 584	14	24.6	2341	4	US-09-925-065A-2569	Sequence 2569, Ap
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586	14	24.6	2346	9	US-10-450-763-25797	Sequence 25797, A
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588	14	24.6	2393	3	US-09-964-824A-281	Sequence 281, App
589	14	24.6	2393	3	US-10-101-510-188	Sequence 188, App
590	14	24.6	2393	8	US-10-622-377-113	Sequence 11, Appl
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C 592	14	24.6	2393	5	US-10-843-641A-5584	Sequence 5584, Ap
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594	14	24.6	2483	6	US-10-117-722-835	Sequence 835, App
595	14	24.6	2483	9	US-10-123-851-835	Sequence 835, App
596	14	24.6	2487	9	US-10-450-763-24633	Sequence 24633, A
C 597	14	24.6	2505	7	US-10-263-929-11	Sequence 11, Appl
C 598	14	24.6	2505	7	US-10-263-929-12	Sequence 12, Appl
C 599	14	24.6	2553	3	US-09-843-552-81	Sequence 81, Appl
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C 602	14	24.6	2595	6	US-10-369-493-33482	Sequence 33482, A
C 603	14	24.6	2596	7	US-10-424-559-49476	Sequence 49476, A
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C 605	14	24.6	2640	7	US-10-437-963-51139	Sequence 51139, A
C 606	14	24.6	2659	7	US-10-424-559-56750	Sequence 56750, A
C 607	14	24.6	2677	3	US-09-070-927A-518	Sequence 518, App
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C 609	14	24.6	2682	7	US-10-425-114-8803	Sequence 8803, Ap
C 610	14	24.6	2706	7	US-10-424-559-56507	Sequence 56507, A
C 611	14	24.6	2722	7	US-10-425-114-89746	Sequence 29746, A
C 612	14	24.6	2727	9	US-10-450-763-38863	Sequence 38863, A
613	14	24.6	2767	9	US-10-282-122A-31551	Sequence 31531, A
614	14	24.6	2764	9	US-10-887-553A-318	Sequence 318, App
615	14	24.6	2764	9	US-10-287-436A-325	Sequence 325, App
616	14	24.6	2764	9	US-10-287-436A-343	Sequence 343, App
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C 619	14	24.6	2808	4	US-10-450-763-24642	Sequence 24642, A
C 620	14	24.6	2815	4	US-09-925-065A-705179	Sequence 705179, A
C 621	14	24.6	2858	7	US-10-191-803-409	Sequence 409, App
C 622	14	24.6	2858	7	US-10-153-319A-2128	Sequence 2128, App
C 623	14	24.6	2858	7	US-10-664-705-18	Sequence 18, Appl
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C 625	14	24.6	2950	3	US-09-814-353-19077	Sequence 19077, A
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C 627	14	24.6	2995	10	US-11-097-143-7790	Sequence 7790, Ap
C 628	14	24.6	3030	10	US-11-097-143-28351	Sequence 28351, A
C 629	14	24.6	3068	4	US-09-925-065A-695382	Sequence 695382, A
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631	14	24.6	3150	7	US-10-282-122A-31370	Sequence 31370, A
632	14	24.6	3207	7	US-10-282-122A-13367	Sequence 13367, A
C 633	14	24.6	3215	9	US-10-450-763-24645	Sequence 24645, A
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635	14	24.6	3277	6	US-10-343-710-87	Sequence 87, Appl1
636	14	24.6	3277	8	US-10-723-860-1058	Sequence 1058, App
637	14	24.6	3293	7	US-10-276-774-853	Sequence 853, App
638	14	24.6	3421	4	US-09-925-065A-2596	Sequence 2596, Ap
C 639	14	24.6	3465	3	US-09-738-626-2264	Sequence 2264, Ap
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641	14	24.6	3532	10	US-11-097-143-4010	Sequence 4010, Ap
642	14	24.6	3561	7	US-10-437-963-51482	Sequence 51482, A
643	14	24.6	3576	10	US-11-097-143-4527	Sequence 527, App
644	14	24.6	3589	10	US-11-097-143-40156	Sequence 40156, A
645	14	24.6	3590	7	US-10-320-797-176	Sequence 176, App
C 646	14	24.6	3595	8	US-10-494-674-53	Sequence 53, Appl
647	14	24.6	3684	6	US-10-094-749-997	Sequence 997, App
C 648	14	24.6	3752	5	US-10-098-841-55	Sequence 55, Appl1
649	14	24.6	3849	6	US-10-259-194A-183	Sequence 183, App
C 650	14	24.6	3882	7	US-10-282-122A-6334	Sequence 6334, Ap
C 651	14	24.6	3903	3	US-09-815-242-3848	Sequence 3848, Ap
C 652	14	24.6	3903	3	US-09-815-242-5809	Sequence 5809, Ap
C 653	14	24.6	3974	5	US-10-087-192-1367	Sequence 1367, Ap
C 654	14	24.6	3990	6	US-10-369-493-24908	Sequence 24908, A
C 655	14	24.6	4091	8	US-10-723-860-5769	Sequence 5769, Ap
C 656	14	24.6	4097	8	US-10-723-860-5604	Sequence 5604, Ap
C 657	14	24.6	4107	9	US-10-764-420-2409	Sequence 2409, Ap
658	14	24.6	4139	10	US-11-097-143-16165	Sequence 16165, A
659	14	24.6	4178	6	US-10-101-510-407	Sequence 407, App
660	14	24.6	4190	6	US-10-388-934-253	Sequence 253, App
661	14	24.6	4260	6	US-10-369-493-45937	Sequence 45937, A
662	14	24.6	4266	7	US-10-437-963-46917	Sequence 46917, A
663	14	24.6	4433	6	US-10-450-763-19466	Sequence 19466, A
C 664	14	24.6	4532	6	US-10-101-510-372	Sequence 372, App
C 665	14	24.6	4532	10	US-11-097-143-4009	Sequence 4009, Ap
C 666	14	24.6	4722	7	US-10-424-559-56505	Sequence 56505, A
C 667	14	24.6	4850	8	US-10-357-930-47478	Sequence 24748, A
C 668	14	24.6	4887	7	US-10-398-231-1753	Sequence 3753, Ap
C 669	14	24.6	5194	3	US-09-978-343-1	Sequence 1, Appl1
670	14	24.6	5194	5	US-10-002-389-1	Sequence 1, Appl1
671	14	24.6	5194	7	US-10-672-408-1	Sequence 1, Appl1
672	14	24.6	5195	3	US-09-964-888-2	Sequence 2, Appl1
C 673	14	24.6	5373	10	US-11-097-143-7789	Sequence 7789, App
C 674	14	24.6	5722	10	US-11-097-143-526	Sequence 526, App
C 675	14	24.6	6049	7	US-10-092-900A-265	Sequence 265, App
C 676	14	24.6	6143	7	US-10-210-838-11	Sequence 11, Appl
677	14	24.6	6628	5	US-10-171-581-57	Sequence 57, Appl1
678	14	24.6	6628	5	US-10-469-780-1	Sequence 1, Appl1
679	14	24.6	6677	8	US-10-335-053-80	Sequence 80, Appl1
680	14	24.6	6929	6	US-10-017-161-723	Sequence 723, App



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C 662	14	24.6	7402	10	US-11-097-143-5197	Sequence 5197, Ap	C 755	13	22.8	25	5	US-10-098-263B-106170	Sequence 106170, A
C 663	14	24.6	7743	8	US-10-357-930-24872	Sequence 24872, A	C 756	13	22.8	25	6	US-10-376-333-12	Sequence 12, Appl
C 664	14	24.6	7743	8	US-10-357-930-25127	Sequence 25127, A	C 757	13	22.8	25	7	US-10-719-966-11395	Sequence 11395, A
C 665	14	24.6	8134	7	US-10-437-963-93461	Sequence 93461, A	C 758	13	22.8	25	7	US-10-719-966-277006	Sequence 277006, A
C 666	14	24.6	8162	7	US-10-398-221-3877	Sequence 3877, Ap	C 759	13	22.8	25	7	US-10-719-966-280937	Sequence 280937, A
C 667	14	24.6	9704	5	US-10-109-860-3	Sequence 3, Appl	C 760	13	22.8	25	7	US-10-719-956-533872	Sequence 333872, A
C 668	14	24.6	9704	10	US-11-134-474-3	Sequence 3, Appl	C 761	13	22.8	25	7	US-10-719-956-452377	Sequence 452377, A
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C 671	14	24.6	12682	8	US-10-719-993-7018	Sequence 7018, Ap	C 764	13	22.8	25	8	US-10-719-900-106529	Sequence 106529, A
C 672	14	24.6	12242	8	US-10-719-993-7000	Sequence 7000, Ap	C 765	13	22.8	25	8	US-10-719-900-106529	Sequence 106529, A
C 673	14	24.6	12810	10	US-11-097-143-6271	Sequence 6271, Ap	C 766	13	22.8	25	8	US-10-719-900-106529	Sequence 106529, A
C 674	14	24.6	19024	3	US-09-070-927A-179	Sequence 179, App	C 767	13	22.8	25	8	US-10-719-900-106529	Sequence 106529, A
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C 678	14	24.6	26064	5	US-10-087-192-1447	Sequence 1447, Ap	C 771	13	22.8	25	8	US-10-719-900-106529	Sequence 106529, A
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C 700	14	24.6	30471	5	US-10-087-192-901	Sequence 901, App	C 773	13	22.8	25	9	US-10-956-157-55564	Sequence 55564, A
C 701	14	24.6	32159	6	US-10-085-959-54	Sequence 54, Appl	C 774	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 702	14	24.6	32177	3	US-09-764-877-3251	Sequence 3251, Ap	C 775	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 703	14	24.6	32177	3	US-09-764-877-3251	Sequence 6957, Ap	C 776	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 704	14	24.6	32177	6	US-10-242-515-3251	Sequence 3251, Ap	C 777	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 705	14	24.6	32207	3	US-09-764-877-3250	Sequence 3250, Ap	C 778	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 706	14	24.6	32207	3	US-09-764-877-3250	Sequence 3250, Ap	C 779	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 707	14	24.6	32207	6	US-10-242-515-3250	Sequence 3250, Ap	C 780	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 708	14	24.6	33488	6	US-10-085-117-235	Sequence 235, App	C 781	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 709	14	24.6	35832	10	US-11-097-143-25330	Sequence 25330, A	C 782	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 710	14	24.6	39052	10	US-11-097-143-1237	Sequence 1237, Ap	C 783	13	22.8	25	9	US-10-956-157-55573	Sequence 55573, A
C 711	14	24.6	44979	6	US-10-292-798-641	Sequence 641, App	C 784	13	22.8	25	10	US-11-018-377-12	Sequence 12, Appl
C 712	14	24.6	46244	5	US-10-087-192-1795	Sequence 1795, Ap	C 785	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
C 713	14	24.6	47686	7	US-10-322-696-97	Sequence 97, Appl	C 786	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
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C 716	14	24.6	84826	5	US-10-087-192-1561	Sequence 1561, Ap	C 789	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
C 717	14	24.6	85859	5	US-10-087-192-562	Sequence 562, App	C 790	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
C 718	14	24.6	92247	5	US-10-087-192-628	Sequence 628, App	C 791	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
C 719	14	24.6	99656	9	US-10-893-315-127	Sequence 127, App	C 792	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
C 720	14	24.6	99656	9	US-10-893-315-177	Sequence 177, App	C 793	13	22.8	25	10	US-11-036-317-47273	Sequence 47273, A
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C 737	14	24.6	684187	7	US-10-367-094-71	Sequence 71, Appl	C 810	13	22.8	25	10	US-10-860-291-15	Sequence 15, Appl
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C 749	14	24.6	9025608	6	US-10-156-761-1	Sequence 1, Appl	C 822	13	22.8	25	10	US-10-860-291-15	Sequence 15, Appl
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871	13	22.8	294	5	US-10-092-154-1272	Sequence 1272, App	944	13	22.8	431	4	US-09-925-065A-765963	Sequence 765963, A
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c 882	13	22.8	326	3	US-09-814-353-3687	Sequence 3687, App	c 955	13	22.8	444	3	US-09-864-761-4991	Sequence 4991, App
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C 974	13	22.8	453	6	US-10-027-633-234643	Sequence 294643, A
C 975	13	22.8	453	8	US-10-674-124A-21727	Sequence 21727, A
C 976	13	22.8	454	3	US-09-770-44A-582	Sequence 582, App
C 977	13	22.8	456	4	US-09-925-065A-561045	Sequence 561045, A
C 978	13	22.8	456	4	US-09-925-065A-561047	Sequence 561047, A
C 979	13	22.8	456	4	US-09-925-065A-561048	Sequence 561048, A
C 980	13	22.8	457	7	US-10-332-855-59	Sequence 59, Appl
C 981	13	22.8	457	7	US-10-437-963-36334	Sequence 36334, A
C 982	13	22.8	458	2	US-08-943-607-8	Sequence 8, Appl
C 983	13	22.8	458	2	US-08-943-607-11	Sequence 11, Appl
C 984	13	22.8	458	3	US-09-957-215-8	Sequence 8, Appl
C 985	13	22.8	458	3	US-09-957-215-11	Sequence 11, Appl
C 986	13	22.8	458	7	US-10-021-321-12394	Sequence 12394, A
C 987	13	22.8	459	2	US-08-943-607-9	Sequence 9, Appl
C 988	13	22.8	459	2	US-08-943-607-10	Sequence 10, Appl
C 989	13	22.8	459	3	US-09-957-215-9	Sequence 9, Appl
C 990	13	22.8	459	3	US-09-957-215-10	Sequence 10, Appl
C 991	13	22.8	460	3	US-09-960-352-4838	Sequence 4838, App
C 992	13	22.8	460	4	US-09-925-065A-490258	Sequence 490258, A
C 993	13	22.8	463	7	US-10-242-538A-47657	Sequence 47657, A
C 994	13	22.8	463	7	US-10-083-783A-47657	Sequence 47657, A
C 995	13	22.8	465	7	US-10-242-535A-39970	Sequence 39970, A
C 996	13	22.8	465	7	US-10-085-783A-39970	Sequence 39970, A
C 997	13	22.8	466	5	US-10-027-633-275534	Sequence 275534, A
C 998	13	22.8	466	6	US-10-027-633-275534	Sequence 275534, A
C 999	13	22.8	468	7	US-10-437-963-42986	Sequence 42986, A
C 1000	13	22.8	470	7	US-10-424-599-92135	Sequence 92135, A

## ALIGNMENTS

```

RESULT 1
US-10-442-502-11
? Sequence 11, Application US/10/442502
? Publication No. US20040009945A1
? GENERAL INFORMATION:
? APPLICANT: LEE, JOHN SCOTT
? APPLICANT: PUSHKO, PETER
? APPLICANT: PARKER, MICHAEL D.
? APPLICANT: SMITH, JONATHAN F.
? APPLICANT: WELSON, SUSAN L.
? TITLE OF INVENTION: ANTHRAX VACCINES
? FILE REFERENCE: ARMY135B
? CURRENT APPLICATION NUMBER: US/10/442,502
? CURRENT FILING DATE: 2003-05-21
? PRIOR APPLICATION NUMBER: 09/350,729
? PRIOR FILING DATE: 1999-07-09
? PRIOR APPLICATION NUMBER: 60/092,416
? PRIOR FILING DATE: 1998-07-10
? NUMBER OF SEQ ID NOS: 18
? SOFTWARE: PatentIn Ver. 2.1
? SEQ ID NO 11
? LENGTH: 267
? TYPE: DNA
? ORGANISM: Bacillus anthracis
US-10-442-502-11

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Query Match	100.0%	Score 57	DB 6	Length 267
Similarity	100.0%	Pred. No. 9.4e-23		
Beet Local	57	Conservative	0	Mismatches 0
Matches	57	Indels	0	Gaps 0

  

Qy	1	GTGCTGACCTACGGTTCGAGACCGCTGACATGATGGAATCCCTTGATTCATTAGAGG	57
Qb	8	GTGCTGACCTACGGTTCGAGACCGCTGACATGATGGAATCCCTTGATTCATTAGAGG	64

RESULT 2  
US-10-332-282-4  
; Sequence 4, Application US/10332282  
; Publication No. US20030170263A1  
; GENERAL INFORMATION:

```

1  APPLICANT: The Secretary of State for Defence
2  APPLICANT: Williamson, Ethel D
3  APPLICANT: Miller, Julie
4  APPLICANT: Walker, Nicola J
5  APPLICANT: Baillie, Leslie WJ
6  APPLICANT: Holden, Paula T
7  APPLICANT: Flick-Smith, Helen C
8  APPLICANT: Bullifent, Helen L
9  APPLICANT: Titball, Richard W
10 TITLE OF INVENTION: Expression System
11 FILE REFERENCE: CG/P/110/MOD
12 CURRENT APPLICATION NUMBER: US/10/0332,282
13 CURRENT FILING DATE: 2003-01-07
14 PRIOR APPLICATION NUMBER: GB 0016702.3
15 PRIOR FILING DATE: 2000-07-08
16 NUMBER OF SEQ ID NOS: 16
17 SOFTWARE: PatentIn Ver. 2.1
18 SEQ ID NO 4
19 LENGTH: 774
20 TYPE: DNA
21 ORGANISM: Artificial Sequence
22 FEATURE:
23 OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
24 OTHER INFORMATION: used to encode SEQ ID NO: 3
25 US-10-332-282-4

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Query Match	100.0%;	Score 57;	DB 6;	Length 774;
Best Local Similarity	100.0%;	Pred. No. 9.5e-23;		
Matches 57;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy 1 GTGCTGGACCTACCGTTCCAGACCCTGGACAATGATGAATCCTTGATTCAATTAGAG 57  
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |  
Db 509 GTGCTGGACCTACCGTTCCAGACCCTGGACAATGATGAATCCTTGATTCAATTAGAG 565

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/ RESULT 3
/ US-10-332-282-8
/ Sequence 8, Application US/10332282
/ Publication No. US20030170263A1
/ GENERAL INFORMATION:
/ APPLICANT: The Secretary of State for Defence
/ APPLICANT: Williamson, Ethel D
/ APPLICANT: Miller, Julie
/ APPLICANT: Walker, Nicola J
/ APPLICANT: Baillie, Leslie WJ
/ APPLICANT: Holden, Paula T
/ APPLICANT: Flick-Smith, Helen C
/ APPLICANT: Bullifent, Helen L
/ APPLICANT: Tibball, Richard W
/ TITLE OF INVENTION: Expression System
/ FILE REFERENCE: CG/P/110/MOD
/ CURRENT APPLICATION NUMBER: US/10/332,282
/ PRIOR FILING DATE: 2003-01-07
/ PRIOR APPLICATION NUMBER: GB 0016702.3
/ PRIOR FILING DATE: 2000-07-08
/ NUMBER OF SEQ ID NOS: 16
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 954

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; ORGANISM: Artificial Sequence
;
; FEATURE:
;
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
;
; OTHER INFORMATION: used to encode SEQ ID NO: 7
US-10-332-282-8

```

Query Match	100.0%	Score 57	DB 6	Length 954
Best Local Similarity	100.0%	Prod. No. 9.5e-23		
Matches 57	Conservative 0	Mismatches 0	Indels 0	Gaps 0
Qy	1	GTGCTGACCTACAGGTTCCAGACCGGTGACATGATGAAATCCCTGATTCATTAAAGG	57	
Db	2	GTGCTGACCTACAGGTTCCAGACCGGTGACATGATGAAATCCCTGATTCATTAAAGG	58	



RESULT 4  
US-10-332-282-10  
; Sequence 10, Application US/10332282  
; Publication No. US20030170263A1  
; GENERAL INFORMATION:  
; APPLICANT: The Secretary of State for Defence  
; APPLICANT: Williamson, Ethel D  
; APPLICANT: Miller, Julie  
; APPLICANT: Walker, Nicola J  
; APPLICANT: Baillie, Leslie WJ  
; APPLICANT: Holden, Paula T  
; APPLICANT: Flick-Smith, Helen C  
; APPLICANT: Bullifent, Helen L  
; APPLICANT: Tibball, Richard W  
; TITLE OF INVENTION: Expression System  
; FILE REFERENCE: CG/P/110/MOD  
; CURRENT APPLICATION NUMBER: US/10/332,282  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: GB 0016702.3  
; PRIOR FILING DATE: 2000-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1278  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
; OTHER INFORMATION: used to encode SEQ ID NO: 9  
US-10-332-282-10

Query Match 100.0%; Score 57; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 9.5e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
Db 2 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 58

RESULT 5  
US-10-332-282-6  
; Sequence 6, Application US/10332282  
; Publication No. US20030170263A1  
; GENERAL INFORMATION:  
; APPLICANT: The Secretary of State for Defence  
; APPLICANT: Williamson, Ethel D  
; APPLICANT: Miller, Julie  
; APPLICANT: Walker, Nicola J  
; APPLICANT: Baillie, Leslie WJ  
; APPLICANT: Holden, Paula T  
; APPLICANT: Flick-Smith, Helen C  
; APPLICANT: Bullifent, Helen L  
; APPLICANT: Tibball, Richard W  
; TITLE OF INVENTION: Expression System  
; FILE REFERENCE: CG/P/110/MOD  
; CURRENT APPLICATION NUMBER: US/10/332,282  
; PRIOR FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: GB 0016702.3  
; PRIOR FILING DATE: 2000-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 6  
; LENGTH: 1461  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
; OTHER INFORMATION: used to encode SEQ ID NO: 5  
US-10-332-282-6

Query Match 100.0%; Score 57; DB 6; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 565

RESULT 6  
US-10-442-502-4  
; Sequence 4, Application US/10442502  
; Publication No. US20040009945A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, JOHN SCOTT  
; APPLICANT: PUSHKO, PETER  
; APPLICANT: PARKER, MICHAEL D.  
; APPLICANT: SMITH, JONATHAN F.  
; APPLICANT: WELKOS, SUSAN L.  
; TITLE OF INVENTION: ANTHRAX VACCINES  
; FILE REFERENCE: ARMY135B  
; CURRENT APPLICATION NUMBER: US/10/442,502  
; PRIOR FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/350,729  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,416  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1710  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
US-10-442-502-4

Query Match 100.0%; Score 57; DB 6; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
Db 11 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 67

RESULT 7  
US-10-402-466A-21  
; Sequence 21, Application US/10402466A  
; Publication No. US20040028695A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Sukjoon  
; APPLICANT: GYI, Lailian  
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
; FILE REFERENCE: 18933-00005  
; CURRENT APPLICATION NUMBER: US/10/402,466A  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: 60/372,152  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 34  
; SEQ ID NO 21  
; LENGTH: 1722  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION:  
; OTHER INFORMATION: DNA coding sequence from pBP11 for a PA deletion mutant PA64.  
US-10-402-466A-21

Query Match 100.0%; Score 57; DB 7; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 57  
Db 23 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 79

RESULT 8  
US-10-332-282-12

/ Sequence 12, Application US/10332282  
/ Publication No. US20030170263A1  
/ GENERAL INFORMATION:  
/ APPLICANT: The Secretary of State for Defence  
/ APPLICANT: Williamson, Ethel D  
/ APPLICANT: Miller, Julie  
/ APPLICANT: Walker, Nicola J  
/ APPLICANT: Baillie, Leslie WJ  
/ APPLICANT: Holden, Paula T  
/ APPLICANT: Flick-Smith, Helen C  
/ APPLICANT: Bullifent, Helen L  
/ APPLICANT: Tibball, Richard W  
/ TITLE OF INVENTION: Expression System  
/ FILE REFERENCE: CG/P/110/MOD  
/ CURRENT APPLICATION NUMBER: US/10/332,282  
/ CURRENT FILING DATE: 2003-01-07  
/ PRIOR APPLICATION NUMBER: GB 0016702.3  
/ PRIOR FILING DATE: 2000-07-08  
/ NUMBER OF SEQ ID NOS: 16  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 12  
/ LENGTH: 1785  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
US-10-332-282-12

Query Match 100.0%; Score 57; DB 6; Length 1785;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 565

## RESULT 9

US-09-848-909-22  
/ Sequence 22, Application US/09848909  
/ Publication No. US20020039588A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Collier, R. John  
/ APPLICANT: Sellman, Brett R.  
/ TITLE OF INVENTION: Compounds and Methods for the Treatment  
/ TITLE OF INVENTION: and Prevention of Bacterial Infection  
/ FILE REFERENCE: 00742/060002  
/ CURRENT APPLICATION NUMBER: US/09/848,909  
/ CURRENT FILING DATE: 2001-05-04  
/ PRIOR APPLICATION NUMBER: US 60/201,800  
/ PRIOR FILING DATE: 2000-04-04  
/ NUMBER OF SEQ ID NOS: 35  
/ SOFTWARE: FastSeq for Windows Version 4.0  
/ SEQ ID NO 22  
/ LENGTH: 2208  
/ TYPE: DNA  
/ ORGANISM: Bacillus anthracis  
US-09-848-909-22

Query Match 100.0%; Score 57; DB 3; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 57  
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Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 565

RESULT 10  
US-10-332-282-14

/ Sequence 14, Application US/10332282  
/ Publication No. US20030170263A1  
/ GENERAL INFORMATION:  
/ APPLICANT: The Secretary of State for Defence  
/ APPLICANT: Williamson, Ethel D  
/ APPLICANT: Miller, Julie  
/ APPLICANT: Walker, Nicola J  
/ APPLICANT: Baillie, Leslie WJ  
/ APPLICANT: Holden, Paula T  
/ APPLICANT: Flick-Smith, Helen C  
/ APPLICANT: Bullifent, Helen L  
/ APPLICANT: Tibball, Richard W  
/ TITLE OF INVENTION: Expression System  
/ FILE REFERENCE: CG/P/110/MOD  
/ CURRENT APPLICATION NUMBER: US/10/332,282  
/ CURRENT FILING DATE: 2003-01-07  
/ PRIOR APPLICATION NUMBER: GB 0016702.3  
/ PRIOR FILING DATE: 2000-07-08  
/ NUMBER OF SEQ ID NOS: 16  
/ SOFTWARE: PatentIn Ver. 2.1  
/ SEQ ID NO 14  
/ LENGTH: 2208  
/ TYPE: DNA  
/ ORGANISM: Artificial Sequence  
/ FEATURE:  
/ OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
US-10-332-282-14

Query Match 100.0%; Score 57; DB 6; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 565

## RESULT 11

US-10-402-466A-8  
/ Sequence 8, Application US/10402466A  
/ Publication No. US20040028695A1  
/ GENERAL INFORMATION:  
/ APPLICANT: Park, Sukjoon  
/ APPLICANT: Giri, Laljan  
/ TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
/ TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS  
/ FILE REFERENCE: 18933-00005  
/ CURRENT APPLICATION NUMBER: US/10/402,466A  
/ CURRENT FILING DATE: 2003-03-20  
/ PRIOR APPLICATION NUMBER: 60/372,152  
/ PRIOR FILING DATE: 2002-04-12  
/ NUMBER OF SEQ ID NOS: 34  
/ SEQ ID NO 8  
/ LENGTH: 2208  
/ TYPE: DNA  
/ ORGANISM: Bacillus anthracis  
/ FEATURE:  
/ NAME/KEY: CDS  
/ LOCATION:  
/ OTHER INFORMATION: DNA coding sequence for B. anthracis PA.  
US-10-402-466A-8

Query Match 100.0%; Score 57; DB 7; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAATCCCTGATTCATTAGAG 57  
|||||



Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 565

RESULT 12  
US-10-402-466A-11  
; Sequence 11, Application US/10402466A  
; Publication No. US20040028695A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Sukjoon  
; APPLICANT: Gilil, Lailan  
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
; FILE REFERENCE: 18933-00005  
; CURRENT APPLICATION NUMBER: US/10/402,466A  
; PRIOR FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: 60/372,152  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 34  
; SEQ ID NO 11  
; LENGTH: 2208  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION:  
; OTHER INFORMATION: DNA coding sequence from pbp105 for B. anthracis PA. The DNA cod  
; OTHER INFORMATION: sequences for rPA (2208 bases) is identical to Sequence 8.  
US-10-402-466A-11

Query Match 100.0%; Score 57; DB 7; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 57  
Db 509 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 565

RESULT 13  
US-10-442-502-2  
; Sequence 2, Application US/10442502  
; Publication No. US20040009945A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, JOHN SCOTT  
; APPLICANT: PUSKHO, PETER  
; APPLICANT: PARKER, MICHAEL D.  
; APPLICANT: SMITH, JONATHAN F.  
; APPLICANT: WELKOS, SUSAN L.  
; TITLE OF INVENTION: ANTHRAX VACCINES  
; FILE REFERENCE: ARMY135B  
; CURRENT APPLICATION NUMBER: US/10/442,502  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/350,729  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,416  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 2211  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
US-10-442-502-2

Query Match 100.0%; Score 57; DB 6; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 57  
Db 512 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 568

RESULT 14  
US-10-442-502-3  
; Sequence 3, Application US/10442502  
; Publication No. US20040009945A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, JOHN SCOTT  
; APPLICANT: PUSKHO, PETER  
; APPLICANT: PARKER, MICHAEL D.  
; APPLICANT: SMITH, JONATHAN F.  
; APPLICANT: WELKOS, SUSAN L.  
; TITLE OF INVENTION: ANTHRAX VACCINES  
; FILE REFERENCE: ARMY135B  
; CURRENT APPLICATION NUMBER: US/10/442,502  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/350,729  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,416  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 2292  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
US-10-442-502-3

Query Match 100.0%; Score 57; DB 6; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 57  
Db 593 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 649

RESULT 15  
US-09-747-521-3  
; Sequence 3, Application US/09747521  
; Patent No. US20020051791A1  
; GENERAL INFORMATION:  
; APPLICANT: Galloway, Darrel  
; APPLICANT: Mateczun, Alfred  
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus  
; FILE REFERENCE: 22727/04079  
; CURRENT APPLICATION NUMBER: US/09/747,521  
; CURRENT FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 3  
; LENGTH: 2295  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2295)  
US-09-747-521-3

Query Match 100.0%; Score 57; DB 3; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;

Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 57  
Db 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGAAATCCCTGATTCAATTAGAGG 652

RESULT 16  
US-10-106-014-3  
; Sequence 3, Application US/10106014  
; Publication No. US20020142002A1  
; GENERAL INFORMATION:  
; APPLICANT: Galloway, Darrel R.  
US-10-106-014-3



```
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106,014
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-106-014-3
```

```
Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 9.6e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57
Db      596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 652
```

```
RESULT 17
US-10-105-695-3
; Sequence 3, Application US/10105695
; Publication No. US20020197272A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04115
; CURRENT APPLICATION NUMBER: US/10/105,695
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-105-695-3
```

```
Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 9.6e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57
Db      596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 652
```

```
RESULT 18
US-10-105-694-3
; Sequence 3, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; CURRENT FILING DATE: 2002-03-25
```

```
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-105-694-3
```

```
Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 9.6e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57
Db      596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 652
```

```
RESULT 19
US-10-442-502-1
; Sequence 1, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARM1135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-1
```

```
Query Match          100.0%; Score 57; DB 6; Length 2295;
Best Local Similarity 100.0%; Pred. No. 9.6e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 57
Db      596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATCCCTGATTCATTAGAGG 652
```

```
RESULT 20
US-10-751-103-3
; Sequence 3, Application US/10751103
; Publication No. US20050148529A1
; GENERAL INFORMATION:
; APPLICANT: Schmaljohn, Connie S.
; APPLICANT: Fuller, James T.
; TITLE OF INVENTION: Nucleic Acid Immunization
; FILE REFERENCE: 033267-021
; CURRENT APPLICATION NUMBER: US/10/751,103
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2605
```



TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (174)...(2465)  
US-10-751-103-3

Query Match 100.0%; Score 57; DB 9; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 9.6e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57  
Db 769 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 825

RESULT 21  
US-10-410-647-29  
Sequence 29, Application US/10410647  
Publication No. US20030235818A1  
GENERAL INFORMATION:  
APPLICANT: PLEXUS VACCINE, INC.  
APPLICANT: Katriitch, Vsevolod  
APPLICANT: Bordner, Andrew  
APPLICANT: Deans, Robert  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME  
FILE REFERENCE: PLEX1110-1  
CURRENT FILING DATE: 2003-04-08  
PRIOR FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: US 60/373,668  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 60/371,256  
PRIOR FILING DATE: 2002-04-08  
PRIOR APPLICATION NUMBER: US 60/371,250  
PRIOR FILING DATE: 2002-04-08  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 4235  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-10-410-647-29

Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 9.7e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57  
Db 2399 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 2455

RESULT 22  
US-10-402-466A-7  
Sequence 7, Application US/10402466A  
Publication No. US20040028695A1  
GENERAL INFORMATION:  
APPLICANT: Park, Sukjoon  
APPLICANT: Giri, Laljan  
TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS  
FILE REFERENCE: 18933-00005  
CURRENT FILING DATE: US/10/402,466A  
PRIOR FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: 60/372,152  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 34  
SEQ ID NO 7  
LENGTH: 8198  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:

NAME/KEY:  
LOCATION:  
OTHER INFORMATION: Expression vector for B. anthracis Protective Antigen (PA). E  
OTHER INFORMATION: sequence is shown since the vector sequence is different from  
OTHER INFORMATION: of the pBP vectors. The PA coding sequence is from 3735 to 59.  
US-10-402-466A-7

Query Match 100.0%; Score 57; DB 7; Length 8198;  
Best Local Similarity 100.0%; Pred. No. 9.7e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57  
Db 4243 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 4299

RESULT 23  
US-10-402-466A-10  
Sequence 10, Application US/10402466A  
Publication No. US20040028695A1  
GENERAL INFORMATION:  
APPLICANT: Park, Sukjoon  
APPLICANT: Giri, Laljan  
TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTIN  
TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS  
FILE REFERENCE: 18933-00005  
CURRENT FILING DATE: US/10/402,466A  
CURRENT FILING DATE: 2003-03-20  
PRIOR FILING DATE: 60/372,152  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 34  
SEQ ID NO 10  
LENGTH: 9286  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY:  
LOCATION:  
OTHER INFORMATION: Dual expression vector pBP105 for B. anthracis PA and LF30. E  
OTHER INFORMATION: sequence is shown since the vector sequence contains two codin  
OTHER INFORMATION: regions. The coding region for PA is from 3735 to 5942 and th  
OTHER INFORMATION: region for LF30 is from 6391 to 7161.  
US-10-402-466A-10

Query Match 100.0%; Score 57; DB 7; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 9.8e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57  
Db 4243 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 4299

RESULT 24  
US-10-638-006-3  
Sequence 3, Application US/10638006  
Publication No. US20040171121A1  
GENERAL INFORMATION:  
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA as  
APPLICANT: represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND  
APPLICANT: HUMAN SERVICES  
APPLICANT: Leppia, Stephen H.  
APPLICANT: Rosovitz, Mary Jo  
APPLICANT: Hau, S. Dana  
TITLE OF INVENTION: METHODS FOR PREPARING BACILLUS ANTHRACIS SPOKULANT DEFICIENT  
TITLE OF INVENTION: MUTANTS AND FOR PRODUCING RECOMBINANT BACILLUS ANTHRACIS  
TITLE OF INVENTION: PROTECTIVE ANTIGEN FOR USE IN VACCINES  
FILE REFERENCE: 4239-66891  
CURRENT FILING DATE: US/10/638,006  
CURRENT FILING DATE: 2003-08-08  
PRIOR APPLICATION NUMBER: 60/402,285  
PRIOR FILING DATE: 2002-08-09  
NUMBER OF SEQ ID NOS: 3



```
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mature double mutant protective antigen
; US-10-638-006-3

Query Match          91.2%; Score 52; DB 7; Length 2235;
Best Local Similarity 100.0%; Pred. No. 7.6e-20;
Matches 52; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 GGACTTAGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 583 GGACCTAGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 634

RESULT 25
; US-10-376-323-13
; Sequence 13, Application US/10376323
; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 225
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment 2
; US-10-376-323-13

Query Match          75.4%; Score 43; DB 6; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 13 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 55

RESULT 26
; US-11-018-377-13
; Sequence 13, Application US/11018377
; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasielecki, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 13
; LENGTH: 225

; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Fragment 2
; US-11-018-377-13

Query Match          75.4%; Score 43; DB 10; Length 225;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 13 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 55

RESULT 27
; US-10-376-323-19
; Sequence 19, Application US/10376323
; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fragment 4
; US-10-376-323-19

Query Match          75.4%; Score 43; DB 6; Length 240;
Best Local Similarity 100.0%; Pred. No. 1.2e-14;
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 28 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 70

RESULT 28
; US-11-018-377-19
; Sequence 19, Application US/11018377
; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasielecki, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 19
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
```



OTHER INFORMATION: Fragment 4  
US-11-018-377-19

Query Match 75.4%; Score 43; DB 10; Length 240;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 28 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 70

RESULT 29  
US-10-376-323-22

Sequence 22, Application US/10376323  
Publication No. US20030211527A1  
GENERAL INFORMATION:  
APPLICANT: Hartman, Laurie J.  
APPLICANT: Norwood Jr., David A.  
TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID  
FILE REFERENCE: P68364US0  
CURRENT APPLICATION NUMBER: US/10/376,323  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 60/361,455  
PRIOR FILING DATE: 2002-03-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 22  
LENGTH: 348  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment 5  
US-10-376-323-22

Query Match 75.4%; Score 43; DB 6; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 163 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 205

RESULT 30  
US-11-018-377-22

Sequence 22, Application US/11018377  
Publication No. US20050095644A1  
GENERAL INFORMATION:  
APPLICANT: U.S. Army Medical Research and Materiel Command  
APPLICANT: Hartman, Laurie J.  
APPLICANT: Norwood, David A.  
APPLICANT: Wasieleski, Leonard  
TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE  
FILE REFERENCE: 034047.023CIP1  
CURRENT APPLICATION NUMBER: US/11/018,377  
PRIOR FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: US 10/376,323  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/361,455  
PRIOR FILING DATE: 2002-03-04  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 22  
LENGTH: 348  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Fragment 5  
US-11-018-377-22

Query Match 75.4%; Score 43; DB 10; Length 348;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 163 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 205

RESULT 31  
US-10-376-323-29

Sequence 29, Application US/10376323  
Publication No. US20030211527A1  
GENERAL INFORMATION:  
APPLICANT: Hartman, Laurie J.  
APPLICANT: Norwood Jr., David A.  
TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID  
FILE REFERENCE: P68364US0  
CURRENT APPLICATION NUMBER: US/10/376,323  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: 60/361,455  
PRIOR FILING DATE: 2002-03-04  
NUMBER OF SEQ ID NOS: 88  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 29  
LENGTH: 415  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: Fragment 7  
US-10-376-323-29

Query Match 75.4%; Score 43; DB 6; Length 415;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 118 GTTCGAGCCGTGACATGATGGAATCCCTGATTCATTAGAG 160

RESULT 32  
US-11-018-377-29

Sequence 29, Application US/11018377  
Publication No. US20050095644A1  
GENERAL INFORMATION:  
APPLICANT: U.S. Army Medical Research and Materiel Command  
APPLICANT: Hartman, Laurie J.  
APPLICANT: Norwood, David A.  
APPLICANT: Wasieleski, Leonard  
TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE  
FILE REFERENCE: 034047.023CIP1  
CURRENT APPLICATION NUMBER: US/11/018,377  
PRIOR FILING DATE: 2004-12-22  
PRIOR APPLICATION NUMBER: US 10/376,323  
PRIOR FILING DATE: 2003-03-03  
PRIOR APPLICATION NUMBER: US 60/361,455  
PRIOR FILING DATE: 2002-03-04  
NUMBER OF SEQ ID NOS: 91  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 29  
LENGTH: 415  
TYPE: DNA  
ORGANISM: Artificial  
FEATURE:  
OTHER INFORMATION: Fragment 7  
US-11-018-377-29

Query Match 75.4%; Score 43; DB 10; Length 415;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 15 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 118 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 160

RESULT 33  
US-10-376-323-35  
; Sequence 35, Application US/10376323  
; Publication No. US20030211527A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Laurie J.  
; APPLICANT: Norwood Jr., David A.  
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID  
; FILE REFERENCE: P68364US0  
; CURRENT APPLICATION NUMBER: US/10/376,323  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 60/361,455  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 427  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Fragment 9  
US-10-376-323-35

Query Match 75.4%; Score 43; DB 6; Length 427;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57  
Db 130 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 172

RESULT 34  
US-11-018-377-35  
; Sequence 35, Application US/11018377  
; Publication No. US20050095644A1  
; GENERAL INFORMATION:  
; APPLICANT: U.S. Army Medical Research and Materiel Command  
; APPLICANT: Hartman, Laurie J.  
; APPLICANT: Norwood, David A.  
; APPLICANT: Masiejowski, Leonard  
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE  
; FILE REFERENCE: 034047.023CIP1  
; CURRENT APPLICATION NUMBER: US/11/018,377  
; PRIOR FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/376,323  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/361,455  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 91  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO 35  
; LENGTH: 427  
; TYPE: DNA  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fragment 9  
US-11-018-377-35

Query Match 75.4%; Score 43; DB 10; Length 427;  
Best Local Similarity 100.0%; Pred. No. 1.2e-14;  
Matches 43; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 130 GTTCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 172

RESULT 35  
US-10-376-323-23  
; Sequence 23, Application US/10376323  
; Publication No. US20030211527A1  
; GENERAL INFORMATION:  
; APPLICANT: Hartman, Laurie J.  
; APPLICANT: Norwood Jr., David A.  
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID  
; FILE REFERENCE: P68364US0  
; CURRENT APPLICATION NUMBER: US/10/376,323  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: 60/361,455  
; PRIOR FILING DATE: 2002-03-04  
; NUMBER OF SEQ ID NOS: 88  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 23  
; LENGTH: 521  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Clone 11  
US-10-376-323-23

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; Sequence 23, Application US/11018377  
; Publication No. US20050095644A1  
; GENERAL INFORMATION:  
; APPLICANT: U.S. Army Medical Research and Materiel Command  
; APPLICANT: Hartman, Laurie J.  
; APPLICANT: Norwood, David A.  
; APPLICANT: Masiejowski, Leonard  
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE  
; FILE REFERENCE: 034047.023CIP1  
; CURRENT APPLICATION NUMBER: US/11/018,377  
; PRIOR FILING DATE: 2004-12-22  
; PRIOR APPLICATION NUMBER: US 10/376,323  
; PRIOR FILING DATE: 2003-03-03  
; PRIOR APPLICATION NUMBER: US 60/361,455  
; PRIOR FILING DATE: 2002-03-04  
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; SOFTWARE: PatentIn version 3.3  
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; TYPE: DNA  
; ORGANISM: Artificial  
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; OTHER INFORMATION: Clone 11  
US-11-018-377-23

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RESULT 37
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; Sequence 36, Application US/10376323
; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
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; TYPE: DNA
; ORGANISM: Artificial Sequence
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; OTHER INFORMATION: Description of Artificial Sequence: Clone 7
US-10-376-323-36

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; Sequence 36, Application US/11018377
; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasieleski, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
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; FEATURE:
; OTHER INFORMATION: Clone 7
US-11-018-377-36

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; Sequence 1, Application US/10376323
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; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 88
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US-10-376-323-1

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; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasieleski, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 91
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Minimum DB seq length: 0

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C 130	14	24.6	470	10	US-10-301-480-470999	Sequence 470999,	C 203	14	24.6	570	6	US-09-925-065A-560657	Sequence 560657,
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134	14	24.6	471	10	US-10-301-480-1043890	Sequence 1043890,	C 207	14	24.6	572	10	US-10-301-480-481353	Sequence 481353,
135	14	24.6	471	10	US-10-301-480-1043890	Sequence 1043890,	208	14	24.6	575	9	US-10-301-480-1094761	Sequence 1094761,
136	14	24.6	476	6	US-09-925-065A-359303	Sequence 359303,	209	14	24.6	575	10	US-10-301-480-712489	Sequence 712489,
137	14	24.6	476	6	US-09-925-065A-359304	Sequence 359304,	C 210	14	24.6	576	6	US-09-925-065A-415660	Sequence 415660,
C 138	14	24.6	479	6	US-09-925-065A-648564	Sequence 648564,	211	14	24.6	576	10	US-10-301-480-339296	Sequence 339296,
C 139	14	24.6	480	6	US-09-925-065A-403987	Sequence 403987,	212	14	24.6	576	10	US-10-301-480-339297	Sequence 339297,
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141	14	24.6	486	9	US-10-932-182A-5793	Sequence 5793, Ap	214	14	24.6	576	10	US-10-301-480-952706	Sequence 952706,
C 142	14	24.6	491	10	US-10-301-480-164649	Sequence 364649,	C 215	14	24.6	577	10	US-10-301-480-69526	Sequence 69526, A
C 143	14	24.6	491	10	US-10-301-480-164650	Sequence 364650,	C 216	14	24.6	577	10	US-10-301-480-682935	Sequence 682935,
C 144	14	24.6	491	10	US-10-301-480-164651	Sequence 364651,	217	14	24.6	580	6	US-09-925-065A-260968	Sequence 260968,
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C 147	14	24.6	491	10	US-10-301-480-978060	Sequence 978060,	C 220	14	24.6	581	9	US-10-301-480-53596	Sequence 53596, A
C 148	14	24.6	497	6	US-09-925-065A-542366	Sequence 542366,	C 221	14	24.6	581	9	US-10-301-480-53597	Sequence 53597, A
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C 151	14	24.6	497	9	US-10-301-480-93305	Sequence 93305, A	C 224	14	24.6	581	10	US-10-301-480-667004	Sequence 667004,
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161	14	24.6	520	10	US-10-301-480-697730	Sequence 697730,	234	14	24.6	590	10	US-10-301-480-874432	Sequence 874432,
162	14	24.6	521	6	US-09-925-065A-200411	Sequence 200411,	235	14	24.6	590	10	US-10-301-480-874433	Sequence 874433,
163	14	24.6	522	6	US-09-925-065A-195110	Sequence 195110,	236	14	24.6	590	10	US-10-301-480-874433	Sequence 874433,
164	14	24.6	522	6	US-09-925-065A-195111	Sequence 195111,	237	14	24.6	592	9	US-10-301-480-18125	Sequence 18125, A



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C 248	14	24.6	612	6	US-09-925-065A-530596	Sequence 530596, A	C 321	14	24.6	1911	8	US-10-750-623-16629	Sequence 16629, A
C 249	14	24.6	613	6	US-09-925-065A-267245	Sequence 267245, A	C 322	14	24.6	1911	8	US-10-750-623-16629	Sequence 16629, A
C 250	14	24.6	613	6	US-09-925-065A-833188	Sequence 833188, A	C 323	14	24.6	1968	6	US-09-925-065A-48764	Sequence 48764, A
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C 256	14	24.6	630	10	US-10-301-480-345027	Sequence 345027, A	329	14	24.6	2031	8	US-10-750-623-29466	Sequence 29466, A
C 257	14	24.6	630	10	US-10-301-480-958436	Sequence 958436, A	C 330	14	24.6	2180	8	US-10-750-185-48791	Sequence 48791, A
C 258	14	24.6	631	6	US-09-925-065A-633364	Sequence 633364, A	C 331	14	24.6	2180	8	US-10-750-623-48791	Sequence 48791, A
C 260	14	24.6	631	6	US-09-925-065A-842003	Sequence 842003, A	C 332	14	24.6	2304	11	US-11-079-463-2970	Sequence 2970, Ap
C 261	14	24.6	631	10	US-10-301-480-100101	Sequence 100101, A	C 333	14	24.6	2341	6	US-09-925-065A-2567	Sequence 2567, Ap
C 262	14	24.6	632	6	US-09-925-065A-713510	Sequence 713510, A	C 334	14	24.6	2341	6	US-09-925-065A-2568	Sequence 2568, Ap
C 263	14	24.6	632	10	US-10-301-480-481353	Sequence 481353, A	C 335	14	24.6	2341	6	US-09-925-065A-2569	Sequence 2569, Ap
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C 266	14	24.6	643	9	US-10-301-480-53159	Sequence 53159, A	C 338	14	24.6	2341	9	US-10-301-480-103805	Sequence 103805, A
C 267	14	24.6	643	10	US-10-301-480-666568	Sequence 666568, A	C 339	14	24.6	2341	9	US-10-301-480-103806	Sequence 103806, A
C 268	14	24.6	656	6	US-09-925-065A-510060	Sequence 510060, A	C 340	14	24.6	2341	9	US-10-301-480-103807	Sequence 103807, A
C 269	14	24.6	656	6	US-09-925-065A-735724	Sequence 735724, A	C 341	14	24.6	2341	10	US-10-301-480-717213	Sequence 717213, A
C 270	14	24.6	659	6	US-09-925-065A-668653	Sequence 668653, A	C 342	14	24.6	2341	10	US-10-301-480-717214	Sequence 717214, A
C 271	14	24.6	672	9	US-10-932-182A-4780	Sequence 4780, Ap	C 343	14	24.6	2341	10	US-10-301-480-717215	Sequence 717215, A
C 272	14	24.6	672	9	US-10-932-182A-4780	Sequence 4780, Ap	C 344	14	24.6	2341	10	US-10-301-480-717216	Sequence 717216, A
C 273	14	24.6	680	6	US-09-925-065A-895130	Sequence 895130, A	C 345	14	24.6	2373	6	US-09-925-065A-669662	Sequence 669662, A
C 274	14	24.6	680	6	US-09-925-065A-895131	Sequence 895131, A	C 346	14	24.6	2474	8	US-10-750-185-43359	Sequence 43359, A
C 275	14	24.6	680	6	US-09-925-065A-916389	Sequence 916389, A	C 347	14	24.6	2474	8	US-10-750-185-43359	Sequence 43359, A
C 276	14	24.6	861	11	US-11-079-463-1940	Sequence 1940, Ap	C 348	14	24.6	2481	8	US-10-750-185-46552	Sequence 46552, A
C 277	14	24.6	878	8	US-10-750-185-62784	Sequence 62784, A	C 349	14	24.6	2481	8	US-10-750-623-46552	Sequence 46552, A
C 278	14	24.6	878	8	US-10-750-623-62784	Sequence 62784, A	C 350	14	24.6	2513	8	US-10-750-185-56860	Sequence 56860, A
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C 280	14	24.6	980	10	US-10-301-480-121383	Sequence 121383, A	C 352	14	24.6	2544	8	US-10-750-185-44237	Sequence 44237, A
C 281	14	24.6	990	6	US-09-925-065A-727916	Sequence 727916, A	C 353	14	24.6	2544	8	US-10-750-623-44237	Sequence 44237, A
C 282	14	24.6	999	10	US-10-301-480-541365	Sequence 541365, A	C 354	14	24.6	2815	6	US-09-925-065A-705179	Sequence 705179, A
C 283	14	24.6	999	10	US-10-301-480-1154774	Sequence 1154774, A	C 355	14	24.6	2821	11	US-11-096-568A-31422	Sequence 31422, A
C 284	14	24.6	1003	6	US-09-925-065A-287772	Sequence 287772, A	C 356	14	24.6	2821	11	US-11-096-568A-31422	Sequence 31422, A
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287	14	24.6	1097	10	US-10-301-480-763227	Sequence 763227, A	C 359	14	24.6	2934	9	US-10-932-182A-683	Sequence 683, App
C 288	14	24.6	1131	9	US-10-301-480-44028	Sequence 44028, A	C 360	14	24.6	3068	6	US-09-925-065A-693382	Sequence 693382, A
C 289	14	24.6	1131	10	US-10-301-480-647437	Sequence 647437, A	C 361	14	24.6	3123	8	US-10-750-185-31501	Sequence 31501, A
C 290	14	24.6	1148	9	US-10-301-480-398823	Sequence 398823, A	C 362	14	24.6	3123	8	US-10-750-623-31501	Sequence 31501, A
C 291	14	24.6	1148	9	US-10-301-480-398823	Sequence 398823, A	C 363	14	24.6	3421	6	US-09-925-065A-2596	Sequence 2596, Ap
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C 293	14	24.6	1148	10	US-10-301-480-653331	Sequence 653331, A	365	14	24.6	3421	10	US-10-301-480-717242	Sequence 717242, A
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C 295	14	24.6	1148	10	US-10-301-480-653333	Sequence 653333, A	C 367	14	24.6	4018	8	US-10-750-185-16840	Sequence 26840, A
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C 297	14	24.6	1191	8	US-10-750-185-33585	Sequence 33585, A	C 369	14	24.6	4703	14	US-11-136-527-3140	Sequence 3140, Ap
C 298	14	24.6	1191	8	US-10-750-623-33585	Sequence 33585, A	C 370	14	24.6	7351	14	US-11-136-527-1993	Sequence 1993, Ap
C 299	14	24.6	1221	9	US-10-540-091-15	Sequence 15, Appl	C 371	14	24.6	46854	14	US-11-124-368A-2892	Sequence 2892, Ap
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301	14	24.6	1278	9	US-10-932-182A-741	Sequence 741, App	C 373	14	24.6	98638	9	US-10-330-773-896	Sequence 86, App
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C 306	14	24.6	1505	6	US-09-925-065A-666360	Sequence 666360, A	C 378	14	24.6	153162	14	US-11-121-086-30	Sequence 30, Appl
C 307	14	24.6	1505	6	US-09-925-065A-666361	Sequence 666361, A	C 379	14	24.6	16020	14	US-11-112-908-28	Sequence 28, Appl
C 308	14	24.6	1505	6	US-10-750-185-53865	Sequence 53865, A	C 380	14	24.6	171247	14	US-11-112-908-57	Sequence 27, Appl
C 309	14	24.6	1505	8	US-10-750-623-53865	Sequence 53865, A	C 381	14	24.6	171247	11	US-11-114-798-23	Sequence 23, Appl
C 310	14	24.6	1520	8	US-10-750-185-45451	Sequence 45451, A	C 382	14	24.6	248999	9	US-10-330-773-342	Sequence 342, App
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387	13	22.8	19	12	US-11-101-244-254108	Sequence 254108, A	C 460	13	22.8	364	6	US-09-925-065A-135060	Sequence 135060, A
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389	13	22.8	19	12	US-11-101-244-952484	Sequence 952484, A	C 462	13	22.8	391	6	US-09-925-065A-581535	Sequence 581535, A
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C 391	13	22.8	19	12	US-11-101-244-1487657	Sequence 1487657, A	C 464	13	22.8	417	6	US-09-925-065A-200605	Sequence 200605, A
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C 393	13	22.8	19	13	US-11-083-784-254104	Sequence 254104, A	C 466	13	22.8	421	10	US-10-301-480-902608	Sequence 902608, A
C 394	13	22.8	19	13	US-11-083-784-254108	Sequence 254108, A	C 467	13	22.8	429	9	US-10-301-480-18616	Sequence 18616, A
C 395	13	22.8	19	13	US-11-083-784-4549702	Sequence 449702, A	C 468	13	22.8	429	9	US-10-301-480-18617	Sequence 18617, A
C 396	13	22.8	19	13	US-11-083-784-952484	Sequence 952484, A	C 469	13	22.8	429	9	US-10-301-480-632025	Sequence 632025, A
C 397	13	22.8	19	13	US-11-083-784-1009657	Sequence 1009657, A	C 470	13	22.8	429	9	US-10-301-480-632026	Sequence 632026, A
C 398	13	22.8	19	13	US-11-083-784-1487657	Sequence 1487657, A	C 471	13	22.8	431	6	US-09-925-065A-765963	Sequence 765963, A
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C 400	13	22.8	19	14	US-11-001-347-750	Sequence 750, App	C 473	13	22.8	432	6	US-09-925-065A-604130	Sequence 604130, A
C 401	13	22.8	22	8	US-10-310-914A-683647	Sequence 683647, A	C 474	13	22.8	432	6	US-09-925-065A-604131	Sequence 604131, A
C 402	13	22.8	22	8	US-10-310-914A-1360282	Sequence 1360282, A	C 475	13	22.8	445	11	US-11-116-881A-1892	Sequence 1892, App
C 403	13	22.8	23	8	US-10-310-914A-683641	Sequence 683641, A	C 476	13	22.8	451	6	US-09-925-065A-184423	Sequence 184423, A
C 404	13	22.8	25	8	US-10-310-914A-1291200	Sequence 1291200, A	C 477	13	22.8	456	6	US-09-925-065A-561045	Sequence 561045, A
C 405	13	22.8	25	9	US-10-932-182A-30043	Sequence 30043, A	C 478	13	22.8	456	6	US-09-925-065A-561047	Sequence 561047, A
C 406	13	22.8	25	9	US-10-932-182A-30043	Sequence 30043, A	C 479	13	22.8	456	6	US-09-925-065A-561048	Sequence 561048, A
C 407	13	22.8	25	9	US-10-934-048A-96585	Sequence 96585, A	C 480	13	22.8	459	9	US-10-301-480-45205	Sequence 45205, A
C 408	13	22.8	25	14	US-11-121-849-105900	Sequence 105900, A	C 481	13	22.8	459	10	US-10-301-480-658614	Sequence 658614, A
C 409	13	22.8	25	14	US-11-121-849-181271	Sequence 181271, A	C 482	13	22.8	460	6	US-09-925-065A-490258	Sequence 490258, A
C 410	13	22.8	25	14	US-11-121-849-253459	Sequence 253459, A	C 483	13	22.8	472	6	US-09-925-065A-321905	Sequence 321905, A
C 411	13	22.8	25	14	US-11-121-849-254954	Sequence 254954, A	C 484	13	22.8	474	10	US-10-301-480-396473	Sequence 396473, A
C 412	13	22.8	25	14	US-11-121-849-280213	Sequence 280213, A	C 485	13	22.8	474	10	US-10-301-480-1009882	Sequence 1009882, A
C 413	13	22.8	25	14	US-11-121-849-295946	Sequence 295946, A	C 486	13	22.8	476	9	US-10-301-480-42804	Sequence 42804, A
C 414	13	22.8	25	14	US-11-121-849-328564	Sequence 328564, A	C 487	13	22.8	476	10	US-10-301-480-656213	Sequence 656213, A
C 415	13	22.8	25	14	US-11-121-849-355657	Sequence 355657, A	C 488	13	22.8	484	6	US-09-925-065A-109775	Sequence 109775, A
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C 419	13	22.8	50	14	US-11-175-859-95550	Sequence 95550, A	C 492	13	22.8	490	10	US-10-301-480-627160	Sequence 627160, A
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C 422	13	22.8	80	8	US-10-310-914A-16934	Sequence 16934, A	C 495	13	22.8	496	11	US-09-925-065A-196327	Sequence 196327, A
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C 427	13	22.8	93	8	US-10-310-914A-210	Sequence 210, App	C 500	13	22.8	501	10	US-10-301-480-822795	Sequence 822795, A
C 428	13	22.8	93	8	US-10-310-914A-213	Sequence 213, App	C 501	13	22.8	504	6	US-09-925-065A-923939	Sequence 923939, A
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C 430	13	22.8	93	8	US-10-310-914A-4550	Sequence 4550, App	C 503	13	22.8	505	6	US-09-925-065A-800805	Sequence 800805, A
C 431	13	22.8	93	8	US-10-310-914A-5015	Sequence 5015, App	C 504	13	22.8	507	6	US-09-925-065A-921182	Sequence 921182, A
C 432	13	22.8	100	11	US-11-274-344-3	Sequence 3, App11	C 505	13	22.8	507	6	US-09-925-065A-921183	Sequence 921183, A
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C 440	13	22.8	201	14	US-11-124-368A-9338	Sequence 9338, App	C 513	13	22.8	522	6	US-09-925-065A-566409	Sequence 566409, A
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C 453	13	22.8	304	6	US-09-925-065A-307333	Sequence 307333, A	C 526	13	22.8	524	6	US-09-925-065A-519361	Sequence 519361, A
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C 455	13	22.8	323	10	US-10-301-480-331661	Sequence 331661, A	C 528	13	22.8	526	6	US-09-925-065A-400718	Sequence 400718, A
C 456	13	22.8	358	10	US-10-301-480-230609	Sequence 230609, A	C 529	13	22.8	526	6	US-09-925-065A-400718	Sequence 400718, A



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629	13	22.8	567	14	US-11-128-049-1440	Sequence 1440, Ap
C 631	13	22.8	567	14	US-11-128-049-5082	Sequence 5082, Ap
C 632	13	22.8	568	6	US-09-925-065A-306893	Sequence 306893,
C 633	13	22.8	568	7	US-10-530-774-82	Sequence 774-82, Ap1
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C 643	13	22.8	572	10	US-10-301-480-965443	Sequence 965443,
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C 656	13	22.8	575	10	US-10-301-480-934725	Sequence 934725,
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C 667	13	22.8	576	10	US-10-301-480-929946	Sequence 929946,
C 668	13	22.8	576	10	US-10-301-480-929947	Sequence 929947,
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C 677	13	22.8	577	10	US-10-301-480-730022	Sequence 730022,	750	13	22.8	589	6	US-09-925-065A-164455	Sequence 164455,
C 678	13	22.8	577	10	US-10-301-480-730023	Sequence 730023,	751	13	22.8	589	6	US-09-925-065A-248017	Sequence 248017,
C 679	13	22.8	578	6	US-09-925-065A-496659	Sequence 496659, A	C 752	13	22.8	589	6	US-09-925-065A-637151	Sequence 637151,
C 680	13	22.8	578	6	US-09-925-065A-163938	Sequence 163938,	C 753	13	22.8	589	6	US-09-925-065A-859116	Sequence 859116,
C 681	13	22.8	578	6	US-09-925-065A-754512	Sequence 754512,	C 754	13	22.8	589	10	US-10-301-480-334689	Sequence 334689,
C 682	13	22.8	578	9	US-10-301-480-73778	Sequence 73778, A	C 755	13	22.8	589	10	US-10-301-480-934609	Sequence 934609,
C 683	13	22.8	578	9	US-10-301-480-73779	Sequence 73779, A	C 756	13	22.8	591	9	US-10-301-480-99361	Sequence 99361, A
C 684	13	22.8	578	9	US-10-301-480-73780	Sequence 73780, A	C 757	13	22.8	591	10	US-10-301-480-712770	Sequence 712770,
C 685	13	22.8	578	9	US-10-301-480-150907	Sequence 150907,	C 758	13	22.8	592	6	US-09-925-065A-255522	Sequence 255522,
C 686	13	22.8	578	10	US-10-301-480-332539	Sequence 332539,	C 759	13	22.8	592	6	US-09-925-065A-357747	Sequence 357747,
C 687	13	22.8	578	10	US-10-301-480-889849	Sequence 389849,	C 760	13	22.8	592	6	US-09-925-065A-357748	Sequence 357748,
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C 690	13	22.8	578	10	US-10-301-480-687189	Sequence 687189,	C 763	13	22.8	593	6	US-09-925-065A-493334	Sequence 493334,
C 691	13	22.8	578	10	US-10-301-480-764316	Sequence 764316,	C 764	13	22.8	593	6	US-09-925-065A-758215	Sequence 758215,
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C 699	13	22.8	579	9	US-10-932-182A-5857	Sequence 5857, Ap	C 772	13	22.8	596	6	US-09-925-065A-674834	Sequence 674834,
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C 702	13	22.8	580	6	US-09-925-065A-426353	Sequence 426353,	C 775	13	22.8	596	6	US-10-301-480-342498	Sequence 342498,
C 703	13	22.8	581	6	US-09-925-065A-239425	Sequence 239425,	C 776	13	22.8	596	10	US-10-301-480-955907	Sequence 955907,
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C 706	13	22.8	581	10	US-10-301-480-1079976	Sequence 1079976,	C 779	13	22.8	597	6	US-09-925-065A-516983	Sequence 516983,
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C 708	13	22.8	582	10	US-10-301-480-316540	Sequence 316540,	C 781	13	22.8	597	10	US-10-301-480-317231	Sequence 317231,
C 709	13	22.8	582	10	US-10-301-480-929948	Sequence 929948,	C 782	13	22.8	597	10	US-10-301-480-569412	Sequence 569412,
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C 722	13	22.8	584	6	US-09-925-065A-601187	Sequence 601187,	C 795	13	22.8	599	10	US-10-301-480-686649	Sequence 686649,
C 723	13	22.8	584	6	US-09-925-065A-601188	Sequence 601188,	C 796	13	22.8	600	6	US-09-925-065A-360068	Sequence 360068,
C 724	13	22.8	584	10	US-10-301-480-445208	Sequence 445208,	C 797	13	22.8	600	6	US-09-925-065A-424622	Sequence 424622,
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C 727	13	22.8	584	10	US-10-301-480-858617	Sequence 858617,	C 800	13	22.8	600	8	US-10-750-633-3348	Sequence 3348, Ap
C 728	13	22.8	584	10	US-10-301-480-973639	Sequence 973639,	C 801	13	22.8	600	10	US-10-301-480-289964	Sequence 289964,
C 729	13	22.8	584	10	US-10-301-480-97027	Sequence 97027,	C 802	13	22.8	600	10	US-10-301-480-429048	Sequence 429048,
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C 738	13	22.8	587	9	US-10-301-480-88267	Sequence 88267, A	C 811	13	22.8	601	6	US-09-925-065A-830776	Sequence 830776,
C 739	13	22.8	587	9	US-10-301-480-88268	Sequence 88268, A	C 812	13	22.8	601	9	US-10-301-480-199339	Sequence 199339,
C 740	13	22.8	587	10	US-10-301-480-511885	Sequence 511885,	C 813	13	22.8	601	9	US-10-301-480-199340	Sequence 199340,
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C 743	13	22.8	587	10	US-10-301-480-701677	Sequence 701677,	C 816	13	22.8	601	10	US-10-301-480-488580	Sequence 488580,
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C 825	13	22.8	602	6	US-09-925-065A-937087	Sequence 937087,	C 898	13	22.8	629	6	US-09-925-065A-797293	Sequence 797293,
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C 827	13	22.8	603	6	US-10-301-480-23456	Sequence 23456, A	900	13	22.8	629	10	US-10-301-480-656377	Sequence 656377,
C 828	13	22.8	603	10	US-10-301-480-636865	Sequence 636865,	C 901	13	22.8	631	6	US-09-925-065A-179201	Sequence 179201,
C 829	13	22.8	604	6	US-09-925-065A-331767	Sequence 331767,	C 902	13	22.8	631	6	US-09-925-065A-315352	Sequence 315352,
C 830	13	22.8	604	6	US-09-925-065A-331768	Sequence 331768,	903	13	22.8	631	10	US-10-301-480-390370	Sequence 390370,
C 831	13	22.8	604	6	US-09-925-065A-331769	Sequence 331769,	904	13	22.8	631	10	US-10-301-480-1003779	Sequence 1003779,
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C 833	13	22.8	604	6	US-09-925-065A-746709	Sequence 746709,	906	13	22.8	635	6	US-09-925-065A-862934	Sequence 862934,
C 834	13	22.8	604	6	US-09-925-065A-746710	Sequence 746710,	907	13	22.8	635	9	US-10-301-480-82913	Sequence 82913, A
C 835	13	22.8	604	6	US-09-925-065A-798627	Sequence 798627,	C 908	13	22.8	636	10	US-10-301-480-666322	Sequence 666322,
C 836	13	22.8	604	6	US-09-925-065A-820529	Sequence 820529,	909	13	22.8	637	10	US-10-301-480-76487	Sequence 76487, A
C 837	13	22.8	604	6	US-09-925-065A-913629	Sequence 913629,	C 910	13	22.8	637	10	US-10-301-480-689896	Sequence 689896,
C 838	13	22.8	605	6	US-09-925-065A-201429	Sequence 201429,	C 911	13	22.8	641	6	US-09-925-065A-188595	Sequence 188595,
C 839	13	22.8	605	6	US-09-925-065A-344785	Sequence 344785,	C 912	13	22.8	642	6	US-09-925-065A-697036	Sequence 697036,
C 840	13	22.8	606	6	US-09-925-065A-98529	Sequence 98529, A	C 913	13	22.8	642	6	US-09-925-065A-800791	Sequence 800791,
C 841	13	22.8	606	6	US-09-925-065A-98530	Sequence 98530, A	C 914	13	22.8	643	6	US-09-925-065A-155570	Sequence 155570,
C 842	13	22.8	607	6	US-09-925-065A-798639	Sequence 798639,	C 915	13	22.8	643	9	US-10-301-480-81470	Sequence 81470, A
C 843	13	22.8	607	6	US-09-925-065A-894110	Sequence 894110,	C 916	13	22.8	643	10	US-10-301-480-6748504	Sequence 6748504,
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C 845	13	22.8	610	6	US-09-925-065A-194638	Sequence 194638,	C 918	13	22.8	643	10	US-10-301-480-891913	Sequence 891913,
C 846	13	22.8	610	6	US-09-925-065A-797033	Sequence 797033,	919	13	22.8	646	6	US-09-925-065A-477419	Sequence 477419,
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C 848	13	22.8	610	10	US-10-301-480-405531	Sequence 405531,	921	13	22.8	646	6	US-09-925-065A-617506	Sequence 617506,
C 849	13	22.8	610	10	US-10-301-480-405532	Sequence 405532,	922	13	22.8	646	6	US-09-925-065A-617507	Sequence 617507,
C 850	13	22.8	610	10	US-10-301-480-405533	Sequence 405533,	C 923	13	22.8	646	6	US-09-925-065A-896137	Sequence 896137,
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C 853	13	22.8	610	10	US-10-301-480-1018941	Sequence 1018941,	C 926	13	22.8	654	6	US-09-925-065A-953730	Sequence 953730,
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C 858	13	22.8	612	10	US-10-301-480-1054076	Sequence 1054076,	931	13	22.8	654	10	US-10-301-480-862358	Sequence 862358,
C 859	13	22.8	613	10	US-10-301-480-270111	Sequence 270111,	C 932	13	22.8	654	10	US-10-301-480-925938	Sequence 925938,
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C 873	13	22.8	619	10	US-10-301-480-769321	Sequence 769321,	946	13	22.8	664	6	US-09-925-065A-685660	Sequence 685660,
C 874	13	22.8	620	6	US-09-925-065A-209969	Sequence 209969,	C 947	13	22.8	667	9	US-10-301-480-53696	Sequence 53696, A
C 875	13	22.8	621	6	US-09-925-065A-735568	Sequence 735568,	C 948	13	22.8	667	9	US-10-301-480-62074	Sequence 62074, A
C 876	13	22.8	621	10	US-10-301-480-297359	Sequence 297359,	C 949	13	22.8	667	9	US-10-301-480-62075	Sequence 62075, A
C 877	13	22.8	621	10	US-10-301-480-343298	Sequence 343298,	C 950	13	22.8	667	9	US-10-301-480-62076	Sequence 62076, A
C 878	13	22.8	621	10	US-10-301-480-910768	Sequence 910768,	C 951	13	22.8	667	10	US-10-301-480-647105	Sequence 647105,
C 879	13	22.8	621	10	US-10-301-480-956707	Sequence 956707,	C 952	13	22.8	667	10	US-10-301-480-675483	Sequence 675483,
C 880	13	22.8	622	6	US-09-925-065A-370632	Sequence 370632,	C 953	13	22.8	667	10	US-10-301-480-675484	Sequence 675484,
C 881	13	22.8	622	6	US-09-925-065A-554454	Sequence 554454,	C 954	13	22.8	667	10	US-10-301-480-675485	Sequence 675485,
C 882	13	22.8	622	10	US-10-301-480-366195	Sequence 366195,	955	13	22.8	668	6	US-09-925-065A-883281	Sequence 883281,
C 883	13	22.8	622	10	US-10-301-480-979604	Sequence 979604,	956	13	22.8	669	6	US-09-925-065A-863571	Sequence 863571,
C 884	13	22.8	623	6	US-09-925-065A-252329	Sequence 252329,	C 957	13	22.8	675	10	US-10-301-480-583071	Sequence 583071,
C 885	13	22.8	623	6	US-09-925-065A-572363	Sequence 572363,	C 958	13	22.8	675	10	US-10-301-480-115640	Sequence 115640,
C 886	13	22.8	623	6	US-09-925-065A-572365	Sequence 572365,	959	13	22.8	685	10	US-10-301-480-502501	Sequence 502501,
C 887	13	22.8	623	6	US-09-925-065A-572366	Sequence 572366,	960	13	22.8	685	10	US-10-301-480-1115910	Sequence 1115910,
C 888	13	22.8	623	6	US-09-925-065A-800127	Sequence 800127,	C 961	13	22.8	689	6	US-09-925-065A-693708	Sequence 693708,
C 889	13	22.8	624	6	US-09-925-065A-830478	Sequence 830478,	C 962	13	22.8	690	6	US-09-925-065A-441759	Sequence 441759,
C 890	13	22.8	627	6	US-09-925-065A-327869	Sequence 327869,	C 963	13	22.8	704	10	US-10-301-480-584045	Sequence 584045,
C 891	13	22.8	627	6	US-09-925-065A-327870	Sequence 327870,	C 964	13	22.8	704	10	US-10-301-480-1193814	Sequence 1193814,
C 892	13	22.8	628	6	US-09-925-065A-543530	Sequence 543530,	C 965	13	22.8	709	10	US-10-301-480-569523	Sequence 569523,
C 893	13	22.8	628	10	US-10-301-480-401869	Sequence 401869,	C 966	13	22.8	709	10	US-10-301-480-1182932	Sequence 1182932,
C 894	13	22.8	628	10	US-10-301-480-401870	Sequence 401870,	C 967	13	22.8	719	6	US-09-925-065A-87525	Sequence 87525, A



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C 968 13 22.8 719 6 US-09-925-065A-87526 Sequence 87526, A
C 969 13 22.8 719 6 US-09-925-065A-87527 Sequence 87527, A
C 970 13 22.8 719 9 US-10-301-480-188766 Sequence 188766,
C 971 13 22.8 719 9 US-10-301-480-188767 Sequence 188767,
C 972 13 22.8 719 9 US-10-301-480-188768 Sequence 188768,
C 973 13 22.8 719 10 US-10-301-480-802175 Sequence 802175,
C 974 13 22.8 719 10 US-10-301-480-802176 Sequence 802176,
C 975 13 22.8 719 10 US-10-301-480-802177 Sequence 802177,
C 976 13 22.8 743 11 US-11-096-568A-27050 Sequence 27050, A
C 977 13 22.8 744 10 US-10-301-480-585193 Sequence 585193,
C 978 13 22.8 744 10 US-10-301-480-1198602 Sequence 1198602,
C 979 13 22.8 762 10 US-10-301-480-591851 Sequence 591851,
C 980 13 22.8 762 10 US-10-301-480-1205260 Sequence 1205260,
C 981 13 22.8 762 11 US-11-232-440-76 Sequence 76, Appl
C 982 13 22.8 765 9 US-09-925-065A-33998 Sequence 33998, A
C 983 13 22.8 765 9 US-10-301-480-135236 Sequence 135236,
C 984 13 22.8 765 10 US-10-301-480-748645 Sequence 748645,
C 985 13 22.8 782 10 US-10-301-480-570915 Sequence 570915,
C 986 13 22.8 782 10 US-10-301-480-1184324 Sequence 1184324,
C 987 13 22.8 787 8 US-10-750-185-59923 Sequence 59923, A
C 988 13 22.8 787 8 US-10-750-623-59923 Sequence 59923, A
C 989 13 22.8 800 8 US-10-750-185-60641 Sequence 60641, A
C 990 13 22.8 800 8 US-10-750-623-60641 Sequence 60641, A
C 991 13 22.8 811 9 US-10-301-480-98496 Sequence 98496, A
C 992 13 22.8 811 10 US-10-301-480-711905 Sequence 711905,
C 993 13 22.8 821 6 US-09-925-065A-726685 Sequence 726685,
C 994 13 22.8 821 6 US-09-925-065A-726686 Sequence 726686,
C 995 13 22.8 821 6 US-09-925-065A-726687 Sequence 726687,
C 996 13 22.8 821 6 US-09-925-065A-726688 Sequence 726688,
C 997 13 22.8 821 6 US-10-750-185-31551 Sequence 31551, A
C 998 13 22.8 827 10 US-10-750-623-31551 Sequence 31551, A
C 999 13 22.8 827 10 US-10-301-480-577409 Sequence 577409,
1000 13 22.8 827 10 US-10-301-480-1190818 Sequence 1190818,
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## ALIGNMENTS

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RESULT 1
US-11-055-557-11
; Sequence 11, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; OTHER INFORMATION: wild-type homo-oligomeric anthrax toxin protective
; US-11-055-557-11
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Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 2,4e-24;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57
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Db 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 652
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RESULT 2
US-11-055-557-15
; Sequence 15, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; US-11-055-557-15
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Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 2,4e-24;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 57
|||||
Db 596 GTGCTGACCTACCGTTCCAGACCGTGACATGATGATGATCCCTGATTCATTAGAGG 652
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RESULT 3
US-11-055-557-19
; Sequence 19, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; US-11-055-557-19
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Query Match 100.0%; Score 57; DB 14; Length 2295;
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Best Local Similarity 100.0%; Pred. No. 2,4e-24;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
DB 596 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 652

## RESULT 4

US-11-055-557-1  
; Sequence 1, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified  
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (Prng) Prng-U2-R200A  
US-11-055-557-1

Query Match 100.0%; Score 57; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 2,4e-24;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
DB 605 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 661

## RESULT 5

US-11-055-557-9  
; Sequence 9, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 2304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified

OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (Prng) Prng-U2-K197A (Pa-U-K197A)  
US-11-055-557-9

Query Match 100.0%; Score 57; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 2,4e-24;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
DB 605 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 661

## RESULT 6

US-11-055-557-13  
; Sequence 13, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 2304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified  
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (Prng) Prng-U2  
US-11-055-557-13

Query Match 100.0%; Score 57; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 2,4e-24;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 57  
DB 605 GTGCTGACCTACGCGTTCCAGACCGTGACATGATGGAATCCCTGATTCTTAGAGG 661

## RESULT 7

US-11-055-557-3  
; Sequence 3, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3



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; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-1210A (PA-M-1210A)
US-11-055-557-3

Query Match          100.0%; Score 57; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.4e-24;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 608 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 664

RESULT 8
US-11-055-557-5
; Sequence 5, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-K214A (PA-M-K214A)
US-11-055-557-5

Query Match          100.0%; Score 57; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.4e-24;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 608 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 664

RESULT 9
US-11-055-557-17
; Sequence 17, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
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; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1
US-11-055-557-17

Query Match          100.0%; Score 57; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.4e-24;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 57
Db 608 GTGCTGACCTACCGTTCCAGACCGTGACATGATGGAATCCCTGATTCATTAGAG 664

RESULT 10
US-10-889-197-39
; Sequence 39, Application US/10889197
; Publication No. US20050271689A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, CHUN-MING
; APPLICANT: ZHANG, JIANPENG
; APPLICANT: TANG, DE-CHU
; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
; TITLE OF INVENTION: THERAPY AGAINST ANTHRAX
; FILE REFERENCE: 858610-2006.1
; CURRENT APPLICATION NUMBER: US/10/889,197
; PRIOR FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,369
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: primer
US-10-889-197-39

Query Match          40.4%; Score 23; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.00079;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GTGCTGACCTACCGTTCCAGAC 23
Db 8 GTGCTGACCTACCGTTCCAGAC 30

RESULT 11
US-11-055-557-7
; Sequence 7, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
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; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-R178A (Pa-M-R178A)
US-11-055-557-7

Query Match          40.4%; Score 23; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 0.00091;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GTGCTGACCTACGCTTCAGAC 23
Db      608 GTGCTGACCTACGCTTCAGAC 630

RESULT 12
US-11-131-479-90
; Sequence 90, Application US/11/131,479
; Publication No. US20060024670A1
; GENERAL INFORMATION:
; APPLICANT: Luke, Catherine J.
; APPLICANT: Vialta, Adrian
; APPLICANT: Wloch, Mary K.
; APPLICANT: Evans, Thomas G.
; APPLICANT: Geall, Andrew J.
; APPLICANT: Jimenez, Gretchen
; TITLE OF INVENTION: Influenza Virus Vaccine Composition and Methods of Use
; FILE REFERENCE: 1530.0640002/EDH/J-H
; CURRENT APPLICATION NUMBER: US/11/131,479
; CURRENT FILING DATE: 2005-05-18
; PRIOR APPLICATION NUMBER: US 60/571,854
; PRIOR FILING DATE: 2004-05-18
; NUMBER OF SEQ ID NOS: 112
; SOFTWARE: Patentn version 3.3
; SEQ ID NO 90
; LENGTH: 6425
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: VR6307, Ligation of VCL6292 into VR6430
US-11-131-479-90

Query Match          36.8%; Score 21; DB 14; Length 6425;
Best Local Similarity 100.0%; Pred. No. 0.015;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      27 GACAATGATGGAATCCCTGAT 47
Db      1726 GACAATGATGGAATCCCTGAT 1746

RESULT 13
US-11-055-557-39
; Sequence 39, Application US/11/055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having

; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:sense primer
; OTHER INFORMATION: Pr178a-2
US-11-055-557-39

Query Match          33.3%; Score 19; DB 14; Length 30;
Best Local Similarity 100.0%; Pred. No. 0.21;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      39 ATCCCTGATTCATTAGAG 57
Db      5 ATCCCTGATTCATTAGAG 23

RESULT 14
US-11-055-557-38/c
; Sequence 38, Application US/11/055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patentn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 39
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:antisense
; OTHER INFORMATION: primer Pr178a-1
US-11-055-557-38

Query Match          31.6%; Score 18; DB 14; Length 39;
Best Local Similarity 100.0%; Pred. No. 0.85;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 GGACCTACGGTTCCAGAC 23
Db      39 GGACCTACGGTTCCAGAC 22

RESULT 15
US-10-750-185-32728
; Sequence 32728, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMT GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
```



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; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 32728
; LENGTH: 2176
; TYPE: DNA
; ORGANISM: Bovine 19866880677481
US-10-750-185-32728

Query Match 29.8%; Score 17; DB 8; Length 2176;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CCTGATTCATTAGAG 57
Db 1935 CCTGATTCATTAGAG 1951

RESULT 16
US-10-750-623-32728
; Sequence 32728, Application US/10750623
; Publication No. US20050287531
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 32728
; LENGTH: 2176
; TYPE: DNA
; ORGANISM: Bovine 19866880677481
US-10-750-623-32728

Query Match 29.8%; Score 17; DB 8; Length 2176;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 41 CCTGATTCATTAGAG 57
Db 1935 CCTGATTCATTAGAG 1951

RESULT 17
US-10-934-048A-31261
; Sequence 31261, Application US/10934048A
; Publication No. US20060051770A1
; GENERAL INFORMATION:
; APPLICANT: Tanya Makeev
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3699
; CURRENT APPLICATION NUMBER: US/10/934,048A
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 12085
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
```

```
; SEQ ID NO 31261
; LENGTH: 25
; TYPE: DNA
; ORGANISM: S. cerevisiae
US-10-934-048A-31261

Query Match 28.1%; Score 16; DB 9; Length 25;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 GACCGTGAATGATG 36
Db 7 GACCGTGAATGATG 22

RESULT 18
US-09-925-065A-627981/c
; Sequence 627981, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 627981
; LENGTH: 533
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-627981

Query Match 28.1%; Score 16; DB 6; Length 533;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 AATCCGTGATTCATTA 53
Db 242 AATCCGTGATTCATTA 227

RESULT 19
US-09-925-065A-648910/c
; Sequence 648910, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
```



;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 648910  
;; LENGTH: 541  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-648910

Query Match 28.1%; Score 16; DB 6; Length 541;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TGACATGATGGAATC 41  
Db 251 TGACATGATGGAATC 236

RESULT 20  
US-09-925-065A-648911/c  
; Sequence 648911, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single  
;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925,065A  
;; PRIOR FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 648911  
;; LENGTH: 541  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-648911

Query Match 28.1%; Score 16; DB 6; Length 541;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TGACATGATGGAATC 41  
Db 251 TGACATGATGGAATC 236

RESULT 21  
US-09-925-065A-892206/c  
; Sequence 892206, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single  
;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925,065A  
;; PRIOR FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30

;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 892206  
;; LENGTH: 715  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-892206

Query Match 28.1%; Score 16; DB 6; Length 715;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 AATCCCTGATTCATTA 53  
Db 170 AATCCCTGATTCATTA 155

RESULT 22  
US-10-750-185-37407  
; Sequence 37407, Application US/10750185  
; Publication No. US20050260603A1  
; GENERAL INFORMATION:

;; APPLICANT: MMT GENOMICS, INC.  
;; APPLICANT: DENISE, Sue K.  
;; APPLICANT: KERR, Richard  
;; APPLICANT: ROSENFELD, David  
;; APPLICANT: HOLM, Tom  
;; APPLICANT: BATES, Stephen  
;; APPLICANT: FANTIN, Dennis  
;; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
;; FILE REFERENCE: MM1100-2  
;; CURRENT APPLICATION NUMBER: US/10/750,185  
;; PRIOR FILING DATE: 2003-12-31  
;; PRIOR APPLICATION NUMBER: US 60/437,482  
;; PRIOR FILING DATE: 2002-12-31  
;; NUMBER OF SEQ ID NOS: 64922  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO 37407  
;; LENGTH: 3012  
;; TYPE: DNA  
;; ORGANISM: Bovine  
US-10-750-185-37407

Query Match 28.1%; Score 16; DB 8; Length 3012;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TGACATGATGGAATC 41  
Db 1336 TGACATGATGGAATC 1351

RESULT 23  
US-10-750-623-37407  
; Sequence 37407, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
;; APPLICANT: MMT GENOMICS, INC.  
;; APPLICANT: DENISE, Sue K.  
;; APPLICANT: KERR, Richard  
;; APPLICANT: ROSENFELD, David  
;; APPLICANT: HOLM, Tom  
;; APPLICANT: BATES, Stephen  
;; APPLICANT: FANTIN, Dennis  
;; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
;; FILE REFERENCE: MM1100-1  
;; CURRENT APPLICATION NUMBER: US/10/750,623  
;; PRIOR FILING DATE: 2003-12-31  
;; PRIOR APPLICATION NUMBER: US 60/437,482



;; PRIOR FILING DATE: 2002-12-31  
;; NUMBER OF SEQ ID NOS: 64922  
;; SOFTWARE: PatentIn version 3.1  
;; SEQ ID NO: 37407  
;; LENGTH: 3012  
;; TYPE: DNA  
;; ORGANISM: Bovine 19866880944975  
US-10-750-623-37407

Query Match 28.1%; Score 15; DB 8; Length 3012;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 26 TGACATGATGGAATC 41  
Db 1336 TGACATGATGGAATC 1351

RESULT 24  
US-10-932-182A-88631/c  
; Sequence 88631, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 88631  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-88631

Query Match 26.3%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 26 TGACATGATGGAAT 40  
Db 19 TGACATGATGGAAT 5

RESULT 25  
US-10-932-182A-88631/c  
; Sequence 88631, Application US/10932182A  
; Publication No. US20060046253A1  
; GENERAL INFORMATION:  
; APPLICANT: NAKAO, YOSHIHIRO  
; APPLICANT: NAKAMURA, NORIHISA  
; APPLICANT: KODAMA, YUKIKO  
; APPLICANT: FUJIMURA, TOMOKO  
; APPLICANT: ASHIKARI, TOSHIHIKO  
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
; FILE REFERENCE: 030685-043  
; CURRENT APPLICATION NUMBER: US/10/932,182A  
; CURRENT FILING DATE: 2004-09-02  
; NUMBER OF SEQ ID NOS: 197023  
; SOFTWARE: PatentIn version 3.3  
; SEQ ID NO: 88631  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-88631

Query Match 26.3%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;

Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 26 TGACATGATGGAAT 40  
Db 19 TGACATGATGGAAT 5

RESULT 26  
US-10-933-982-192853/c  
; Sequence 192853, Application US/10933982  
; Publication No. US20060051769A1  
; GENERAL INFORMATION:  
; APPLICANT: Barts, Jennifer  
; TITLE OF INVENTION: Methods of Genetic Analysis of E. coli  
; FILE REFERENCE: 3700  
; CURRENT APPLICATION NUMBER: US/10/933,982  
; CURRENT FILING DATE: 2004-09-03  
; NUMBER OF SEQ ID NOS: 224976  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 192853  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: E. coli  
US-10-933-982-192853

Query Match 26.3%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 13 CGTTCCAGACCGTG 27  
Db 15 CGTTCCAGACCGTG 1

RESULT 27  
US-10-934-048A-48980/c  
; Sequence 48980, Application US/10934048A  
; Publication No. US20060051770A1  
; GENERAL INFORMATION:  
; APPLICANT: Tanya Makeev  
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast  
; FILE REFERENCE: 3699  
; CURRENT APPLICATION NUMBER: US/10/934,048A  
; CURRENT FILING DATE: 2004-09-03  
; NUMBER OF SEQ ID NOS: 120855  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO: 48980  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: S. cerevisiae  
US-10-934-048A-48980

Query Match 26.3%; Score 15; DB 9; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 26 TGACATGATGGAAT 40  
Db 23 TGACATGATGGAAT 9

RESULT 28  
US-11-121-849-340613  
; Sequence 340613, Application US/11121849  
; Publication No. US20050272080A1  
; GENERAL INFORMATION:  
; APPLICANT: John Palma  
; TITLE OF INVENTION: Methods of Genetic Analysis of Formalin Fixed Paraffin Embedded  
; FILE REFERENCE: 3684.1  
; CURRENT APPLICATION NUMBER: US/11/121,849  
; CURRENT FILING DATE: 2005-05-03  
; PRIOR APPLICATION NUMBER: 60/567,949



;; PRIOR FILING DATE: 2004-05-03  
;; NUMBER OF SEQ ID NOS: 673904  
;; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
;; SEQ ID NO 340613  
;; LENGTH: 25  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-11-121-849-340613

Query Match 26.3%; Score 15; DB 14; Length 25;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 36 GGAATCCTGATTC 50  
Db 8 GGAATCCTGATTC 22

RESULT 29  
US-11-175-859-41848/C  
;; Sequence 41848, Application US/11175859  
;; Publication No. US20060024715A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Affymetrix, Inc.  
;; APPLICANT: Liu, Guoying et al.  
;; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
;; FILE REFERENCE: 3690.1  
;; CURRENT APPLICATION NUMBER: US/11/175, 859  
;; CURRENT FILING DATE: 2005-07-05  
;; PRIOR APPLICATION NUMBER: US 60/585,352  
;; PRIOR FILING DATE: 2004-07-02  
;; NUMBER OF SEQ ID NOS: 116251  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 41848  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-11-175-859-41848

Query Match 26.3%; Score 15; DB 14; Length 50;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 GTGCAATGATGAA 39  
Db 50 GTGCAATGATGAA 36

RESULT 30  
US-11-175-859-87027  
;; Sequence 87027, Application US/11175859  
;; Publication No. US20060024715A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Affymetrix, Inc.  
;; APPLICANT: Liu, Guoying et al.  
;; TITLE OF INVENTION: Method of Analysis of Human Polymorphism  
;; FILE REFERENCE: 3690.1  
;; CURRENT APPLICATION NUMBER: US/11/175, 859  
;; CURRENT FILING DATE: 2005-07-05  
;; PRIOR APPLICATION NUMBER: US 60/585,352  
;; PRIOR FILING DATE: 2004-07-02  
;; NUMBER OF SEQ ID NOS: 116251  
;; SOFTWARE: PatentIn version 3.2  
;; SEQ ID NO 87027  
;; LENGTH: 50  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-11-175-859-87027

Query Match 26.3%; Score 15; DB 14; Length 50;  
Best Local Similarity 100.0%; Pred. No. 56;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 TGACATGATGAA 40  
Db 9 TGACATGATGAA 23

RESULT 31  
US-09-925-065A-840059/C  
;; Sequence 840059, Application US/09925065A  
;; Publication No. US20040181048A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925, 065A  
;; CURRENT FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 840059  
;; LENGTH: 466  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-840059

Query Match 26.3%; Score 15; DB 6; Length 466;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 AATCCTGATTCATT 52  
Db 296 AATCCTGATTCATT 282

RESULT 32  
US-10-301-480-323739  
;; Sequence 323739, Application US/10301480  
;; Publication No. US20060057564A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
;; FILE REFERENCE: 108827.137  
;; CURRENT APPLICATION NUMBER: US/10/301, 480  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US 10/215,598  
;; PRIOR FILING DATE: 2002-08-09  
;; PRIOR APPLICATION NUMBER: US 60/311,695  
;; PRIOR FILING DATE: 2001-08-10  
;; NUMBER OF SEQ ID NOS: 1226818  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 323739  
;; LENGTH: 505  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-10-301-480-323739

Query Match 26.3%; Score 15; DB 10; Length 505;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TGATGAATCCCTGA 46  
Db 192 TGATGAATCCCTGA 206



## RESULT 33

US-10-301-480-937148  
; Sequence 937148, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 937148  
; LENGTH: 505  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-301-480-937148

## Query Match

Best Local Similarity 26.3%; Score 15; DB 10; Length 505;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TGATGAATCCCTGA 46  
|||||  
Db 192 TGATGAATCCCTGA 206

## RESULT 34

US-09-925-065A-850695/c  
; Sequence 850695, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 850695  
; LENGTH: 507  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-850695

## Query Match

Best Local Similarity 26.3%; Score 15; DB 6; Length 507;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TGATGAATCCCTGA 46  
|||||  
Db 223 TGATGAATCCCTGA 209

## RESULT 35

## US-09-925-065A-850696/c

; Sequence 850696, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 850696  
; LENGTH: 507  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-850696

## Query Match

Best Local Similarity 26.3%; Score 15; DB 6; Length 507;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TGATGAATCCCTGA 46  
|||||  
Db 223 TGATGAATCCCTGA 209

## RESULT 36

US-09-925-065A-242775  
; Sequence 242775, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 242775  
; LENGTH: 509  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-242775

## Query Match

Best Local Similarity 26.3%; Score 15; DB 6; Length 509;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 TGATGAATCCCTGA 46  
|||||  
Db 192 TGATGAATCCCTGA 206



```
RESULT 37
US-09-925-065A-242776
; Sequence 242776, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 242776
; LENGTH: 509
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-242776

Query Match      26.3%; Score 15; DB 6; Length 509;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32 TGATGATCCCTGA 46
Db      192 TGATGATCCCTGA 206

RESULT 38
US-09-925-065A-538602
; Sequence 538602, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 538602
; LENGTH: 532
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-538602

Query Match      26.3%; Score 15; DB 6; Length 532;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      32 TGATGATCCCTGA 46
Db      256 TGATGATCCCTGA 270

RESULT 39
US-09-925-065A-584969/c
; Sequence 584969, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 584969
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-584969

Query Match      26.3%; Score 15; DB 6; Length 547;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      43 CTGATTCATTAGAG 57
Db      390 CTGATTCATTAGAG 376

RESULT 40
US-09-925-065A-584970/c
; Sequence 584970, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 584970
; LENGTH: 547
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-584970

Query Match      26.3%; Score 15; DB 6; Length 547;
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Best Local Similarity 100.0%; Pred. No. 61;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 43 CTGATTCAATTAGAGG 57  
|||||  
Db 390 CTGATTCAATTAGAGG 376

Search completed: April 12, 2006, 07:07:09  
Job time : 240.795 secs

---



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 784.814 Seconds  
(without alignments)  
3398.084 Million cell updates/sec

Title: US-10-712-654-21

Perfect score: 57

Sequence: 1 gtgtgtgacctacgttcca.....aatccctgattcattagagg 57

Scoring table: OLIGO\_NUC

Searched: 41078325 seqs, 23393541228 residues

Word size: 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*  
10: gb\_est10: \*  
11: gb\_est11: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	20	35.1	768	2	BE889641 601512663
2	19	33.3	825	10	CZ060909 OM_BA005
3	18	31.6	555	2	BE130454 L48-642T3
4	18	31.6	558	1	AM053908 L30-2348T
5	18	31.6	637	3	BM658306 MCR058E05
6	18	31.6	690	3	BI869110 603395428
7	17	29.8	197	1	AI788617 UK47C09.x
8	17	29.8	267	3	BP926030 BP926030
9	17	29.8	366	2	BG731863 ps07a06.y
10	17	29.8	397	1	AA910388 OK89b07.s
11	17	29.8	398	10	CZ233273 A1AA-aae8
12	17	29.8	433	5	BM880236 BM880236
13	17	29.8	441	7	CN056216 Salamande
14	17	29.8	450	2	BG731918 ps07a06.y
15	17	29.8	453	7	CK614921 LPS1.M02
16	17	29.8	483	6	CD188515 MS1-0063U
17	17	29.8	501	2	BG302319 ps07a06.y
18	17	29.8	510	1	AJ735313 AJ735313
19	17	29.8	513	5	BQ738090 pc27f12.y
20	17	29.8	513	7	CK142714 AGENCOURT
21	17	29.8	514	2	BE492067 WHE0551.B
22	17	29.8	533	1	AL925807 AL925807

23	17	29.8	563	3	BU268532
24	17	29.8	567	8	CK399264
25	17	29.8	576	6	CD279894
26	17	29.8	580	2	BE492082
27	17	29.8	589	6	CD279643
28	17	29.8	599	7	CV059002
29	17	29.8	599	11	CPA562939
30	17	29.8	638	6	CA191493
31	17	29.8	639	3	BU268492
32	17	29.8	651	9	BE2843563
33	17	29.8	672	1	AJ735325
34	17	29.8	676	3	BI326765
35	17	29.8	691	2	BF030782
36	17	29.8	704	7	CV053951
37	17	29.8	710	5	BU442399
38	17	29.8	742	8	DT063771
39	17	29.8	745	5	BU479295
40	17	29.8	746	5	BU484191
41	17	29.8	754	6	CD757777
42	17	29.8	760	7	CK139961
43	17	29.8	762	8	DT076647
44	17	29.8	763	8	CK976694
45	17	29.8	765	6	CD750747
46	17	29.8	784	7	CK140864
47	17	29.8	785	1	AJ448217
48	17	29.8	786	7	CK143661
49	17	29.8	787	6	CD752592
50	17	29.8	788	7	CN057630
51	17	29.8	799	7	CK144127
52	17	29.8	799	7	CN054495
53	17	29.8	802	7	CK143665
54	17	29.8	805	5	BU483110
55	17	29.8	811	7	CK145712
56	17	29.8	816	2	BE618414
57	17	29.8	820	7	CK148369
58	17	29.8	823	7	CK144020
59	17	29.8	835	6	CD751521
60	17	29.8	838	8	CK078543
61	17	29.8	840	8	DR882435
62	17	29.8	845	7	CK141467
63	17	29.8	846	6	CD755449
64	17	29.8	846	8	CK836929
65	17	29.8	847	8	CK971896
66	17	29.8	851	8	CK979341
67	17	29.8	859	7	CR581457
68	17	29.8	862	6	CD752750
69	17	29.8	868	6	CA475980
70	17	29.8	873	6	CD757459
71	17	29.8	873	7	CO104643
72	17	29.8	878	8	CK982708
73	17	29.8	891	6	CA470016
74	17	29.8	896	8	CK398954
75	17	29.8	897	6	CA476490
76	17	29.8	900	6	CA476448
77	17	29.8	901	6	CA470843
78	17	29.8	908	6	CA477082
79	17	29.8	921	6	CA477186
80	17	29.8	934	6	CA470172
81	17	29.8	944	6	CA476686
82	17	29.8	1049	10	CL102788
83	17	29.8	1061	7	CA496795
84	17	29.8	1173	7	CK206602
85	17	29.8	1723	4	AK015643
86	17	29.8	1760	2	BE541790
87	16	28.1	174	5	BF733442
88	16	28.1	199	5	BM522866
89	16	28.1	289	9	AQ028577
90	16	28.1	323	6	CF050085
91	16	28.1	324	6	CF048270
92	16	28.1	335	6	CF047563
93	16	28.1	347	2	BF872116
94	16	28.1	349	2	BG837518
95	16	28.1	362	3	BP058403
96	16	28.1	362	3	BP058403

BU268532	BU268532
CA399264	JGI_XZT37
CD279894	G44222.48
BE492082	WHE0551.C
CD279643	G44222.B3
CV059002	BNE43c8
CPA562939	CYP108PO
CA191493	SCCCT2C0
BU268492	BU268492
BE2843563	CH240.291
AJ735325	AJ735325
BI326765	STRO0027
BF030782	601557518
CV053951	BNE410585
BU442399	604147742
DT063771	AGENCOURT
BU479295	603472492
BU484191	AGENCOURT
CD757777	AGENCOURT
CK139961	AGENCOURT
DT076647	AGENCOURT
CK976694	JGI_CAAp9
CD750747	AGENCOURT
CK140864	AGENCOURT
AJ448217	AGENCOURT
CK143661	AGENCOURT
CD752592	AGENCOURT
CN057630	Salamande
CK144127	AGENCOURT
CN054495	Salamande
CK143665	AGENCOURT
BU483110	603842425
CK145712	HVSMEC000
BE618414	AGENCOURT
CK148369	AGENCOURT
CK144020	AGENCOURT
CD751521	AGENCOURT
CK078543	UCRCS08_9
DR882435	JGI_CABK1
CK141467	AGENCOURT
CD755449	AGENCOURT
CK836929	JGI_CAAK7
CK971896	JGI_CAAp7
CK979341	JGI_CAAp1
CR581457	CR581457
CD752750	AGENCOURT
CA475980	AGENCOURT
CD757459	AGENCOURT
CO104643	GR_EB003
CK982708	JGI_CAAp1
CA470016	AGENCOURT
CK398954	JGI_XZT35
CA476490	AGENCOURT
CA476448	AGENCOURT
CA470843	AGENCOURT
CA477082	AGENCOURT
CA477186	AGENCOURT
CA470172	AGENCOURT
CA476686	AGENCOURT
CL102788	ISB1-40J9
CA496795	AGENCOURT
CK206602	FGAS01820
AK015643	MuB_muBcu
BE541790	601063759
BF733442	MRI-AN003
BM522866	BMS22866
AQ028577	CIT-HSP-2
CF050085	QCL7e05.y
CF048270	QCL1a11.y
CF047563	QCL10b10.
BF872116	IL3-ET011
BG837518	Zm10_08f0
BP058403	BP058403



C 96	16	28.1	383	9	CC152741	CC152741	CSU-K34.1	169	16	28.1	734	8	DR725888	DR725888	AGENCOURT
97	16	28.1	388	10	AG979204	AG979204	Drosophila	170	16	28.1	736	9	BH088822	BH088822	RPCI-24-3
98	16	28.1	395	10	CM858394	CM858394	Btze1n2-4	171	16	28.1	738	10	CM073101	CM073101	104_332.1
99	16	28.1	410	7	CK770631	CK770631	958829 MA	172	16	28.1	742	6	CD916444	CD916444	6G08_001M
C 100	16	28.1	412	1	AM669077	AM669077	112230 MA	173	16	28.1	744	5	BM452383	BM452383	BM452383
C 101	16	28.1	454	3	BP074661	BP074661	BP074661	174	16	28.1	746	5	BM403118	BM403118	BM403118
C 102	16	28.1	454	7	CM993243	CM993243	MdTw2047K	175	16	28.1	749	5	BM018846	BM018846	BM018846
C 103	16	28.1	454	7	BZ140886	BZ140886	CH230-245	176	16	28.1	754	7	CN825114	CN825114	LjPES13M1
C 104	16	28.1	462	1	A1978185	A1978185	614041C08	177	16	28.1	754	1	AJ452237	AJ452237	AJ452237
C 105	16	28.1	462	3	BP066295	BP066295	BP066295	178	16	28.1	761	7	CN825104	CN825104	LjPES12H3
C 106	16	28.1	472	3	BM732174	BM732174	sa174a07.	179	16	28.1	761	10	CL150343	CL150343	104_332.1
C 107	16	28.1	482	7	CV388323	CV388323	OVI-MT022	180	16	28.1	780	11	CR804006	CR804006	GR05AA25A
C 108	16	28.1	483	7	AW719571	AW719571	LjNHE563	181	16	28.1	781	10	AG588062	AG588062	Mus muscu
C 109	16	28.1	485	2	BF426121	BF426121	880606.y	182	16	28.1	784	9	BH725571	BH725571	BOMPT21TF
C 110	16	28.1	491	3	BP058424	BP058424	AP0828506 HS_5255_B	183	16	28.1	812	9	CC368525	CC368525	PUMDL27TD
C 111	16	28.1	498	3	CK519974	CK519974	rswa00_00	184	16	28.1	812	9	CC368525	CC368525	PUMDL27TD
C 112	16	28.1	514	7	BP028038	BP028038	BP028038	185	16	28.1	829	6	CF636624	CF636624	ZmTw00_0
C 113	16	28.1	518	3	CO360672	CO360672	DR-ATE-SU	186	16	28.1	832	2	BG029493	BG029493	602297042
C 114	16	28.1	520	7	BP073227	BP073227	BP073227	187	16	28.1	832	2	BX878368	BX878368	BX878368
C 115	16	28.1	525	3	AP061538	AP061538	AP061538	188	16	28.1	834	2	BP167305	BP167305	601775781
C 116	16	28.1	530	9	BM517590	BM517590	BM517590	189	16	28.1	838	9	CC359832	CC359832	PUM8Y95TB
C 117	16	28.1	543	10	CL412933	CL412933	RPCT4_43	190	16	28.1	842	5	BU908637	BU908637	AGENCOURT
C 118	16	28.1	548	11	DR10N105	DR10N105	AL735918 Danio rer	191	16	28.1	853	11	CR252910	CR252910	Forward
C 119	16	28.1	551	6	CD323732	CD323732	StrPu537.	192	16	28.1	853	11	CR252910	CR252910	Forward
C 120	16	28.1	557	1	AV390250	AV390250	AV390250	193	16	28.1	853	11	CR252910	CR252910	Forward
C 121	16	28.1	558	1	AV620959	AV620959	AV620959	194	16	28.1	860	8	DN520890	DN520890	1263690 M
C 122	16	28.1	560	2	BE344757	BE344757	946028F10	195	16	28.1	868	8	DR069179	DR069179	RTDK1.5 H
C 123	16	28.1	563	7	CN876430	CN876430	020814MAR	196	16	28.1	871	6	CD753113	CD753113	AGENCOURT
C 124	16	28.1	564	5	BM517590	BM517590	BM517590	197	16	28.1	874	10	DU037032	DU037032	NDL.1A7.T
C 125	16	28.1	566	2	BE642214	BE642214	Cr12.5.H0	198	16	28.1	875	9	CC130893	CC130893	AJ456273
C 126	16	28.1	568	3	BI942077	BI942077	af08h05.y	199	16	28.1	897	4	AJ456273	AJ456273	Zea mays
C 127	16	28.1	580	3	BM177365	BM177365	af180d10	200	16	28.1	903	4	AG1616103	AG1616103	PUGJ121TD
C 128	16	28.1	582	6	CD916443	CD916443	6G08_001M	201	16	28.1	913	9	CC005180	CC005180	PUGJ121TD
C 129	16	28.1	591	9	AZ766797	AZ766797	1M0564A11	202	16	28.1	931	10	CZ514566	CZ514566	GMW2-78F1
C 130	16	28.1	594	1	AV390181	AV390181	AV390181	203	16	28.1	945	2	BC297726	BC297726	602395941
C 131	16	28.1	595	8	DN228039	DN228039	MEST1215	204	16	28.1	963	10	CG1616103	CG1616103	PURV953TB
C 132	16	28.1	596	8	DR825970	DR825970	ZM-BFb006	205	16	28.1	964	9	CC442231	CC442231	mgae0004A
C 133	16	28.1	597	1	AV390916	AV390916	AV390916	206	16	28.1	1003	4	AY107718	AY107718	PuHLX42TB
C 134	16	28.1	606	9	BZ520981	BZ520981	BOMSK16TR	207	16	28.1	1005	9	BZ433886	BZ433886	Zea mays
C 135	16	28.1	611	10	CM188877	CM188877	104_608_1	208	16	28.1	1014	10	CNS01QFD	CNS01QFD	Andopheles
C 136	16	28.1	613	7	CO692535	CO692535	DG11-49n1	209	16	28.1	1014	10	CNS01QFD	CNS01QFD	Andopheles
C 137	16	28.1	617	2	BE186492	BE186492	946007B08	210	16	28.1	1172	7	CK209164	CK209164	AGENCOURT
C 138	16	28.1	621	2	BE186454	BE186454	946009G03	211	16	28.1	1280	4	BM914014	BM914014	AGENCOURT
C 139	16	28.1	621	9	AZ702127	AZ702127	RPCI-23-2	212	16	28.1	1380	4	AK082926	AK082926	Mus muscu
C 140	16	28.1	622	9	BH514588	BH514588	BOG1039TR	213	16	28.1	154	7	CK048707	CK048707	45848r81C
C 141	16	28.1	624	9	CC094373	CC094373	CSU-K34.1	214	16	28.1	165	3	B1788432	B1788432	sa070G01.
C 142	16	28.1	625	10	CE310524	CE310524	CE310524	215	16	28.1	175	1	AA442673	AA442673	zvf09G02.r
C 143	16	28.1	637	11	CR865755	CR865755	Sub scroF	216	16	28.1	181	10	CL280331	CL280331	Ggal.51.y
C 144	16	28.1	640	2	BF439233	BF439233	bab61d04.	217	16	28.1	183	1	AA039083	AA039083	m19d01.y
C 145	16	28.1	643	9	BZ641103	BZ641103	OGCB119TM	218	16	28.1	188	1	A1510189	A1510189	m19d01.y
C 146	16	28.1	653	5	BM725336	BM725336	BM725336	219	16	28.1	193	5	BO458647	BO458647	HA04J19r
C 147	16	28.1	656	9	BZ817055	BZ817055	PUGCB06TB	220	16	28.1	196	9	BO458647	BO458647	HA04J19r
C 148	16	28.1	659	10	AG089454	AG089454	Pan trogl	221	16	28.1	196	9	BH638578	BH638578	1008021F0
C 149	16	28.1	665	3	BM937091	BM937091	UI-M-CRO	222	16	28.1	202	2	BH530553	BH530553	1008023D0
C 150	16	28.1	665	6	CF626070	CF626070	zmrw06.5	223	16	28.1	205	9	BH410221	BH410221	1007017B1
C 151	16	28.1	665	10	BZ817060	BZ817060	PUGCB06TD	224	16	28.1	206	5	BX525007	BX525007	1119001C0
C 152	16	28.1	665	9	CE174603	CE174603	CE174603	225	16	28.1	212	10	CG707114	CG707114	Aradidops
C 153	16	28.1	669	10	AG302518	AG302518	Mus muscu	226	16	28.1	217	10	BX662173	BX662173	Aradidops
C 154	16	28.1	670	10	AG157185	AG157185	Pan trogl	227	16	28.1	233	2	BA116221	BA116221	Sheared D
C 155	16	28.1	677	5	BM169203	BM169203	BM169203	228	16	28.1	246	9	AQ951628	AQ951628	BP042324
C 156	16	28.1	698	2	BF165336	BF165336	601777236	229	16	28.1	247	8	BP042324	BP042324	BP042324
C 157	16	28.1	704	8	DR816223	DR816223	ZM-BFb001F2	230	16	28.1	251	8	D39468	D39468	R1C80815A R
C 158	16	28.1	706	4	CM459072	CM459072	CM459072	231	16	28.1	253	2	BB355645	BB355645	BB355645
C 159	16	28.1	712	7	CN825782	CN825782	LjPES110d	232	16	28.1	256	1	BB005997	BB005997	BB005997
C 160	16	28.1	714	7	CN825186	CN825186	LjPES131d	233	16	28.1	256	2	BB060400	BB060400	BB060400
C 161	16	28.1	714	8	DN224678	DN224678	MEST1162	234	16	28.1	263	3	AZ800803	AZ800803	2M0059F06
C 162	16	28.1	715	5	BM428416	BM428416	LjPES11G8	235	16	28.1	264	3	BI741735	BI741735	9C90B11.y
C 163	16	28.1	716	5	BM428416	BM428416	LjPES11G8	236	16	28.1	267	2	BF290609	BF290609	EGT455200
C 164	16	28.1	718	10	CL151911	CL151911	104_334_1	237	16	28.1	268	7	CR472834	CR472834	CR472834
C 165	16	28.1	719	7	CN825706	CN825706	LjPES19F2	238	16	28.1	274	1	AA442249	AA442249	zvf1508.r
C 166	16	28.1	725	7	CV497892	CV497892	62127.1 M	239	16	28.1	274	8	DN499032	DN499032	T0190G06.5
C 167	16	28.1	730	9	BH122838	BH122838	RPCT-24-3	240	16	28.1	280	2	BB472734	BB472734	BB472734
C 168	16	28.1	730	9	BH122838	BH122838	RPCT-24-3	241	16	28.1	280	2	BB472734	BB472734	BB472734



[illegible]



C 388	15	26.3	5077	2	BE422455	WHE0055_A	461	15	560	8	CY963111	CY963111	PYrPCV_13
C 389	15	26.3	5077	2	BE474401	sp623h10_Y	462	15	561	3	BM233230	BM233230	K0334A11-
C 390	15	26.3	5077	6	CD673230	fg22d09_Y	463	15	561	7	CK105483	CK105483	UA15CP11
C 391	15	26.3	508	4	CR625121	full1-1lemg	464	15	561	11	TA338E08Q	TA338E08Q	AL45179T_T_ bruce1
C 392	15	26.3	508	5	BW542261	BM542261	465	15	562	1	AL958518	AL958518	AL958518
C 393	15	26.3	508	5	BX396625	BX396625	466	15	562	7	CW542104	CW542104	RT9_115_G
C 394	15	26.3	509	8	CD917180	CG608_1.04F	467	15	564	1	A1259362	A1259362	LP03067-5
C 395	15	26.3	510	8	DN955059	1t81d08_9	468	15	564	1	AM859585	AM859585	MR1_-C0035
C 396	15	26.3	511	6	BN964534	BAL15G03_	469	15	564	7	CK657353	CK657353	LP23567.5
C 397	15	26.3	511	6	CU109263	SCSGHR106	470	15	565	3	B1685197	B1685197	CM258364
C 398	15	26.3	512	6	B1320673	8ae47a11_	471	15	567	7	CN258363	CN258363	170004245
C 399	15	26.3	512	6	CD137389	W01_-0047U	472	15	567	9	AO733979	AO733979	HS_2151_A
C 400	15	26.3	513	2	BG702886	602684817	473	15	568	3	B5656679	B5656679	BJ565679
C 401	15	26.3	515	2	BF460628	UI-M-CGDP	474	15	569	6	CD485219	CD485219	MB8F486_U
C 402	15	26.3	516	5	BT706350	UI-M-F00-	475	15	569	6	CC821493	CC821493	B1162180
C 403	15	26.3	516	6	CD913632	G550_1181	476	15	570	2	BM092302	BM092302	BaH11C04_
C 404	15	26.3	517	6	BU162301	BU162301	477	15	570	3	CK062879	CK062879	557808r1c
C 405	15	26.3	517	6	CB503946	CB503946	478	15	572	7	B6991643	B6991643	BJ691643
C 406	15	26.3	518	9	CC091784	CC091784	479	15	573	3	B0611121	B0611121	BJ061121
C 407	15	26.3	518	9	CC154114	CSU-K34_1	480	15	573	10	CB509208	CB509208	LTgr-g88-
C 408	15	26.3	520	1	AM523402	UI-R-B00-	481	15	574	6	CB159158	CB159158	K-BST0218
C 409	15	26.3	520	3	BU464643	BU464643	482	15	576	5	BO630410	BO630410	BAQ07a05_
C 410	15	26.3	520	6	CF002757	CF002757	483	15	576	5	BO630410	BO630410	BAQ07a05_
C 411	15	26.3	521	5	BX250365	BX250365	484	15	577	3	BT785013	BT785013	BAE69G10_
C 412	15	26.3	521	6	CA952489	1q12f05_X	485	15	578	10	CM731117	CM731117	MARC_7780
C 413	15	26.3	522	6	BM177467	8a181902_	486	15	580	8	DK019579	DK019579	STR81_31
C 414	15	26.3	522	6	CFP05605	OB113B01_	487	15	580	8	CA784490	CA784490	BAE97a10_
C 415	15	26.3	524	1	AU023367	AU023367	488	15	581	7	CK782472	CK782472	UI-D-GC1-
C 416	15	26.3	524	9	AO715097	AO715097	489	15	581	7	BP292973	BP292973	BP292973
C 417	15	26.3	527	1	AU215567	AU215567	490	15	582	3	BP67328	BP67328	BP67328
C 418	15	26.3	527	6	CD133048	MG1_-0024U	491	15	582	9	AO688487	AO688487	BP67328
C 419	15	26.3	528	6	CA8000430	8aui16a11_	492	15	582	9	AO688487	AO688487	BP67328
C 420	15	26.3	529	3	BM725455	UI-E-BJ0-	493	15	585	3	BP275322	BP275322	BP275322
C 421	15	26.3	529	3	CA752388	UI-M-F00-	494	15	585	6	CB160355	CB160355	BP243007
C 422	15	26.3	530	3	BM614563	BU614563	495	15	586	3	BP243007	BP243007	BP243007
C 423	15	26.3	531	7	BU554293	BU554293	496	15	586	8	DT104268	DT104268	JGI_A00N6
C 424	15	26.3	531	7	CF861467	pe200091A	497	15	586	10	CM059491	CM059491	OC__Ba005
C 425	15	26.3	531	10	CE460439	CE460439	498	15	587	9	AZ851353	AZ851353	2M0153M02
C 426	15	26.3	532	9	CC110034	NDL_50J20	499	15	587	9	BP272595	BP272595	BP272595
C 427	15	26.3	536	2	BR843985	RCO-TMN07	500	15	593	11	FR0043928	FR0043928	FR0043928
C 428	15	26.3	536	2	BU767069	BU767069	501	15	593	11	FR0043928	FR0043928	FR0043928
C 429	15	26.3	537	10	AG251128	AG251128	502	15	594	1	FR0043928	FR0043928	FR0043928
C 430	15	26.3	538	8	BM195824	C0317E03-	503	15	594	1	FR0043928	FR0043928	FR0043928
C 431	15	26.3	538	8	CK683239	yde12b11_	504	15	595	10	AG972805	AG972805	AG972805
C 432	15	26.3	540	1	AJ872848	AJ872848	505	15	595	11	FR0011718	FR0011718	FR0011718
C 433	15	26.3	541	1	AM704843	AM704843	506	15	596	6	CA935454	CA935454	CA935454
C 434	15	26.3	541	10	CM033021	104_262.1	507	15	597	7	CO455342	CO455342	CO455342
C 435	15	26.3	543	7	AM010470	ST07B09_F	508	15	597	7	CO455342	CO455342	CO455342
C 436	15	26.3	543	7	CK440188	GQ0024D_B	509	15	599	7	CO455342	CO455342	CO455342
C 437	15	26.3	544	2	BF989596	MR2-GN012	510	15	600	2	BG801818	BG801818	BG801818
C 438	15	26.3	544	2	BM233744	K0344G02-	511	15	600	2	BG801818	BG801818	BG801818
C 439	15	26.3	544	3	BM233987	BM233987	512	15	600	6	CA952733	CA952733	CA952733
C 440	15	26.3	544	7	CK661482	LP21030_3	513	15	602	2	BE6611705	BE6611705	BE6611705
C 441	15	26.3	544	9	AO756650	HS_2128_B	514	15	602	6	CF245570	CF245570	CF245570
C 442	15	26.3	546	3	BU032154	BU032154	515	15	603	6	CA377303	CA377303	CA377303
C 443	15	26.3	546	10	CZ751357	OC__Ba010	516	15	605	1	AL877674	AL877674	AL877674
C 444	15	26.3	549	10	CL792462	OR_CBa000	517	15	605	7	CK113731	CK113731	CK113731
C 445	15	26.3	549	11	CM046285	Rebera_s	518	15	606	3	BU059222	BU059222	BU059222
C 446	15	26.3	550	9	AZ007790	AZ007790	519	15	606	6	CB504283	CB504283	CB504283
C 447	15	26.3	550	9	CC968945	CC968945	520	15	606	6	DN198088	DN198088	DN198088
C 448	15	26.3	551	10	CE358063	CE358063	521	15	607	6	CA082572	CA082572	CA082572
C 449	15	26.3	552	6	CB214898	OML05178	522	15	608	3	BU038511	BU038511	BU038511
C 450	15	26.3	554	3	BM419051	BM419051	523	15	610	7	CNS24976	CNS24976	CNS24976
C 451	15	26.3	554	5	BO806711	BO806711	524	15	611	7	CVS69333	CVS69333	CVS69333
C 452	15	26.3	555	7	CN876879	CN876879	525	15	611	6	CA499416	CA499416	CA499416
C 453	15	26.3	555	7	AL856800	AL856800	526	15	611	6	AZ793654	AZ793654	AZ793654
C 454	15	26.3	556	6	CB863572	CB863572	527	15	611	6	AZ793654	AZ793654	AZ793654
C 455	15	26.3	556	6	AO933673	RPCI-23-2	528	15	612	1	A1257060	A1257060	A1257060
C 456	15	26.3	557	2	BE378142	601237871	529	15	612	3	BU555398	BU555398	BU555398
C 457	15	26.3	557	8	DN198055	USDA-FP_1	530	15	612	7	CN464546	CN464546	CN464546
C 458	15	26.3	558	7	BP496682	AT10573_5	531	15	613	5	BQ611421	BQ611421	BQ611421
C 459	15	26.3	558	7	CK392586	K0847F01-	532	15	613	10	CZ714570	CZ714570	CZ714570
C 460	15	26.3	559	5	CA041979	88a1p1nD5	533	15	613	10	CE558175	CE558175	CE558175



534	15	26.3	614	1	A1256927	A1256927 LP03687.5	C 607	15	26.3	654	6	CA698065	CA698065 w14.pK00
535	15	26.3	615	6	CA073360	CA073360 SCRAM105	C 608	15	26.3	654	6	CD913195	CD913195 G550.117C
536	15	26.3	616	10	CZ576313	CZ576313 OA_BBa015	C 609	15	26.3	654	10	CZ763052	CZ763052 OC_BBa011
537	15	26.3	616	9	BZ804850	BZ804850 PUF6U76TB	C 610	15	26.3	655	9	Bj689989	Bj689989 Bj689989
538	15	26.3	617	11	CR875695	CR875695 Sub scrof	C 611	15	26.3	655	6	CA912185	CA912185 PCS04234
539	15	26.3	617	2	BB634742	BB634742 BB634742	C 612	15	26.3	656	2	BG401241	BG401241 602465339
540	15	26.3	617	6	CD0808759	CD0808759 LCa04P07C	C 613	15	26.3	656	7	CV088159	CV088159 est_C_v1r
541	15	26.3	618	3	BP957067	BP957067 BP957067	C 614	15	26.3	656	7	CV088159	CV088159 est_C_v1r
542	15	26.3	618	10	CL335241	CL335241 RRC144_47	C 615	15	26.3	657	2	BB353325	BB353325 BB353325
543	15	26.3	619	11	FR0035952	FR0035952	C 616	15	26.3	657	7	CK429573	CK429573 oJ38d11.Y
544	15	26.3	620	6	CF168864	CF168864 B0805G03-	C 617	15	26.3	658	1	AM546010	AM546010 L0001A07-
545	15	26.3	621	2	BB584145	BB584145 6-9A-HA P	C 618	15	26.3	658	2	BB612338	BB612338 BB612338
546	15	26.3	621	8	CK716237	CK716237 1332635 N	C 619	15	26.3	658	6	CB526565	CB526565 UT-M-PY0-
547	15	26.3	622	1	A1257956	A1257956 LP06810.5	C 620	15	26.3	658	10	CG249429	CG249429 OCYDM94TH
548	15	26.3	623	1	AL850784	AL850784 AL850784	C 621	15	26.3	660	2	BB385048	BB385048 9-6A-ZO P
549	15	26.3	623	1	AL850784	AL850784 AL850784	C 622	15	26.3	660	10	CM636692	CM636692 OA_ABa017
550	15	26.3	623	8	CK716236	CK716236 1332634 N	C 623	15	26.3	661	6	CA115901	CA115901 SCVPLB101
551	15	26.3	623	8	AZ036611	AZ036611 RPCI-23-2	C 624	15	26.3	661	6	CD412457	CD412457 Gm_CK4356
552	15	26.3	624	2	BE346171	BE346171 RPI-206	C 625	15	26.3	661	6	CD685708	CD685708 EST2229 h
553	15	26.3	625	2	BE346171	BE346171 RPI-206	C 626	15	26.3	662	1	AL873155	AL873155 AL873155
554	15	26.3	625	5	BU433543	BU433543 603221611	C 627	15	26.3	662	6	CB647442	CB647442 OSUNED10G
555	15	26.3	626	3	BU467032	BU467032 BU467032	C 628	15	26.3	663	8	DN224765	DN224765 MEST1163
556	15	26.3	626	3	BH706091	BH706091 BOWDT83TF	C 629	15	26.3	663	9	CC321101	CC321101 TAM32-21H
557	15	26.3	627	8	CK295377	CK295377 C05071E11	C 630	15	26.3	664	7	CK080980	CK080980 81710r81C
558	15	26.3	628	3	BI462453	BI462453 603203934	C 631	15	26.3	664	10	AG061955	AG061955 Pan_trog1
559	15	26.3	628	6	CF540293	CF540293 UT-M-P00-	C 632	15	26.3	665	5	BU705637	BU705637 UT-M-P00-
560	15	26.3	629	2	BG086782	BG086782 H1330B03-	C 633	15	26.3	666	7	CV132736	CV132736 est_C_v1r
561	15	26.3	629	2	BG086782	BG086782 H1330B03-	C 634	15	26.3	666	7	AZ286835	AZ286835 RPCI-23-1
562	15	26.3	629	2	BG086782	BG086782 H1330B03-	C 635	15	26.3	667	7	CK432133	CK432133 UI-D-GC1-
563	15	26.3	629	2	BG086782	BG086782 H1330B03-	C 636	15	26.3	668	7	CO980620	CO980620 GMB9008B1
564	15	26.3	630	7	CA041823	CA041823 603203934	C 637	15	26.3	668	10	AG148847	AG148847 Pan_trog1
565	15	26.3	630	7	CA041823	CA041823 603203934	C 638	15	26.3	669	2	BI143567	BI143567 602907590
566	15	26.3	631	5	CA014231	CA014231 HT10M04r	C 639	15	26.3	669	8	CK202589	CK202589 MNS04583
567	15	26.3	631	6	CB522002	CB522002 UI-M-GH0-	C 640	15	26.3	670	8	CK886409	CK886409 JG1_CAA05
568	15	26.3	632	1	AU212916	AU212916 AU212916	C 641	15	26.3	671	1	AM835061	AM835061 RC2-LT000
569	15	26.3	633	8	CK141953	CK141953 1281469 N	C 642	15	26.3	671	6	CB523346	CB523346 UI-M-GH0-
570	15	26.3	633	8	DT045569	DT045569 Le_lvo_32	C 643	15	26.3	671	6	CF532351	CF532351 UT-M-GH0-
571	15	26.3	634	1	AL852007	AL852007 AL852007	C 644	15	26.3	671	7	CN875077	CN875077 010131NAR
572	15	26.3	634	1	AL852007	AL852007 AL852007	C 645	15	26.3	672	2	BG017653	BG017653 dab09d05.
573	15	26.3	634	1	AL852007	AL852007 AL852007	C 646	15	26.3	672	2	BG017653	BG017653 dab09d05.
574	15	26.3	636	6	CA061753	CA061753 88A1rB51	C 647	15	26.3	672	2	BG017653	BG017653 dab09d05.
575	15	26.3	636	6	CA061753	CA061753 88A1rB51	C 648	15	26.3	672	2	BG017653	BG017653 dab09d05.
576	15	26.3	636	6	CA061753	CA061753 88A1rB51	C 649	15	26.3	672	11	CN8504HSQ	CN8504HSQ ZMMBBD019
577	15	26.3	637	10	CG134558	CG134558 PUFVT02TB	C 650	15	26.3	673	5	BU482998	BU482998 603469148
578	15	26.3	637	10	CG134558	CG134558 PUFVT02TB	C 651	15	26.3	674	3	BM107850	BM107850 a01n15 CD
579	15	26.3	638	5	BM272466	BM272466 BM272466	C 652	15	26.3	674	10	AG069958	AG069958 Pan_trog1
580	15	26.3	638	5	BM272466	BM272466 BM272466	C 653	15	26.3	675	8	DR798066	DR798066 Gm_BFD002
581	15	26.3	639	10	AG941709	AG941709 Drosophila	C 654	15	26.3	675	10	CM671481	CM671481 OG_BBa003
582	15	26.3	640	6	CA295825	CA295825 SCRLV102	C 655	15	26.3	676	9	BZ138051	BZ138051 CH230-338
583	15	26.3	640	6	CA295825	CA295825 SCRLV102	C 656	15	26.3	677	6	CA119177	CA119177 SCGSHR106
584	15	26.3	641	1	AL847248	AL847248 AL847248	C 657	15	26.3	677	10	CL573592	CL573592 OB_Ba001
585	15	26.3	641	7	CV089366	CV089366 est_C_v1r	C 658	15	26.3	678	9	AZ433504	AZ433504 1M0219G21
586	15	26.3	642	2	BB617638	BB617638 BB617638	C 659	15	26.3	678	10	CZ571289	CZ571289 OB_Ba003
587	15	26.3	642	2	BB617638	BB617638 BB617638	C 660	15	26.3	679	8	CK559069	CK559069 yda6f08
588	15	26.3	643	8	W73221	W73221 2d53g11.r1	C 661	15	26.3	679	9	CE163930	CE163930 CSU-K34.1
589	15	26.3	644	1	A1258174	A1258174 LP01305.5	C 662	15	26.3	679	9	CE163930	CE163930 CSU-K34.1
590	15	26.3	644	10	CL321858	CL321858 CH242-15K	C 663	15	26.3	680	7	CK765837	CK765837 atf02-12m
591	15	26.3	645	7	CN220898	CN220898 WLA025E09	C 664	15	26.3	680	7	CK765837	CK765837 atf02-12m
592	15	26.3	647	1	AL887137	AL887137 AL887137	C 665	15	26.3	682	5	BU029387	BU029387 UT-M-HS0-
593	15	26.3	648	2	BF500861	BF500861 AT16012.5	C 666	15	26.3	682	6	CD648076	CD648076 AUF_101.M
594	15	26.3	648	2	BF500861	BF500861 AT16012.5	C 667	15	26.3	683	7	CR438197	CR438197 CR438197
595	15	26.3	648	6	CB505188	CB505188 B8a1mge50	C 668	15	26.3	684	7	CR438197	CR438197 CR438197
596	15	26.3	648	6	CB505188	CB505188 B8a1mge50	C 669	15	26.3	684	9	BH993147	BH993147 oe111e02.
597	15	26.3	649	3	BU138966	BU138966 BU138966	C 670	15	26.3	685	2	BE015329	BE015329 EST555 Ma
598	15	26.3	651	7	CK569253	CK569253 HO12K3W	C 671	15	26.3	685	5	BE015329	BE015329 EST555 Ma
599	15	26.3	651	10	CL801724	CL801724 OR_CBA001	C 672	15	26.3	685	5	BE015329	BE015329 EST555 Ma
600	15	26.3	652	5	BU389364	BU389364 603511694	C 673	15	26.3	685	5	BE015329	BE015329 EST555 Ma
601	15	26.3	652	7	CN825254	CN825254 LjPEST4e9	C 674	15	26.3	686	1	A1612632	A1612632 AEMTB065
602	15	26.3	652	9	AO578387	AO578387 nbdx0092D	C 675	15	26.3	686	11	CR044627	CR044627 Forward_s
603	15	26.3	653	10	CM271401	CM271401 104_743_1	C 676	15	26.3	686	11	CR344050	CR344050 mte1-7706
604	15	26.3	653	1	AL891710	AL891710 AL891710	C 677	15	26.3	688	10	CL814128	CL814128 OR_CBA003
605	15	26.3	653	2	BF646250	BF646250 NF072D04E	C 678	15	26.3	689	7	CK661635	CK661635 LP21258.5
606	15	26.3	653	7	CK637147	CK637147 UT-M-H00-	C 679	15	26.3	690	6	CA751321	CA751321 UT-M-P00-



C 680	15	26.3	691	5	BW074453	BW074453		C 753	15	26.3	734	10	AG412566
C 681	15	26.3	692	6	CD770684	CD770684	AGENCOURT	C 754	15	26.3	735	10	CV538022
C 682	15	26.3	692	6	CF522615	CF522615	AGENCOURT	C 755	15	26.3	735	10	AG417283
C 683	15	26.3	693	9	CC099931	CC099931	CSU -K34.1	C 756	15	26.3	736	1	AA820595
C 684	15	26.3	694	3	BM677877	BM677877	UI-E-BJ0-	C 757	15	26.3	736	1	AU123828
C 685	15	26.3	694	3	BZ478045	BZ478045	BONPDQ3TR	C 758	15	26.3	736	1	AV928303
C 686	15	26.3	695	9	CE114869	CE114869	tigr-gsm-	C 759	15	26.3	736	8	DN880918
C 687	15	26.3	695	7	CV132403	CV132403	eac_c_vlr	C 760	15	26.3	737	3	BP694197
C 688	15	26.3	695	8	DR542383	DR542383	MSO1038.B	C 761	15	26.3	737	6	CA945454
C 689	15	26.3	695	8	DN084489	DN084489	JGI_AIZU4	C 762	15	26.3	739	6	CD364758
C 690	15	26.3	695	10	CL390717	CL390717	ZMMBDB019	C 763	15	26.3	739	8	DR682953
C 691	15	26.3	696	7	CK657867	CK657867	LP24494.5	C 764	15	26.3	741	3	BI458933
C 692	15	26.3	697	9	AZ539949	AZ539949	IM0103F03	C 765	15	26.3	741	3	BI686243
C 693	15	26.3	697	9	AZ539949	AZ539949	CP39F12.F	C 766	15	26.3	741	5	BM495228
C 694	15	26.3	698	11	CR285159	CR285159	meb4-17YL	C 767	15	26.3	742	7	CK635832
C 695	15	26.3	698	11	CR662351	CR662351	meb4-17YL	C 768	15	26.3	742	9	BZ061972
C 696	15	26.3	699	3	BJ273444	BJ273444		C 769	15	26.3	743	10	AG520614
C 697	15	26.3	699	5	BU480388	BU480388	603469256	C 770	15	26.3	743	10	CL863153
C 698	15	26.3	699	7	CO196757	CO196757	GEOI_1_H0	C 771	15	26.3	744	7	CNS37446
C 699	15	26.3	699	11	CNS031H1	AL245583	Tetraodon	C 772	15	26.3	744	9	AQ933157
C 700	15	26.3	700	9	CA062144	CA062144	ssta1rpb51	C 773	15	26.3	745	10	AG608582
C 701	15	26.3	700	9	BN972887	BN972887	odj33f05.	C 774	15	26.3	745	10	CL849676
C 702	15	26.3	701	10	CM641148	CM641148	OA_ABA017	C 775	15	26.3	746	2	BF493933
C 703	15	26.3	701	10	CZ754015	CZ754015	OC_B8010	C 776	15	26.3	746	6	CF522041
C 704	15	26.3	702	9	BH822915	BH822915	BACP18-G	C 777	15	26.3	747	8	DN279853
C 705	15	26.3	702	9	BH974573	BH974573	cdj06a07.	C 778	15	26.3	747	10	CL678277
C 706	15	26.3	702	6	CG301536	CG301536	OQVDRS1TV	C 779	15	26.3	748	7	CO091907
C 707	15	26.3	703	10	CF729319	CF729319	UI-M-HD0-	C 780	15	26.3	749	15	AM688034
C 708	15	26.3	703	10	CM221970	CM221970	104_657.1	C 781	15	26.3	749	6	CB520498
C 709	15	26.3	705	7	CNS33084	CNS33084	UI-M-H00-	C 782	15	26.3	750	8	CK543202
C 710	15	26.3	705	7	CV088109	CV088109	eac_c_vlr	C 783	15	26.3	753	8	CK543202
C 711	15	26.3	706	6	CA325071	CA325071	UI-M-FY0-	C 784	15	26.3	753	8	CK543202
C 712	15	26.3	706	6	CD649879	CD649879	CVG110058	C 785	15	26.3	755	8	BI078927
C 713	15	26.3	707	2	BBS53809	BBS53809		C 786	15	26.3	757	7	CX151561
C 714	15	26.3	707	7	CV556388	CV556388	UI-M-HZ0-	C 787	15	26.3	757	11	BP677920
C 715	15	26.3	707	10	CE828317	CE828317	tigr-gsm-	C 788	15	26.3	758	10	CT020497
C 716	15	26.3	708	5	BM271224	BM271224	BM271224	C 789	15	26.3	759	8	CM648310
C 717	15	26.3	710	5	BM373158	BM373158	BM436311	C 790	15	26.3	760	9	DN932231
C 718	15	26.3	711	9	BH937295	BH937295	BM373158	C 791	15	26.3	761	10	BH339208
C 719	15	26.3	713	3	BM121554	BM121554	BM121554	C 792	15	26.3	763	7	CG927650
C 720	15	26.3	713	3	BM121554	BM121554	BM121554	C 793	15	26.3	763	8	CG927650
C 721	15	26.3	715	7	CK637329	CK637329	CGF110035	C 794	15	26.3	764	8	CG927650
C 722	15	26.3	715	7	CK637329	CK637329	CGF110035	C 795	15	26.3	764	8	CG927650
C 723	15	26.3	717	9	AQ840603	AQ840603	170006001	C 796	15	26.3	765	6	CB685449
C 724	15	26.3	717	9	AQ840603	AQ840603	170006001	C 797	15	26.3	766	2	BE744067
C 725	15	26.3	718	2	BF933036	BF933036	602253996	C 798	15	26.3	766	8	CB962185
C 726	15	26.3	718	7	CV088762	CV088762	eac_c_vlr	C 799	15	26.3	768	10	DR895315
C 727	15	26.3	718	8	CX368578	CX368578	JGI_XZT54	C 800	15	26.3	768	10	CM006909
C 728	15	26.3	718	8	CX368578	CX368578	JGI_XZT54	C 801	15	26.3	769	10	CM006909
C 729	15	26.3	719	8	CX707297	CX707297	gmtrDRN80	C 802	15	26.3	770	9	CC627024
C 730	15	26.3	719	8	CX707297	CX707297	gmtrDRN80	C 803	15	26.3	771	10	CL858372
C 731	15	26.3	719	10	AG454269	AG454269	mue musecu	C 804	15	26.3	773	5	BM774686
C 732	15	26.3	720	5	BQ850744	BQ850744	OGB13H05.	C 805	15	26.3	773	7	CK461105
C 733	15	26.3	721	8	CX707641	CX707641	gmtrDRN80	C 806	15	26.3	773	7	CK461105
C 734	15	26.3	721	10	AG045358	AG045358	Pan t1c01	C 807	15	26.3	773	7	CK461105
C 735	15	26.3	722	9	CC072062	CC072062	CSU-K33r.	C 808	15	26.3	774	6	CB674259
C 736	15	26.3	723	1	AU123775	AU123775	BM433598	C 809	15	26.3	774	6	CB674259
C 737	15	26.3	723	5	BZ467789	BZ467789	BONBQ39TF	C 810	15	26.3	774	6	CB674259
C 738	15	26.3	724	10	AG399918	AG399918	mue musecu	C 811	15	26.3	774	10	CZ133447
C 739	15	26.3	725	8	DN205789	DN205789	MST823_A	C 812	15	26.3	776	9	CN459324
C 740	15	26.3	725	10	CL754252	CL754252	OR_BBA012	C 813	15	26.3	776	9	CN459324
C 741	15	26.3	726	7	CK661618	CK661618	LP21239.5	C 814	15	26.3	777	10	CC109644
C 742	15	26.3	726	7	CK661618	CK661618	LP21239.5	C 815	15	26.3	778	10	CC109644
C 743	15	26.3	726	7	CK661618	CK661618	LP21239.5	C 816	15	26.3	778	10	CC109644
C 744	15	26.3	727	6	CF520269	CF520269	AGENCOURT	C 817	15	26.3	781	1	BM463095
C 745	15	26.3	727	6	CF520269	CF520269	AGENCOURT	C 818	15	26.3	781	1	BM463095
C 746	15	26.3	728	6	CF520548	CF520548	AGENCOURT	C 819	15	26.3	781	1	BM463095
C 747	15	26.3	728	6	CF520548	CF520548	AGENCOURT	C 820	15	26.3	781	1	BM463095
C 748	15	26.3	730	3	BI560034	BI560034	603253214	C 821	15	26.3	782	8	DR792409
C 749	15	26.3	730	3	BI560034	BI560034	603253214	C 822	15	26.3	782	8	DR792409
C 750	15	26.3	731	6	CF532481	CF532481	UI-M-GH0-	C 823	15	26.3	784	5	BM963280
C 751	15	26.3	732	10	AG277640	AG277640	mue musecu	C 824	15	26.3	785	7	CN525049
C 752	15	26.3	733	10	DR729193	DR729193	AGENCOURT	C 825	15	26.3	785	9	BE975609
C 753	15	26.3	734	10	AG412566	AG412566	mue musecu	C 826	15	26.3	786	10	CM006909
C 754	15	26.3	735	10	CV538022	CV538022	NOD_249_C	C 827	15	26.3	787	11	CM006909
C 755	15	26.3	735	10	AG417283	AG417283	mue musecu	C 828	15	26.3	788	12	CM006909
C 756	15	26.3	736	1	AA820595	AA820595	LD24408.5	C 829	15	26.3	789	13	CM006909
C 757	15	26.3	736	1	AU123828	AU123828		C 830	15	26.3	790	14	CM006909
C 758	15	26.3	736	1	AV928303	AV928303		C 831	15	26.3	791	15	CM006909
C 759	15	26.3	736	8	DN880918	DN880918	1162065_M	C 832	15	26.3	792	16	CM006909
C 760	15	26.3	737	3	BP694197	BP694197		C 833	15	26.3	793	17	CM006909
C 761	15	26.3	737	6	CA945454	CA945454		C 834	15	26.3	794	18	CM006909
C 762	15	26.3	739	6	CD364758	CD364758		C 835	15	26.3	795	19	CM006909
C 763	15	26.3	739	8	DR682953	DR682953		C 836	15	26.3	796	20	CM006909
C 764	15	26.3	741	3	BI458933	BI458933		C 837	15	26.3	797	21	CM006909
C 765	15	26.3	741	3	BI686243	BI686243		C 838	15	26.3	798	22	CM006909
C 766	15	26.3	741	5	BM495228	BM495228		C 839	15	26.3	799	23	CM006909
C 767	15	26.3	742	7	CK635832	CK635832		C 840	15	26.3	800	24	CM006909
C 768	15	26.3	742	9	BZ061972	BZ061972		C 841	15	26.3	801	25	CM006909
C 769	15	26.3	743	10	AG520614	AG520614		C 842	15	26.3	802	26	CM006909
C 770	15	26.3	743	10	CL863153	CL863153		C 843	15	26.3	803	27	CM006909
C 771	15	26.3	744	7	CNS37446	CNS37446		C 844	15	26.3	804	28	CM006909
C 772	15	26.3	744	9	AQ933157	AQ933157		C 845	15	26.3	805	29	CM006909
C 773	15	26.3	745	10	AG608582	AG608582		C 846	15	26.3	806	30	CM006909
C 774	15	26.3	745	10	CL849676	CL849676		C 847	15	26.3	807	31	CM006909
C 775	15	26.3	746	2	BF493933	BF493933		C 848	15	26.3	808	32	CM006909
C 776	15	26.3	746	6	CF522041	CF522041		C 849	15	26			



826	15	26.3	786	6	BJ385598	BJ385598	BJ385598	899	15	26.3	838	3	B1658582	B1658582	603284315
827	15	26.3	787	7	CK872355	CK872355	AGENCOCURT	900	15	26.3	842	2	BF780828	BF780828	602105714
828	15	26.3	788	2	BG170894	BG170894	602323657	901	15	26.3	843	7	CK3971148	CK3971148	AGENCOCURT
829	15	26.3	789	6	CB622958	CB622958	OS1IEA10F	902	15	26.3	843	9	AQ329432	AQ329432	nbxb0045A
830	15	26.3	789	5	BUT50552	BUT50552	CH3K034.B	903	15	26.3	844	8	CK387359	CK387359	UCI_XRT21
831	15	26.3	789	9	BZ680791	PUBCK03TD		904	15	26.3	844	10	CZ702256	CZ702256	OC_Ba001
832	15	26.3	790	10	CL356576	OB_Ba003		905	15	26.3	844	10	AG864331	AG864331	Oryza sat
833	15	26.3	791	7	CO045168			906	15	26.3	845	2	BG031293	BG031293	602299278
834	15	26.3	791	11	CR871751	Sue sciof		907	15	26.3	845	2	BG031293	BG031293	602299278
835	15	26.3	793	10	CZ292783			908	15	26.3	845	10	CG298195	CG298195	OSG0FA19TH
836	15	26.3	795	6	CB622795	OS1IEA10A		909	15	26.3	849	9	BZ838223	BZ838223	CH240_204
837	15	26.3	795	10	CM614402	OA_Aba015		910	15	26.3	851	5	BF718961	BF718961	BX718961
838	15	26.3	796	8	DR667550	ZM_BFP008		911	15	26.3	851	7	CV558154	CV558154	UI-M-H2O-
839	15	26.3	797	10	CG311016			912	15	26.3	851	10	CZ698163	CZ698163	OC_Ba001
840	15	26.3	798	8	CK807899	CG311016	OGXEO70TH	913	15	26.3	853	1	AU123662	AU123662	OC_Ba001
841	15	26.3	798	8	CV556934	UI-M-H2O-		914	15	26.3	854	4	CU189049	CU189049	AGENCOCURT
842	15	26.3	800	7	CK969813	ZP101-P00		915	15	26.3	856	7	CK095594	CK095594	UA15CP11
843	15	26.3	801	7	CK969813	CR414419		916	15	26.3	856	7	BH136200	BH136200	ENTNK89TR
844	15	26.3	801	8	CK464638	JGI_XZG47		917	15	26.3	858	7	CY283632	CY283632	WS0187_B2
845	15	26.3	801	8	CK464638	JGI_XZG47		918	15	26.3	860	2	BG242605	BG242605	602354019
846	15	26.3	802	7	CK708313	gmTDCNSO		919	15	26.3	862	8	CV883995	CV883995	UI-M-H2O-
847	15	26.3	802	7	CJ038924	CJ038924		920	15	26.3	863	1	AU121955	AU121955	AU121955
848	15	26.3	806	8	CV887290	UCRCG04_2		921	15	26.3	864	5	BU187033	BU187033	AGENCOCURT
849	15	26.3	807	5	BU744504	CH1M002_F		922	15	26.3	865	6	CB560973	CB560973	AGENCOCURT
850	15	26.3	807	10	CG134559	CG134559	PUPFYV02TD	923	15	26.3	866	9	CC100325	CC100325	CSU-K34.1
851	15	26.3	808	1	AU119381	AU119381		924	15	26.3	866	10	AG833844	AG833844	Oryza sat
852	15	26.3	809	7	CV559957	UI-M-H2O-		925	15	26.3	869	5	BG906952	BG906952	AGENCOCURT
853	15	26.3	809	10	CG075229	PUCO46TB		926	15	26.3	869	8	DR538523	DR538523	WS0227_B2
854	15	26.3	809	10	CL620647	OR_BBa001		927	15	26.3	871	10	CL097878	CL097878	ISB1-30H1
855	15	26.3	811	10	AG472624	Mvb_muscu		928	15	26.3	872	10	CG954407	CG954407	MBEKC58TF
856	15	26.3	812	8	CK376780	JGI_XZT33		929	15	26.3	874	5	BQ799935	BQ799935	EST_2104
857	15	26.3	812	8	DR924210	ZM_BFP001		930	15	26.3	875	9	CB865463	CB865463	NDL_109M2
858	15	26.3	813	9	BH570150	BH570150	BOHBT48PT	931	15	26.3	875	3	B1860163	B1860163	603387355
859	15	26.3	813	10	CL957625	OBIFCC036		932	15	26.3	877	10	CL475397	CL475397	SA1L_238
860	15	26.3	814	8	CK783213	HMSC3_19		933	15	26.3	878	7	CO247267	CO247267	AGENCOCURT
861	15	26.3	815	8	CC105765	CSU-K34.1		934	15	26.3	878	8	DR497035	DR497035	WS02911.C
862	15	26.3	815	8	DT089717	JGI_AANX2		935	15	26.3	880	6	CA980021	CA980021	AGENCOCURT
863	15	26.3	816	9	BZ540122			936	15	26.3	880	6	CF578838	CF578838	MBEKC58TF
864	15	26.3	817	10	CM645265	OA_ABa018		937	15	26.3	880	10	CG922368	CG922368	MBCDC79TR
865	15	26.3	818	9	CC125910	NDL_28M17		938	15	26.3	881	5	BU183778	BU183778	AGENCOCURT
866	15	26.3	819	2	BH869858	60144696		939	15	26.3	881	10	CM648168	CM648168	OA_ABa018
867	15	26.3	819	9	BZ744912	OGFCC68TM		940	15	26.3	881	10	CL664253	CL664253	PRI0146C
868	15	26.3	820	7	CK639225	UI-M-HO0-		941	15	26.3	882	6	CD105895	CD105895	AGENCOCURT
869	15	26.3	821	6	CB624302	OS1IEA12M		942	15	26.3	882	10	CL475424	CL475424	SA1L_238
870	15	26.3	821	9	CC094095	CSU-K34.1		943	15	26.3	883	9	CC099962	CC099962	CSU-K34.1
871	15	26.3	821	9	CC931299	PURHC67TB		944	15	26.3	883	10	AG831691	AG831691	Oryza sat
872	15	26.3	822	6	CB647515	OSUNEB10H		945	15	26.3	884	6	CA788363	CA788363	AGENCOCURT
873	15	26.3	822	7	CO466329	MCCCL2003		946	15	26.3	884	9	CC391303	CC391303	PURHC67TD
874	15	26.3	822	9	BH572493	BQGMPT0TR		947	15	26.3	886	2	BF338640	BF338640	602034328
875	15	26.3	822	8	CC550264	CH240_434		948	15	26.3	887	10	CM967749	CM967749	AI1AA-aac0
876	15	26.3	823	8	DR553522	KS03226.C		949	15	26.3	888	3	BM012843	BM012843	603637573
877	15	26.3	823	9	CC892513	ZMMBEC052		950	15	26.3	889	7	CR438208	CR438208	CR438208
878	15	26.3	825	6	CB651100	OSUNEB15P		951	15	26.3	890	8	DR503410	DR503410	WS0298_B2
879	15	26.3	826	1	AM016031	AM016031		952	15	26.3	890	10	CZ717361	CZ717361	OC_Ba004
880	15	26.3	826	3	BI454210	603170634		953	15	26.3	891	9	CC354827	CC354827	PURHNV09TD
881	15	26.3	826	9	CC130079	NDL_42117		954	15	26.3	893	2	BF701310	BF701310	602128403
882	15	26.3	826	9	CC155107	CSU-K34.1		955	15	26.3	894	3	BI407330	BI407330	602919460
883	15	26.3	827	7	CC438184	PURHC67TB		956	15	26.3	894	7	CV558583	CV558583	UI-M-H2O-
884	15	26.3	828	7	CO115697	CO115697		957	15	26.3	896	8	CV922190	CV922190	PURHC67TB
885	15	26.3	828	11	CNS03SGK	AL258509	Tetraodon	958	15	26.3	897	9	CC097564	CC097564	CSU-K34.1
886	15	26.3	829	9	CC152814	CSU-K34.1		959	15	26.3	897	8	CV705415	CV705415	gmTDCNSO
887	15	26.3	830	1	AJ823787	AG823787		960	15	26.3	898	6	DR650363	DR650363	EST105048
888	15	26.3	830	10	AG879849	AG879849	Oryza sat	961	15	26.3	904	2	BZ559919	BZ559919	601345472
889	15	26.3	832	10	CG311006	OGXEO70TH		962	15	26.3	905	10	CZ871513	CZ871513	OC_Ba027
890	15	26.3	833	7	CK238020	AGENCOCURT		963	15	26.3	906	7	CO468475	CO468475	MCCS1504
891	15	26.3	833	10	CM581130	OA_ABa011		964	15	26.3	907	7	CK424693	CK424693	AUF_IPSto
892	15	26.3	834	9	B2135191	CH230-385		965	15	26.3	907	7	CV558778	CV558778	UI-M-H2O-
893	15	26.3	834	10	CL677469	PRI0120B		966	15	26.3	908	7	BX849792	BX849792	BX849792
894	15	26.3	835	3	BP714990	BP714990		967	15	26.3	908	9	AZ550512	AZ550512	ENTG333TF
895	15	26.3	835	10	CG932675	MBEKC02TR		968	15	26.3	909	5	BQ931560	BQ931560	AGENCOCURT
896	15	26.3	837	7	CO457465	CO457465		969	15	26.3	909	8	CV711293	CV711293	gmTDCNSO
897	15	26.3	837	7	CV529266	AIIV_O10A		970	15	26.3	910	2	BF568701	BF568701	602184346
898	15	26.3	837	9	CC438187	PURHC67TD		971	15	26.3	910	8	CV712613	CV712613	RRPQ1_3.D







SOURCE  
ORGANISM Mesembryanthemum crystallinum (common iceplant)  
Mesembryanthemum crystallinum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Alzaceae; Mesembryanthemum.  
REFERENCE  
AUTHORS Cushman, J.C.  
TITLE An expressed sequence tag database for the common ice plant,  
Mesembryanthemum crystallinum  
JOURNAL  
COMMENT Unpublished (1997)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T7  
BACKWARD: T3  
Plate: L48-7 row: D column: 6  
Seq primer: T3  
High quality sequence stop: 350  
POLYA=No.  
FEATURES  
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1. 555  
Location/Qualifiers  
/organism="Mesembryanthemum crystallinum"  
/mol\_type="mRNA"  
/db\_xref="taxon:3544"  
/clone="L48-642"  
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/dev\_stage="Six week old"  
/clone\_lib="Ice plant Lambda Uni-Zap XR expression  
library, 48 hours NaCl treatment"  
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
ORIGIN  
Query Match 31.6%; Score 18; DB 2; Length 555;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 34 ATGGAATCCCTGATTGAT 51  
Db 209 ATGGAATCCCTGATTGAT 226  
RESULT 4  
AM053908 558 bp mRNA linear EST 20-FEB-2001  
LOCUS L30-234873 Ice plant Lambda Uni-Zap XR expression library, 30 hours  
NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-2348  
5', mRNA sequence.  
ACCESSION  
VERSION AM053908  
KEYWORDS AM053908.1 GI:5917101  
SOURCE EST.  
ORGANISM Mesembryanthemum crystallinum (common iceplant)  
Mesembryanthemum crystallinum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Alzaceae; Mesembryanthemum.  
REFERENCE  
AUTHORS Cushman, J.C.  
TITLE An expressed sequence tag database for the common ice plant,  
Mesembryanthemum crystallinum  
JOURNAL  
COMMENT Unpublished (1997)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu

Poly(A) tail, 24 nt: 559. .582  
PCR Primers  
FORWARD: T7  
BACKWARD: T3  
Insert Length: 582 Std Error: 2.00  
Plate: L30-24 row: E column: 4  
Seq primer: T3  
High quality sequence stop: 450.  
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/organism="Mesembryanthemum crystallinum"  
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/db\_xref="taxon:3544"  
/clone="L30-2348"  
/tissue\_type="leaf, 30 h 0.4M NaCl"  
/dev\_stage="Six week old"  
/clone\_lib="Ice plant Lambda Uni-Zap XR expression  
library, 30 hours NaCl treatment"  
/note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1:  
EcoRI; Site\_2: XhoI"  
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Query Match 31.6%; Score 18; DB 1; Length 558;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 34 ATGGAATCCCTGATTGAT 51  
Db 422 ATGGAATCCCTGATTGAT 405  
RESULT 5  
BM658306 637 bp mRNA linear EST 26-FEB-2002  
LOCUS MCR058E05 70395 Ice plant Lambda Uni-Zap XR expression library, 48  
hours NaCl treatment prescreened for removal of highly abundant  
transcripts Mesembryanthemum crystallinum cDNA clone MCR058E05 5,  
mRNA sequence.  
ACCESSION  
VERSION BM658306  
KEYWORDS BM658306.1 GI:18957817  
SOURCE EST.  
ORGANISM Mesembryanthemum crystallinum (common iceplant)  
Mesembryanthemum crystallinum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Caryophyllales; Alzaceae; Mesembryanthemum.  
REFERENCE  
AUTHORS Cushman, J.C.  
TITLE An expressed sequence tag database for the common ice plant,  
Mesembryanthemum crystallinum  
JOURNAL  
COMMENT Unpublished (1997)  
Contact: Cushman JC  
Department of Biochemistry  
University of Nevada  
MS200, Reno, NV 89557-0014, USA  
Tel: 775-784-1918  
Fax: 775-784-1650  
Email: jcushman@unr.edu  
PCR Primers  
FORWARD: T3 20mer  
BACKWARD: T7 21mer  
Plate: 058 row: E column: 05  
Seq primer: T3 20mer  
High quality sequence stop: 637.  
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/clone="MCR058E05"  
/tissue\_type="leaf"  
/dev\_stage="six-week-old"  
/clone\_lib="Ice plant Lambda Uni-Zap XR expression



library, 48 hours NaCl treatment prescreened for removal of highly abundant transcripts" /note="Vector: Lambda Uni-Zap XR, Bluescript SK-; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 31.6%; Score 18; DB 3; Length 637;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 ATGGAATCCCTGATTCAT 51  
|||||  
Db 570 ATGGAATCCCTGATTCAT 553

RESULT 6  
BI869110/c 690 bp mRNA linear EST 11-OCT-2001  
LOCUS 603395428F1 NIH\_MGC\_90 Homo sapiens cDNA clone IMAGE:5405238 5',  
DEFINITION  
BI869110  
BI869110  
BI869110.1 GI:16042783  
RNA sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 690)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-rcmail.nih.gov  
Tissue Procurement: ATCC  
cDNA Library Preparation: Life Technologies, Inc.  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
plate: LLAM12033 row: h column: 07  
High quality sequence stop: 660.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT  
Location/Qualifiers  
1. 690  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/lab\_host="PH10B (phage-resistant)"  
/clone\_lib="NIH MGC 90"  
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Site 2: SalI; cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC library."

## FEATURES

## source

1. 690  
/organism="Homo sapiens"  
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/note="Organ: liver; Vector: PCMV-SPORT6; Site 1: NotI;  
Site 2: SalI; cloned unidirectionally; oligo-dT primed.  
Average insert size 1.7 kb. Library enriched for  
full-length clones and constructed by Life Technologies.  
Note: this is a NIH\_MGC library."

## ORIGIN

Query Match 31.6%; Score 18; DB 3; Length 690;  
Best Local Similarity 100.0%; Pred. No. 20;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 19 CAGACCGTGACATGATG 36  
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Db 351 CAGACCGTGACATGATG 334

RESULT 7  
A1788617 197 bp mRNA linear EST 02-JUL-1999  
LOCUS UK47C09.x1 Sugano mouse kidney m1a Mus musculus cDNA clone  
DEFINITION IMAGE:1972144 3' similar to gb:116919 Mus musculus (MOUSE);, mRNA

sequence.  
A1788617  
A1788617.1 GI:5336333  
EST.  
Mus musculus (house mouse)  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murine; Mus.  
1 (bases 1 to 197)  
Marr, M., Haller, U., Kucaba, T., Martin, J., Beck, C., Wylie, T.,  
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y.,  
Person, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R.,  
Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,  
Waterston, R. and Wilson, R.  
The Mashu-NCI Mouse EST Project 1999  
Unpublished (1999)  
Other ESTs: uk47c09.y1  
Contact: Marra M/Mashu-NCI Mouse EST Project 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@watsn.wustl.edu  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:968884  
Trace considered overall poor quality  
Seq primer: custom primer used  
High quality sequence stop: 1.  
Location/Qualifiers  
1. 197  
/organism="Mus musculus"  
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/strain="C57BL"  
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/sex="female"  
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/lab\_host="DH10B"  
/clone\_lib="Sugano mouse kidney m1a"  
/note="Organ: kidney; Vector: pME18S-FL3; Site 1: DraIII  
(CACTGCTG); Site 2: DraIII (CACCATGTG); 1st strand cDNA  
was primed with an oligo(dT) primer  
[ATGTCGCTTTTCTTTTCTTTT]; double-stranded cDNA was  
ligated to a DraIII adaptor [GTGACCTACTGG] digested  
and cloned into distinct DraIII sites of the pME18S-FL3  
vector (5' site CACTGCTG, 3' site CACCATGTG). XhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTTCGCTTAAAGCTGCG and 3' end  
primer CGACCTGACGCTCGACACA."

## ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 197;  
Best Local Similarity 100.0%; Pred. No. 73;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 ATGATGATCCCTGAT 47  
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Db 69 ATGATGATCCCTGAT 85

RESULT 8  
BP926030 267 bp mRNA linear EST 23-FEB-2005  
LOCUS BP926030 full-length enriched poplar cDNA library Populus nigra  
DEFINITION BP926030  
BP926030  
BP926030.1 GI:60207656  
CDNA clone FmFL1-053\_p13.f 5', mRNA sequence.  
ACCESSION  
VERSION  
KEYWORDS  
EST.



**SOURCE**  
**ORGANISM** *Populus nigra*  
*Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.*  
**REFERENCE** 1 (bases 1 to 267)  
**AUTHORS** Nanjo,T., Futamura,N., Nishiguchi,M., Igasaki,T., Shinzaki,K. and Shiohara,K.  
**TITLE** Characterization of full-length enriched expressed sequence tags of stress-treated poplar leaves  
**JOURNAL** Plant Cell Physiol. 45 (12), 1738-1748 (2004)  
**PUBMED** 15653793  
**COMMENT** Contact: Tokihiko Nanjo  
Molecular and Cell Biology  
Forestry and Forest Products Research Institute (FFPRI)  
1 Matsunosato, Tsukuba, Ibaraki, 305-8687, Japan  
Tel: 81-29-873-3211  
Fax: 81-29-873-0507  
Email: nanjo@affrc.go.jp.  
**FEATURES**  
**source**  
1..267  
/organism="Populus nigra"  
/mol\_type="mRNA"  
/db\_xref="taxon:3691"  
/clone="PnPII-053\_P13.f"  
/sex="female"  
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/dev\_stage="juvenile"  
/clone\_lib="full-length enriched poplar cDNA library"  
/notes="synonym: Populus nigra var. italica"  
**ORIGIN**  
Query Match 29.8%; Score 17; DB 3; Length 267;  
Best Local Similarity 100.0%; Pred. No. 74;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 27 GACATGATGGAATCCC 43  
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**Db** 75 GACATGATGGAATCCC 91  
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**RESULT 9**  
BG731863 366 bp mRNA linear EST 09-MAY-2001  
ps07a06.y3 Trichinella spiralis ML CMTSPT JASMER Trichinella  
spALICE cDNA 5' similar to TR:Q18136 Q18136 SIMILAR TO EF-HAND  
CALCIUM BINDING PROTEIN. NCBI GI: 1065541. [1] ; mRNA sequence.  
**ACCESSION** BG731863  
**VERSION** BG731863.1 GI:14016938  
**KEYWORDS** EST.  
**SOURCE** Trichinella spiralis  
**ORGANISM** Trichinella spiralis  
Eukaryota; Metazoa; Nematoda; Trichocephalida;  
Trichinellidae; Trichinella.  
1 (bases 1 to 366)  
McGarter,J., Clifton,S., Chiapelli,B., Page,D., Martin,J.,  
Wyllie,I., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Rittler,E., Bennett,J., Franklin,C.,  
Tsagarashvili,I., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
Harvey,N., Schurk,Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCamr,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
**TITLE** The Washington Univ. Nematode EST Project, 1999  
**JOURNAL** Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watsn.wustl.edu  
(djasmervetmed.wu.edu) at Washington State University, Dept. of

**FEATURES**  
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1..366  
/organism="Trichinella spiralis"  
/mol\_type="mRNA"  
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/dev\_stage="muscle stage larvae"  
/lab\_host="DH10B"  
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/notes="vector: pCMTSPT-7.neo; Site 1: NotI; Site 2:  
SalI; The library was constructed using mRNA isolated from  
total RNA with oligo-dT cellulose. Total RNA was generated  
from muscle larvae that were isolated from infected rats.  
Larvae were liberated by pepsin/HCl digestion, incubated  
with 1% SDS, treated with RNase and DNase to eliminate  
host nucleic acid contamination, and purified on a Percoll  
gradient. The T. spiralis isolate was obtained from  
Dickson Despommer (Columbia University). The library was  
provided by Dr. Doug Jasmer (djasmervetmed.wu.edu) and  
colleagues at Washington State University. DNA Sequencing  
by: Washington University Genome Sequencing Center St.  
Louis."  
**ORIGIN**  
Query Match 29.8%; Score 17; DB 2; Length 366;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**QY** 21 GACCGTGACATGATGG 37  
|||||  
**Db** 232 GACCGTGACATGATGG 248  
|||||  
**RESULT 10**  
AA910388 397 bp mRNA linear EST 09-JUN-1998  
LOCUS OK89b07.s1 NCI CGAP\_Lus Homo sapiens cDNA clone IMAGE:1521109 3',  
DEFINITION mRNA sequence.  
**ACCESSION** AA910388  
**VERSION** AA910388.1 GI:3049678  
**KEYWORDS** EST.  
**SOURCE** Homo sapiens (human)  
**ORGANISM** Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 397)  
Email: cgabbs-r@mail.nih.gov  
Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.  
Emmett-Buck, M.D., Ph.D.  
cDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www.bio.llnl.gov/bbrp/image/image.html  
Insert length: 756 Std Error: 0.00  
Seq primer: -40m3 fwd. RT from Amersham  
High quality sequence stop: 374.  
Location/Qualifiers  
1..397  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1521109"



/issue\_type="carcinoid"  
/lab\_host="DH10B"  
/clone\_id="NCI CGAP Lu5"  
/note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; 1st strand cDNA was prepared from neuroendocrine lung carcinoid, and was then primed with a Not I - oligo(dT) primer. Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT73 vector. Library is normalized. Library was constructed by Bento Soares and M. Fatima Bonaldo. "

## ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 397;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 TCCCGATTCATTAGAG 56  
Db 140 TCCCTGATTCATTAGAG 156

RESULT 11  
LOCUS C2233273 398 bp DNA linear GSS 10-FEB-2005  
DEFINITION A1AA-aas86g17.b1 Ancylostoma caninum whole genome shotgun library  
(A1AAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.  
ACCESSION C2233273  
VERSION C2233273.1 GI:59266406  
KEYWORDS GSS.  
SOURCE Ancylostoma caninum (dog hookworm)  
ORGANISM Ancylostoma caninum  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida;  
Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
1 (bases 1 to 398)

## REFERENCE

## AUTHORS

Mitreva, M., McCarter, J.P., Page, D., Rilter, R., Tsagaris, J.L., R.,  
Ronko, I., Martin, J., Wylie, T., Dante, M., Meyer, R., Messina, D.,  
Waterston, R.H., Clifton, S.W. and Wilson, R.  
Genome Survey sequences from the parasitic nematode Ancylostoma  
caninum

## TITLE

## JOURNAL

Unpublished (2004)  
Contact: Mitreva M  
Washington University in St. Louis  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: nematode@wustl.wustl.edu  
Genomic DNA provided by John Hawdon (ntmjnh@gwumc.edu) DNA  
sequenced by Washington University Genome Sequencing Center  
Class: Shotgun.  
Location/Qualifiers

## FEATURES

## Source

1..398  
/organism="Ancylostoma caninum"  
/mol\_type="genomic DNA"  
/strain="Baltimore"  
/db\_xref="taxon:29170"  
/dev\_stage="Adult"  
/lab\_host="GS10"  
/clone\_id="Ancylostoma caninum whole genome shotgun  
library (A1AAGSS 001)"  
/note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI;  
Ancylostoma caninum genomic DNA was randomly sheared,  
end-repaired and size fractionated to enrich for 2-4 kb  
fragments. Genomic DNA was provided by John Hawdon  
(ntmjnh@gwumc.edu) at George Washington University.  
Sequencing by Washington University Genome Sequencing  
Center, St. Louis, MO."

## ORIGIN

Query Match 29.8%; Score 17; DB 10; Length 398;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 GTGACATGATGGAATC 41  
Db 114 GTGACATGATGGAATC 98

## RESULT 12

LOCUS BM80236 433 bp mRNA linear EST 24-MAY-2005  
DEFINITION BM80236 Amphioxus Branchiostoma floridae unpublished cDNA library,  
neurula whole animal Branchiostoma floridae cDNA clone b0ne03e19  
5', mRNA sequence.

## ACCESSION

BM80236  
EST.  
BM80236.1 GI:66494913

## KEYWORDS

## SOURCE

Branchiostoma floridae (Florida lancelet)  
Branchiostoma floridae  
Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;  
Branchiostoma.

## REFERENCE

## AUTHORS

Yu, J., Holland, L.Z., Shin, J., Kohara, Y., Satou, Y. and Satoh, N.  
Expressed genes in Branchiostoma floridae  
Unpublished (2005)  
Contact: Tadao Shin-1  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.  
Location/Qualifiers

## FEATURES

## Source

1..433  
/organism="Branchiostoma floridae"  
/mol\_type="mRNA"  
/db\_xref="taxon:7739"  
/clone\_id="b0ne03e19"  
/issue\_type="whole animal"  
/dev\_stage="neurula"  
/clone\_id="Amphioxus Branchiostoma floridae unpublished  
cDNA library, neurula whole animal"

## ORIGIN

Query Match 29.8%; Score 17; DB 5; Length 433;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 AATCCTGATTCATTAG 54  
Db 198 AATCCTGATTCATTAG 214

## RESULT 13

LOCUS CN056216 441 bp mRNA linear EST 30-MAR-2004  
DEFINITION Salamander\_23\_B13.ab1 AG Ambystoma tigrinum tigrinum cDNA, mRNA  
sequence.

## ACCESSION

## VERSION

CN056216  
EST.  
CN056216.1 GI:45832279

## KEYWORDS

## SOURCE

Ambystoma tigrinum tigrinum (Eastern tiger salamander)  
Ambystoma tigrinum tigrinum  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;

## ORGANISM

## REFERENCE

## AUTHORS

1 (bases 1 to 441)  
Putta, S., Smith, J.J., Walker, J.A., Rondet, M., Weisrock, D.,  
Monaghan, J., Samuels, A.K., Kump, K., King, D.C., Maness, N.J.,  
Hebermann, B., Tanaka, E., Bryant, S.V., Gardiner, D.M., Parichy, D.M.  
and Voss, S.R.  
From biomedicine to natural history research: EST resources for  
Ambystomatid Salamanders  
BMC Genomics 5 (1), 54 (2004)  
15310386



COMMENT Contact: SR Voss  
Department of Biology  
University of Kentucky  
TH Morgan Building, Lexington, KY 40506, USA  
Tel: 859 257 9888  
Fax: 859 257 1717  
Email: sryos@uky.edu  
The EST is quality trimmed at the ends with a 20 base window and  
quality threshold of 15 (phred quality score). Please visit  
http://salamander.uky.edu for any information (trace, quality files  
etc) regarding this EST.

FEATURES  
source  
1..441  
/organism="Ambystoma tigrinum tigrinum"  
/mol\_type="mRNA"  
/sub\_species="tigrinum"  
/db\_xref="taxon:43116"  
/tissue\_type="Liver, Lung, Kidney, Heart, gonad, brain and  
gill tissues collected from metamorphosing larvae"  
/clone\_lib="AG"

ORIGIN  
Query Match 29.8%; Score 17; DB 7; Length 441;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 ACAATGATGAAATCCCT 44  
|||||  
DB 310 ACAATGATGAAATCCCT 326

RESULT 14  
BG731918 450 bp mRNA linear EST 09-MAY-2001  
LOCUS ps07a06.y4 Trichinella spiralis ML CWSport Jasmer Trichinella  
DEFINITION spiralis cDNA 5' similar to TR:018136 Q18136 SIMILAR TO BR-HAND  
ACCESSION BG731918 GI:14016993  
VERSION BG731918.1 GI:14016993  
KEYWORDS EST.  
SOURCE Trichinella spiralis  
ORGANISM Trichinella spiralis  
Eukaryota; Metazoa; Nematoda; Enopleae; Trichocephalida;  
Trichinellidae; Trichinella.  
1 (bases 1 to 450)  
McCart, J., Clifton, S., Chhapelli, B., Pape, D., Martin, J.,  
Wyllie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B.,  
Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C.,  
Tsagarashvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
Underwood, K., Steptoe, M., Allen, M., Peterson, B., Swaller, T.,  
Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
McCann, R., Waterston, R. and Wilson, R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCart, J.P.  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watscn.wustl.edu  
The library was constructed by Dr. Doug Jasmer  
(djasmer@vetmed.wsu.edu) at Washington State University, Dept. of  
Veterinary Microbiology and Pathology DNA Sequencing by: Washington  
University Genome Sequencing Center St. Louis.  
Seq primer: Sp6  
High quality sequence stop: 448.  
Location/Qualifiers  
1..450  
/organism="Trichinella spiralis"  
/mol\_type="mRNA"  
/db\_xref="taxon:6334"  
/dev\_stage="muscle stage larvae"

ORIGIN  
Query Match 29.8%; Score 17; DB 2; Length 450;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACCGTGACATGATGG 37  
|||||  
DB 252 GACCGTGACATGATGG 268

RESULT 15  
CK614921 453 bp mRNA linear EST 26-JAN-2004  
LOCUS LPS1 M02 LPS stimulated Chicken PBL Macrophage Gallus gallus CDNA  
DEFINITION clone LPS1\_M02 5' similar to GP|6013425|gb|AA01332.1| evectln-2  
(Mus musculus), partial (66%), mRNA sequence.  
ACCESSION CK614921 GI:41335979  
VERSION CK614921.1 GI:41335979  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
ORGANISM Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 453)  
Blies, T.W., Emare, M.G., Dohms, J.E., Lillehoj, H.S. and Keeler, C.L.  
Analysis of gene expression in differentially stimulated avian  
macrophages  
Unpublished (2004)  
Contact: Calvin Keeler  
Dept. of Animal and Food Sciences  
University of Delaware  
040 Townsend Hall, Newark, DE 19716-2150, USA  
Tel: 302-831-6473  
Fax: 302-831-2822  
Email: ckeeler@udel.edu  
www.avlangenomics.udel.edu  
PCR Primers  
FORWARD: T7.  
BACKWARD: T7.  
Location/Qualifiers  
1..453  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/strain="Broiler"  
/db\_xref="taxon:9031"  
/clone="LPS1\_M02"  
/sex="Female and male combined"  
/tissue\_type="Blood"  
/cell\_type="Macrophage"  
/clone\_lib="LPS stimulated Chicken PBL Macrophage"  
/note="Vector: pBluescript sk+, Site\_1: EcoRI; Site\_2:  
XhoI"

ORIGIN  
Query Match 29.8%; Score 17; DB 7; Length 453;  
Best Local Similarity 100.0%; Pred. No. 75;



Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATGGA 38  
 Db 365 ACCGTGACATGATGGA 381

RESULT 16  
 CD188515/c  
 LOCUS  
 DEFINITION MS1-0063U-A243-G02-U-B MS1-0063 Schistosoma mansoni cDNA clone  
 MS1-0063U-A243-G02-B, mRNA sequence.  
 CD188515  
 CD188515.1 GI:34718537  
 EST  
 SOURCE Schistosoma mansoni  
 ORGANISM Schistosoma mansoni  
 BUKARYOTA; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigeidida; Schistosomatoidae; Schistosomatidae; Schistosoma.  
 1 (bases 1 to 483)

REFERENCE  
 AUTHORS Verjovski-Almeida, S., DeMarco, R., Martins, E.A.L., Guimaraes, P.E.M.,  
 Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y. Jr.,  
 Kitajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,  
 Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.D.,  
 Leite, R.A., Malaquias, L.C.C., Marques, R.C.P., Miyasato, P.A.,  
 Nascimento, A.L.T.O., Ohlweiler, F.P., Reis, E.M., Ribeiro, T.,  
 Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,  
 Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,  
 Setubal, J.C., Leite, L.C.C. and Dias-Neto, E.  
 Transcriptionome analysis of the acclimated human parasite Schistosoma  
 mansoni  
 Nat. Genet. 35 (2), 148-157 (2003)

JOURNAL  
 PUBMED 12973350  
 COMMENT Contact: Dr. Sergio Verjovski-Almeida  
 Departamento de Bioquimica  
 Instituto de Quimica - Universidade de Sao Paulo  
 Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 Sao Paulo - SP,  
 Brasil  
 Tel: +55-11-3091-2173  
 Fax: +55-11-3091-2186  
 Email: verjov@iq.usp.br  
 This sequence was derived from the FAPESP Schistosoma mansoni EST  
 Genome Project. All sequences in the project were assembled and  
 annotated. This entry and all the assembled sequences can be seen  
 in the following URL: <http://bioinfo.iq.usp.br/schisto/>  
 Plate: MS1-0063U-A243 row: 2 column: G.  
 Location/Qualifiers  
 1..483  
 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6183"  
 /clone="MS1-0063U-A243-G02-B"  
 /sex="mixed pool"  
 /dev\_stage="schistosomulum"  
 /lab\_host="in vitro culture"  
 /clone\_lib="MS1-0063"  
 /note="Vector: pGEM T-easy"

ORIGIN  
 Query Match 29.8%; Score 17; DB 6; Length 483;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 TGGATCCCTGATTCAT 51  
 Db 135 TGGATCCCTGATTCAT 119

RESULT 17  
 BG302319 501 bp mRNA linear EST 10-MAY-2001  
 LOCUS p807a06.v1 Trichinella spiralis ML CWSport JASMER Trichinella  
 DEFINITION spiralis cDNA 5' similar to TR:Q18136 Q18136 SIMILAR TO EF-HAND

ACCESSION  
 BG302319  
 VERSION BG302319.1 GI:13099846  
 KEYWORDS EST  
 SOURCE Trichinella spiralis  
 ORGANISM Trichinella spiralis  
 BUKARYOTA; Metazoa; Nematoda; Enopliea; Trichocephalida;  
 Trichinellidae; Trichinella.  
 1 (bases 1 to 501)

REFERENCE  
 AUTHORS McCarter, J., Clifton, S., Chiapelli, B., Page, D., Martin, J.,  
 Wylie, T., Dance, M., Maira, M., Hillier, L., Kucada, T., Theising, B.,  
 Bowers, Y., Gibbons, M., Ritter, E., Bennett, U., Franklin, C.,  
 Tsagaris, W., R., Ronko, I., Kennedy, S., Maguire, L., Beck, C.,  
 Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T.,  
 Harvey, N., Schurt, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterson, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 The Washington Univ. Nematode EST Project, 1999  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@wustl.wustl.edu  
 The library was constructed by Dr. Doug Jasmer  
 (djasmer@vetmed.wsu.edu) at Washington State University, Dept. of  
 Veterinary Microbiology and Pathology DNA Sequencing by: Washington  
 University Genome Sequencing Center St. Louis.  
 Seq primer: Sp6  
 High quality sequence stop: 489.

FEATURES  
 source  
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 /organism="Trichinella spiralis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6334"  
 /dev\_stage="muscle stage larvae"  
 /lab\_host="DH10B"  
 /clone\_lib="Trichinella spiralis ML CWSport JASMER"  
 /note="Vector: pCMVSPORT-7.neo; site 1: NotI; site 2:  
 SalI; The library was constructed using mRNA isolated from  
 total RNA with oligo-dT cellulose. Total RNA was generated  
 from muscle larvae that were isolated from infected rats.  
 Larvae were liberated by pepsin/HCl digestion, incubated  
 with 1% SDS, treated with RNase and DNase to eliminate  
 host nucleic acid contamination, and purified on a Percoll  
 gradient. The T. spiralis isolate was obtained from  
 Dickson Despommer (Columbia University). The library was  
 provided by Dr. Doug Jasmer (djasmer@vetmed.wsu.edu) and  
 colleagues at Washington State University. DNA Sequencing  
 by: Washington University Genome Sequencing Center St.  
 Louis."

ORIGIN  
 Query Match 29.8%; Score 17; DB 2; Length 501;  
 Best Local Similarity 100.0%; Pred. No. 75;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 GACCGTACATGATGG 37  
 Db 260 GACCGTACATGATGG 276

RESULT 18  
 AJ735313 510 bp mRNA linear EST 17-FEB-2005  
 LOCUS AJ735313 riken1 Gallus gallus cDNA clone 8b5r2, mRNA sequence.  
 DEFINITION AJ735313  
 ACCESSION AJ735313  
 VERSION AJ735313.1 GI:53900698  
 KEYWORDS EST.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
Phasianinae; Gallus.  
1 (bases 1 to 510)  
Caldwell,R.B., Kierzek,A.M., Arakawa,H., Bezubov,Y., Zaim,J.,  
Fiedler,P., Kuter,S., Blagodatki,A., Kostovska,D., Kotex,M.,  
Plachy,J., Carninci,P., Hayashizaki,Y. and Buerstedde,J.M.  
Full-length cDNAs from chicken bursal lymphocytes to facilitate  
gene function analysis  
Genome Biol. 6 (1), R6 (2005)  
15642098  
JOURNAL PUBMED  
COMMENT  
Contact: Caldwell RB  
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.  
Location/Qualifiers  
1. 510  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9031"  
/clone="8B5r2"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/clone\_lib="rikeni"  
/note="CB indred strain"

ORIGIN  
Query Match 29.8%; Score 17; DB 1; Length 510;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 22 ACCGTGACATGATGCA 38  
|||||  
88 ACCGTGACATGATGCA 104

Db

RESULT 19  
BOJ78090 513 bp mRNA linear EST 16-JUN-2002  
LOCUS  
DEFINITION  
PC27f2.2.y1 Trichinella spiralis immature L1 PAMP1 v1 Trichinella  
spiralis CDNA 5' similar to TR:Q18136 Q18136 SIMILAR TO EF-HAND  
CALCIUM BINDING PROTEIN. NCBI GI: 1065541. [1] ; mRNA sequence.  
BOJ78090  
BOJ78090.1 GI:21883302  
EST.  
Trichinella spiralis  
Trichinella spiralis  
Eukaryota; Metazoa; Nematoda; Emophea; Trichocephalida;  
Trichinelidae; Trichinella.  
1 (bases 1 to 513)  
McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
Bowers,Y., Gibbons,M., Ralter,E., Bennett,J., Franklin,C.,  
Tagaretskhvili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
Underwood,K., Steptoe,M., Allen,M., Person,B., Sallier,T.,  
Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
McCaan,R., Waterston,R. and Wilson,R.  
The Washington Univ. Nematode EST Project, 1999  
Unpublished (1999)  
Contact: McCarter JP  
The Washington Univ. Nematode EST Project, 1999  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
The library was constructed by Claire Murphy and Dr. James McCarter  
at Washington University, St. Louis. Newborn larvae were collected  
from infected rats and provided by Dr. Judith Appleton of Cornell  
University, Ithaca, NY (ja2@cornell.edu).  
Seq primer: -40RP from Gibco  
High quality sequence stop: 415.  
Location/Qualifiers  
1. 513  
/organism="Trichinella spiralis"

FEATURES  
source

/mol\_type="mRNA"  
/db\_xref="taxon:6334"  
/dev\_stage="immature L1"  
/ab\_host="DH10B"  
/clone\_lib="Trichinella spiralis immature L1 PAMP1 v1"  
/note="Vector: PAMP1 (Gibco); Site 1: NotI; Site 2: SalI;  
The library was constructed by Claire Murphy and Dr. James  
McCarter at Washington University, St. Louis. The cDNA was  
made by using Dynabead oligo-dT priming (Dynal). PCR based  
library using a modified protocol from the SMART PCR cDNA  
Synthesis Kit from Clontech. Directionally cloned into the  
UDG sites of PAMP1. Newborn larvae were collected from  
infected rats and provided by Dr. Judith Appleton of  
Cornell University, Ithaca, NY (ja2@cornell.edu)."

ORIGIN  
Query Match 29.8%; Score 17; DB 5; Length 513;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 21 GACCGTGACATGATG 37  
|||||  
451 GACCGTGACATGATG 467

Db

RESULT 20  
CK142714 513 bp mRNA linear EST 03-DEC-2003  
LOCUS  
DEFINITION  
AGENCOURT 16719882 NIH\_ZGC\_10 Danio rerio cDNA IMAGE:7047455  
5', mRNA sequence.  
CK142714  
CK142714.1 GI:38647911  
EST.  
Danio rerio (zebrafish)  
SOURCE  
Danio rerio  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 513)  
NIH-MGC <http://mgc.nci.nih.gov/>.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: c9apbs-remail.nih.gov  
Tissue Procurement: Len Zou, Harvard  
cDNA Library Preparation: Open Biosystems  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
plate: LLNL4813 row: 1 column: 21  
High quality sequence stop: 273.  
Location/Qualifiers  
1. 513  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:7047455"  
/tissue\_type="whole body"  
/ab\_host="DH10B"  
/clone\_lib="NIH\_ZGC\_10"  
/note="Vector: pEXpress1; Site 1: NotI; Site 2: EcoRV;  
Bulk tissue was collected from a whole adult individual  
from the Tuebingen strain. 1st strand cDNA was primed with  
a Not I - oligo(dT) primer, double-stranded cDNA was  
cloned into the Not I and EcoRV sites of pEXpress-1.  
Library was size-selected for >1 kb fragments. A  
normalized version of this library is also available  
(NIH\_ZGC\_7). Library was constructed by Open Biosystems

FEATURES  
source



ORIGIN (Huntsville, AL)."

Query Match 29.8%; Score 17; DB 7; Length 513;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 CAATGATGAATCCCTG 45  
|||||  
Db 178 CAATGATGAATCCCTG 194

RESULT 21 514 bp mRNA linear EST 16-APR-2001  
BE492067  
LOCUS  
DEFINITION Wheat551\_B02\_B022E Triticum monococcum vegetative apex cDNA library  
Triticum monococcum cDNA clone Wheat551\_B02\_B02, mRNA sequence.  
ACCESSION BE492067 GI:9658576  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Triticum monococcum

REFERENCE  
AUTHORS Anderson, O.D., Chao, S., Dubcovsky, J., Echenique, V., Han, P.S., Heita, C.C., Kang, Y., Izzo, G.R., Miller, R., Rauech, C.J., Seaton, C.L., Stamova, B. and Tong, J.C.  
The structure and function of the expressed portion of the wheat genomes - Vegetative apex cDNA library from Triticum monococcum Unpublished (2001)

JOURNAL  
COMMENT Contact: Olin Anderson  
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
800 Buchanan Street, Albany, CA 94710, USA  
Tel: 5105595773  
Fax: 5105595818  
Email: oanderson@pw.usda.gov

Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20  
Seq primer: StrataGene T3 primer.  
Location/Qualifiers

FEATURES  
source 1..514

/organism="Triticum monococcum"  
/mol\_type="mRNA"  
/cultivar="DV92"  
/db\_xref="taxon:4568"  
/clone="Wheat551\_B02\_B02"  
/issue\_type="Vegetative shoot apex"  
/dev\_stage="Three weeks-old plants"  
/lab\_host="E. coli XL04"  
/clone\_lib="Triticum monococcum vegetative apex cDNA library"  
/note="Vector: Lambda pBK-CMV (Lambda Zap Express), excised phagemid; Site 1: ScaI; Site 2: XhoI; The tissue, total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised at the University of California, Davis (V. Echenique, B. Stamova, J. Dubcovsky). Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."

ORIGIN

Query Match 29.8%; Score 17; DB 2; Length 514;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 CAGACCGTACATGAT 35  
|||||  
Db 239 CAGACCGTACATGAT 255

RESULT 22

AL925807 533 bp mRNA linear EST 06-JUN-2004

DEFINITION AL925807 PUR-Z1+Z2 Danio rerio cDNA clone 160-F06-2, mRNA sequence.

ACCESSION AL925807  
VERSION AL925807.1 GI:23192387  
KEYWORDS  
SOURCE  
ORGANISM Danio rerio (zebrafish)

REFERENCE  
AUTHORS Lo, J., Lee, S., Xu, M., Liu, P., Ruan, H., Sun, A., He, Y., Ma, W., Wang, W., Wen, Z. and Peng, J.  
15000 unique zebrafish EST clusters and their future use in microarray for profiling gene expression patterns during embryogenesis  
Genome Res. 13 (3), 455-466 (2003)

JOURNAL  
PUBMED  
COMMENT Contact: Peng J  
Lab of Functional Genomics  
Institute of Molecular and Cell Biology  
30 Medical Drive, Singapore, 117603, Singapore  
Email: pengj@imcb.a-star.edu.sg  
Clone requests: info@openbioystems.com  
Open Bioystems,  
6705 Odyssey Drive, Huntsville, AL 35806.

FEATURES  
source 1..533

/organism="Danio rerio"  
/mol\_type="mRNA"  
/strain="local wildtype"  
/db\_xref="taxon:7955"  
/clone="160-F06-2"  
/issue\_type="whole embryo or fish"  
/dev\_stage="mixed stages"  
/clone\_lib="PUR-Z1+Z2"

ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 533;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 CAATGATGAATCCCTG 45  
|||||  
Db 440 CAATGATGAATCCCTG 456

RESULT 23

BU268532 563 bp mRNA linear EST 09-APR-2002

DEFINITION BU268532 Y. Ogihara unpublished cDNA library, whole Triticum aestivum cDNA clone wnoh17g15 5', mRNA sequence.

ACCESSION BU268532  
VERSION BU268532.1 GI:20088527  
KEYWORDS  
SOURCE  
ORGANISM Triticum aestivum (bread wheat)

REFERENCE  
AUTHORS Ogihara, Y. and Murai, K.  
Expressed genes in Triticum aestivum  
Unpublished (2002)  
Contact: Tadasu Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tahini@gene.nig.ac.jp.

JOURNAL  
COMMENT



FEATURES  
source  
1.563  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="whohl7919"  
/tissue\_type="blast at heading date"  
/dev\_stage="Fekkes" scale 10.5"  
/clone\_lib="Y. Ogihara unpublished cDNA library, wh\_oh"

ORIGIN  
Query Match 29.8%; Score 17; DB 3; Length 563;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CAGACCGTGACATGAT 35  
|||||  
185 CAGACCGTGACATGAT 201  
|||||

RESULT 24  
CX399264 567 bp mRNA linear EST 06-JAN-2005  
LOCUS JGI\_XZT3719.fwd NIH\_XGC\_tropTad5 Xenopus tropicalis cDNA clone  
DEFINITION IMAGE:7582268 5', mRNA sequence.  
ACCESSION CX399264 GI:57179952  
VERSION CX399264  
KEYWORDS EST.  
SOURCE Xenopus tropicalis (western clawed frog)  
ORGANISM Xenopus tropicalis

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;  
Xenopodinae; Xenopus; Silurana.  
1 (bases 1 to 567)  
Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C.,  
Brookstein, P., and Lindquist, E.A., Richardson, P.  
DOE Joint Genome Institute Xenopus tropicalis EST project  
Unpublished (2004)  
Other ESTs: JGI\_XZT3719.rev  
Contact: Lindquist, E.A., Richardson, P.  
DOE Joint Genome Institute  
2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
Tel: 925 296 5600  
Fax: 925 296 5710  
Email: cdna@jgi-psf.org  
Tissue Procurement: Richard M. Harland Laboratory, University of  
California, Berkeley: <http://tropicalis.berkeley.edu/home>  
CDNA library Preparation: Richard M. Harland Laboratory, University  
of California, Berkeley  
DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
Clone Distribution: I.M.A.G.E. Consortium/LNL: <http://image.llnl.gov>  
Naming Conventions: EST name is generated by the concatenation of  
the JGI Clone ID and the direction of sequencing. The suffix '.fwd'  
indicates a forward sequencing read of the insert. It does not  
necessarily reflect the orientation of the insert.  
Plate: XZT 0037 row: m column: 18  
High quality sequence stop: 405.  
Location/Qualifiers  
1.567  
/organism="Xenopus tropicalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8364"  
/clone="IMAGE:7582268"  
/tissue\_type="whole embryo"  
/dev\_stage="Tadpole (st. 36-41)"  
/lab\_host="E. coli XL1-Blue derivative, Stratagene  
Electrofen-Blue"  
/clone\_lib="NIH\_XGC\_tropTad5"  
/note="Vector: PCS108; Site 1: SalI; Site 2: NotI; Tadpole  
library constructed by Russell B. Fletcher in R. Harland's  
lab using poly A RNA and oligo dT primers (Invitrogen

SuperScript Plasmid System for cDNA Synthesis and  
Cloning). SalI (5' end) -NotI (3' end) cDNA was inserted  
into vector PCS108  
(<http://mcb.berkeley.edu/labs/harland/pages/plasmids.html>)  
"

ORIGIN  
Query Match 29.8%; Score 17; DB 8; Length 567;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 TGACATGATGGAATCC 42  
|||||  
Db 330 TGACATGATGGAATCC 346  
|||||

RESULT 25  
CD279894 576 bp mRNA linear EST 23-MAY-2003  
LOCUS G44222.48 NCI\_CGAP\_Zemb3 Danio rerio cDNA clone IMAGE:6321634 5',  
DEFINITION mRNA sequence.  
ACCESSION CD279894 GI:31057670  
VERSION CD279894  
KEYWORDS EST.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Danio rerio

REFERENCE  
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Osteichthyes;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 576)  
Amundsen, C., Cachuela, N., Chen, F., Cheung, L.M., Chong, A.,  
Murray, L., Oliva, J., Park, C., Reyes, J., Yungen, J., and Swimmer, C.  
Expressed sequence tags from NCI\_CGAP\_Zemb3, a Danio rerio  
embryonic library  
Unpublished (2003)  
Contact: Chen F.  
Exelixis, Inc.  
170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA  
Tel: 650 837 7000  
Fax: 650 837 8300  
Email: [fchen@exelixis.com](mailto:fchen@exelixis.com)  
DNA Sequencing by: Exelixis, Inc. Clone distribution information  
can be found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: 13761 row: O column: 11  
High quality sequence stop: 576.  
Location/Qualifiers  
1.576  
/organism="Danio rerio"  
/mol\_type="mRNA"  
/db\_xref="taxon:7955"  
/clone="IMAGE:6321634"  
/tissue\_type="embryo"  
/lab\_host="DH10B (TI-resistant)"  
/clone\_lib="NCI\_CGAP\_Zemb3"  
/note="Vector: pCMV-SPORT6.1; Site 1: EcoRV; Site 2: NotI;  
Cloned unidirectionally. Primer: Oligo dT. Average insert  
size 2.1 kb. Constructed by J. Wang (Research Genetics,  
Invitrogen Corp) from tissue donated by L. Zon (Harvard  
University). Note: this is a NCI\_CGAP Library."

ORIGIN  
Query Match 29.8%; Score 17; DB 6; Length 576;  
Best Local Similarity 100.0%; Pred. No. 75;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CAATGATGGAATCCCTG 45  
|||||  
Db 456 CAATGATGGAATCCCTG 472  
|||||

RESULT 26  
BE492082



```

LOCUS       BE492082                580 bp    mRNA    linear    EST 16-APR-2001
DEFINITION  WHE0551_C12_C12ZE Triticum monococcum vegetative apex cDNA library
ACCESSION   BE492082
VERSION     BE492082
KEYWORDS    BE492082.1  GI:9658591
SOURCE      EST.
            Triticum monococcum
ORGANISM    Triticum monococcum
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
            Poideae; Triticeae; Triticum.
            1 (bases 1 to 580)
AUTHORS      Anderson,O.D., Chao,S., Dubcovsky,J., Echenique,V., Han,P.S.,
            Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rauech,C.D., Seaton,C.L.,
            Stemove,B., and Tong,J.C.
            The structure and function of the expressed portion of the wheat
            genomes - Vegetative apex cDNA library from Triticum monococcum
            Unpublished (2001)
JOURNAL
COMMENT      Contact: Olin Anderson
            US Department of Agriculture, Agriculture Research Service, Pacific
            West Area, Western Regional Research Center
            800 Buchanan Street, Albany, CA 94710, USA
            Tel: 5105595773
            Fax: 5105595818
            Email: oanderson@pw.usda.gov
            Sequence have been trimmed to remove vector sequence and low
            quality sequence with phred score less than 20
            Seq primer: StrataGene T3 primer.
FEATURES
            location/Qualifiers
            1..580
            /organism="Triticum monococcum"
            /mol_type="mRNA"
            /cultivar="DV92"
            /db_xref="taxon:4568"
            /clone="WHE0551_C12_C12"
            /tissue_type="vegetative shoot apex"
            /dev_stage="three weeks-old plants"
            /lab_host="E. coli XL0LR"
            /clone_id="Triticum monococcum vegetative apex cDNA
            library"
            /note="Vector: lambda pBK-CMV (lambda Zap Express),
            excised phagemid; Site_1: EcoRI; Site_2: XhoI; The tissue,
            total RNA, and poly(A) RNA were prepared; a cDNA library
            was made, and the cDNA clones were in vivo excised at the
            University of California, Davis (V. Echenique, B.
            Stanova, J. Dubcovsky). Plasmid DNA preparations and DNA
            sequencing were performed in the OD Anderson lab (all
            other authors)."
```

AUTHORS	Amundsen, C., Cachuela, N., Chen, F., Cheng, L. M., Chong, A., Murray, L., Oliva, J., Park, C., Reyes, J., Tingen, J. and Swimmer, C.
TITLE	Expressed sequence tags from NCI_CGAP_Zemds, a Danio rerio embryonic library
JOURNAL	Unpublished (2003)
COMMENT	Contact: Chen F. Exelixis, Inc. 170 Harbor Way, PO Box 511, South San Francisco, CA 94083-0511, USA Tel.: 650 837 7000 Fax: 650 837 8300 Email: fchen@exelixis.com DNA Sequencing by: Exelixis, Inc. Clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: 13761 row: B column: 21 High quality sequence stop: 589. Location/Qualifiers
FEATURES	1..589 /organism="Danio rerio" /mol_type="mRNA" /db_xref="taxon:7955" /clone="IMAGE:6321404" /tissue_type="embryo" /lab_host="DH10B (Ti-resistant)" /clone_id="NCI_CGAP_Zemds3" /note="Vector: pCMV-Sport6.1, Site1: EcoRV, Site2: NotI; Cloned unidirectionally. Primer: Oligo dt. Average insert size 2.1 kb. Constructed by J. Wang (Research Genetics, Invitrogen Corp) from tissue donated by L. Zon (Harvard University). Note: this is a NCI_CGAP library."
ORIGIN	
Query Match	29.8%; Score 17; DB 6; Length 589;
Best Local Similarity	100.0%; Pred. No. 75;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
Or	29 CAATGATGGAATCCCTG 45       
Db	469 CAATGATGGAATCCCTG 485
RESULT 28	
LOCUS	CV059002 599 bp mRNA linear EST 24-AUG-2004
DEFINITION	BNEI43c8 Barley EST endosperm library Hordeum vulgare subsp. vulgare cDNA clone BNEI43c8 5' similar to e1P4-gamma-elf5/elf2-epsilon domain-containing protein, mRNA sequence.
ACCESSION	CV059002
VERSION	CV059002.1 GI:51522141
KEYWORDS	EST.
SOURCE	Hordeum vulgare subsp. vulgare Hordeum vulgare subsp. vulgare Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Hordeum.
ORGANISM	1 (bases 1 to 599) Alf, S. Holloway, B. and Taylor, M. C. Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis Plant Mol. Biol. Rep. 18, 123-132 (2000) Contact: Bill Taylor Commonwealth Scientific and Industrial Research Organisation Division of Plant Industry. CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia Tel.: 61 2 6246 5223 Fax: 61 2 6246 5000 Email: Bill.Taylor@csiro.au Seq primer: M13 reverse primer High quality sequence stop: 599. Location/Qualifiers
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
SOURCE	1..599 /organism="Hordeum vulgare subsp. vulgare"



/mol\_type="mRNA"  
/cultivar="Himalaya"  
/sub\_species="vulgaris"  
/db\_xref="taxon:112509"  
/clone="BNEL43c8"  
/tissue\_type="endosperm"  
/dev\_stage="developing endosperm tissue 10, 12, 15 dpa  
(days post anthesis)"  
/lab\_host="DH10B (Life Technology)"  
/clone\_lib="Barley EST endosperm library"  
/note="Vector: \_Ziplox; Site 1: Sal I; Site 2: Not I; mRNA  
was prepared from endosperm tissues of the barley cultivar  
Himalaya. cDNA was synthesised from pooled 10, 12, and 15  
dpa endosperm using Not I-oligo(dT)18 primer/adaptor  
(Pharmacia Biotech), and then ligated to the Sal I-Not I  
site of \_Ziplox vector (Life Technology) after adding a  
Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan  
Ali and Bill Taylor."

## ORIGIN

Query Match 29.8%; Score 17; DB 7; Length 599;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 CAGACCGTGACATGAT 35  
|||||  
Db 2 CAGACCGTGACATGAT 18

RESULT 29  
CPA562939 599 bp DNA linear GSS 11-AUG-2003  
LOCUS Cryptosporidium parvum GSS; PMC clone pica\_0012\_e12, Sp6 end  
DEFINITION Sequence, genomic survey sequence.  
ACCESSION AJ562939  
VERSION AJ562939.1 GI:31337759  
KEYWORDS GSS; genome survey sequence.  
SOURCE Cryptosporidium parvum  
ORGANISM Cryptosporidium parvum  
Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida;  
Cryptosporidiidae; Cryptosporidium.

REFERENCE 1  
AUTHORS Barker,A.T., Spriggs,H.F., Fartmann,B., Konfortov,B.A., Madera,M.,  
Vogel,C., Teichmann,S.A., Ivens,A. and Dear,P.H.  
TITLE Integrated mapping, chromosomal sequencing and sequence analysis of  
Cryptosporidium parvum  
JOURNAL Genome Res. 13 (8), 1787-1799 (2003)  
PUBMED 12869580  
REFERENCE 2 (bases 1 to 599)  
AUTHORS Dear,P.H.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2003) Dear P.H., PNAC Biotech Division, MRC  
Laboratory of Molecular Biology, Hills Road, Cambridge, Cambs CB2  
2QH, UNITED KINGDOM

## FEATURES

## SOURCE

Location/Qualifiers  
1..599  
/organism="Cryptosporidium parvum"  
/mol\_type="genomic DNA"  
/serotype="Type 2"  
/isolate="Iowa"  
/db\_xref="taxon:5807"  
/chromosome="6"  
/clone\_lib="pica\_0012\_e12"  
/dev\_stage="oocyst"  
/note="Sp6 end sequence"

## ORIGIN

Query Match 29.8%; Score 17; DB 11; Length 599;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 38 AATCCCTGATTCATGAG 54

|||||  
Db 398 AATCCCTGATTCATGAG 382

RESULT 30  
CA191493 638 bp mRNA linear EST 24-SEP-2003  
LOCUS SCCCR2C08E08.g RT2 Saccharum officinarum cDNA clone SCCCR2C08E08  
DEFINITION 5', mRNA sequence.

ACCESSION CA191493  
VERSION CA191493.1 GI:35136711  
KEYWORDS EST.  
SOURCE Saccharum officinarum  
ORGANISM Saccharum officinarum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
complex.

1 (bases 1 to 638)

REFERENCE Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
AUTHORS The libraries that made SOCEST  
TITLE Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
JOURNAL Contact: Arruda P  
COMMENT Centro de Biologia Molecular e Engenharia Genetica  
Universidade Estadual de Campinas  
Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
Tel: 55 19 3788 1137  
Fax: 55 19 3788 1089  
Email: parrruda@unicamp.br  
Clone distribution: clone distribution information can be found  
through the Brazilian Clone Collection Center (BCCC) at  
http://www.bcccenter.fcav.unicamp.br  
Plate: C08 row: E column: 08  
Seq primer: T7 Promoter Primer.

## FEATURES

## SOURCE

Location/Qualifiers  
1..638  
/organism="Saccharum officinarum"  
/mol\_type="mRNA"  
/db\_xref="taxon:4547"  
/clone="SCCCR2C08E08"  
/lab\_host="DH10B"  
/clone\_lib="RT2"  
/note="Organ: Root tips (0.3cm-long) from adult plants;  
Vector: pSport1; Site 1: SalI; Site 2: NotI; An  
unidirectional cDNA library generated from [Root  
tips (0.3cm-long) from adult plants]. cDNA was prepared  
from polyA+ mRNA using Superscript Plasmid System Kit  
(Invitrogen). The double-strand cDNAs were fractionated  
in a sepharose CL-2B 40cm-columns and fragments sizing  
between 0.8 and 1.5 kb were directionally cloned into the  
vector. Details of each source of RNA and library  
construction can be obtained at  
http://succec.lad.ic.unicamp.br/public"

## ORIGIN

Query Match 29.8%; Score 17; DB 6; Length 638;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 GGACTACGGTCCAGA 22  
|||||  
Db 185 GGACTACGGTCCAGA 169

RESULT 31  
B2768492 639 bp mRNA linear EST 09-APR-2002  
LOCUS B2768492 Y. Ogihara unpublished cDNA library, wh\_oh Triticum  
DEFINITION B2768492  
ACCESSION B2768492  
VERSION B2768492.1 GI:20088497  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)



ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 639)  
Ogihara, Y. and Murai, K.  
TITLE Expressed genes in *Triticum aestivum*  
JOURNAL Unpublished (2002)  
COMMENT Contact: Tadao Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.

FEATURES  
source  
1..639  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="whon17d19"  
/issue\_type="Distil at heading date"  
/dev\_stage="Fleeker" scale 10.5"  
/clone\_lib="Y. Ogihara unpublished cDNA library, wh\_oh"

ORIGIN  
Query Match 29.8%; Score 17; DB 3; Length 639;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CAGACCGTCAATGAT 35  
|||||  
187 CAGACCGTCAATGAT 203

RESULT 32  
B2843563 651 bp DNA linear GSS 18-MAR-2003  
LOCUS CH240\_29118.TU CHORI-240 Bos taurus genomic clone CH240\_29118,  
DEFINITION genomic survey sequence.  
ACCESSION B2843563  
VERSION B2843563  
KEYWORDS B2843563.1 GI:29070922  
SOURCE GSS.  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 651)  
Zhao, S., Shetty, J., Shateman, S., Teegaye, G., Geer, K., Shvartsbeyn, A., Gebregorgis, E., Chen, D., Riggs, F., de Jong, P., Crawford, A.M. and McEwan, J.C.  
Bovine BAC End Sequences from Library CHORI-240  
Unpublished (2003)  
Contact: Shiyang Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@igir.org  
Clones are derived from the bovine BAC library CHORI-240  
(http://www.chori.org/bacpac/bovine240.htm). For BAC library availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources  
(http://www.chori.org/bacpac/ordering/information.htm). This work was undertaken as part of the International Bovine BAC Mapping Consortium (IBMC) by AgResearch Ltd., New Zealand and The Institute of Genomic Research (TIGR), USA.  
Plate: 291 row: I column: 8  
Seq primer: SP6  
Class: BAC ends.

TITLE JOURNAL  
COMMENT

REFERENCE  
AUTHORS

FEATURES  
source  
Location/Qualifiers  
1..651  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/strain="bred: Hereford"  
/db\_xref="taxon:9913"  
/clone="CH240\_29118"  
/sex="Male"  
/cell\_type="Blood"  
/clone\_lib="CHORI-240"  
/note="Vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI; Hereford bull 11 Domino 99375; CHORI-240 Bovine BAC library (Male) produced by Pieter de Jong"

ORIGIN  
Query Match 29.8%; Score 17; DB 9; Length 651;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 CCTGATTCATTGAGG 57  
|||||  
295 CCTGATTCATTGAGG 311

RESULT 33  
AJ735325 672 bp mRNA linear EST 17-FEB-2005  
LOCUS AJ735325/c  
DEFINITION AJ735325 riken1 Gallus gallus cDNA clone 8b567, mRNA sequence.  
ACCESSION AJ735325  
VERSION AJ735325.1 GI:53900710  
KEYWORDS EST.  
SOURCE Gallus gallus (chicken)  
Gallus gallus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.  
1 (bases 1 to 672)  
Caldwell, R.B., Kierzek, A.M., Arakawa, H., Bezubov, Y., Zaim, J., Fiedler, P., Kutter, S., Blasodatski, A., Kostovska, D., Kotar, M., Plachy, J., Carnici, P., Hayashizaki, Y. and Buerstedde, J.M.  
Full-length cDNAs from chicken bursal lymphocytes to facilitate gene function analysis  
Genome Biol. 6 (1), R6 (2005)  
15642098  
JOURNAL PUBMED  
COMMENT Contact: Caldwell RB  
GSF - Forschungszentrum, Institut fuer Molekulare Strahlenbiologie  
Ingolstaedter Landstr. 1, D-85764 Neuherberg, GERMANY.  
Location/Qualifiers  
1..672  
/organism="Gallus gallus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9931"  
/clone="8b567"  
/cell\_type="bursal lymphocyte"  
/dev\_stage="2-3 weeks old"  
/clone\_lib="riken1"  
/note="CB inbred strain"

FEATURES  
source

ORIGIN  
Query Match 29.8%; Score 17; DB 1; Length 672;  
Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATGA 38  
|||||  
269 ACCGTGACATGATGA 253

RESULT 34  
B1326765 676 bp mRNA linear EST 01-OCT-2001  
LOCUS B1326765  
DEFINITION B1326765 STR00027 random primed zebrafish embryo danio rerio cDNA clone C821  
5' similar to SW:CA11\_CHICK P02457 COLLAGEN ALPRA 1(1) CHAIN



PRECUSOR, mRNA sequence.  
 B1326765  
 VERSION B1326765.1 GI:15811937  
 KEYWORDS EST.  
 SOURCE Dario rerio (zebrafish)  
 ORGANISM Dario rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 676)  
 Loppin,B., Steffan,T., Kempf,J., Heyer,V., Thisse,C. and Thisse,B.  
 Expression of the zebrafish genome during embryogenesis  
 Unpublished (2001)  
 JOURNAL Other ESTs: STR00028  
 COMMENT Contact: Thisse B  
 Institut de Genetique et de Biologie Molculaire et Cellulaire  
 CNRS, INSERM, ULP  
 1, rue Laurent Fries, BP163, CU de Strasbourg, 67404 Illkirch  
 Cedex, France  
 Tel: 33 3 88 65 33 60  
 Fax: 33 3 88 65 32 01  
 Email: thisse@igmc.u-strasbg.fr  
 EST from a cDNA of a gene whose expression is spatially restricted during embryogenesis. We have established its expression pattern on zebrafish embryos from the gastrula stage to 2 days of development. The corresponding data are available on the zebrafish community database at <http://zfinfo.org/> CDNA library preparation: C. Fromental and J-M. Garnier. DNA Sequencing by: IGMC sequencing facility. Clone distribution: zebrafish international resource center at the University of Oregon (Institute of Neuroscience, 1254 University of Oregon, Eugene, OR 97403-1254)  
 Seq primer: T3 ATTAACCTCACTAAGGGA  
 High quality sequence stop: 518.  
 Location/Qualifiers  
 1..676  
 /organism="Dario rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="CB21"  
 /dev\_stage="18 hrs to 48 hrs old embryos"  
 /clone\_lib="random primed zebrafish embryo"  
 /note="Vector: Lambda Zap; Site\_1: EcoRI; Site\_2: EcoRI; Random primed cDNA library constructed from RNA pooled from embryos from 18 to 48 hpf."  
 ORIGIN  
 Query Match 29.8%; Score 17; DB 3; Length 676;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 29 CAATGATGATCCCTG 45  
 |||||||  
 Db 460 CAATGATGATCCCTG 476  
 RESULT 35  
 BFO30782 691 bp mRNA linear EST 10-OCT-2000  
 LOCUS 601557518F1 NIH\_MGC\_58 Homo sapiens cDNA IMAGE:3827261 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BFO30782  
 VERSION BFO30782.1 GI:10738494  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 691)  
 NIH-MGC <http://mgc.nci.nih.gov/>.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 FEATURES  
 source

COMMENT Contact: Robert Straubeberg, Ph.D.  
 Email: cgabs-remail.nih.gov  
 Tissue Procurement: ATCC  
 CDNA Library Preparation: CLONETECH Laboratories, Inc.  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCM496 row: C column: 06  
 High quality sequence stop: 309.  
 Location/Qualifiers  
 1..691  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:3827261"  
 /tissue\_type="hypernephroma"  
 /lab\_host="DH10B (T1 phage-resistant)"  
 /clone\_lib="NIH MGC\_58"  
 /note="Organ: Kidney; Vector: pDNA-LIB (Clontech); Site\_1: SfiI (ggccattcgcc); Site\_2: SfiI (ggccattcgcc); Double-stranded cDNA was prepared from cell line RNA. 5' and 3' adaptors were used in cloning as follows: 5' adaptor sequence: 5'-ATTCTAGAGCCGAGGCGCCGACATG-dT(30)BN-3' (where B = A, C, G or G and N = A, C, G, or T). Average insert size 1.35 kb (range 0.9-4.0 kb). 15/15 colonies contained inserts by PCR. This library was enriched for full-length clones and was constructed by Clontech Laboratories (Palo Alto, CA)."  
 ORIGIN  
 Query Match 29.8%; Score 17; DB 2; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 8 ACTTACGTTCCAGACC 24  
 |||||||  
 Db 575 ACTTACGTTCCAGACC 591  
 RESULT 36  
 CV053951 704 bp mRNA linear EST 24-AUG-2004  
 LOCUS BNEL105as Barley EST endosperm library Hordeum vulgare subsp.  
 DEFINITION vulgare cDNA clone BNEL105as 5' similar to  
 e1F4-gamma/e1F5/e1F2-epsilon domain-containing protein, mRNA  
 sequence.  
 ACCESSION CV053951  
 VERSION CV053951.1 GI:51516972  
 KEYWORDS EST.  
 SOURCE Hordeum vulgare subsp. vulgare  
 ORGANISM Hordeum vulgare subsp. vulgare  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Hordeum.  
 1 (bases 1 to 704)  
 Ali,S, Holloway,B. and Taylor,W.C.  
 Normalisation of cereal endosperm EST libraries for structural and functional genomic analysis  
 Plant Mol. Biol. Rep. 18, 123-132 (2000)  
 Contact: Bill Taylor  
 Commonwealth Scientific and Industrial Research Organisation  
 Division of Plant Industry.  
 CSIRO Plant Industry, GPO Box 1600, Canberra, ACT 2601, Australia  
 Tel: 61 2 6246 5223  
 Fax: 61 2 6246 5000  
 Email: Bill.Taylor@csiro.au  
 Seq primer: M13 reverse primer  
 High quality sequence stop: 704.  
 Location/Qualifiers  
 1..704  
 FEATURES  
 source



/organism="Hordelum vulgare subsp. vulgare"  
 /mol\_type="mRNA"  
 /cultivar="Himalaya"  
 /sub\_species="vulgare"  
 /db\_xref="taxon:112509"  
 /clone="BNEL105a5"  
 /tissue\_type="endosperm"  
 /dev\_stage="developing endosperm tissue 10, 12, 15 dpa  
 (days post anthesis)"  
 /lab\_host="DH10B (Life Technology)"  
 /clone\_lib="Barley EST endosperm library"  
 /note="Vector: Ziplox; Site 1: Sal I; Site 2: Not I; mRNA  
 was prepared from endosperm tissues of the barley cultivar  
 Himalaya. cDNA was synthesised from pooled 10, 12, and 15  
 dpa endosperm using Not I-oligo(dT)18 primer/adaptor  
 (Pharmacia Biotech), and then ligated to the Sal I-Not I  
 site of Ziplox vector (Life Technology) after adding a  
 Sal I-Xho I adaptor (Stratagene). Constructed by Shahjahan  
 Ali and Bill Taylor."

## ORIGIN

Query Match 29.8%; Score 17; DB 7; Length 704;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 CAGACCGTGAATGAT 35  
 |||||  
 DB 2 CAGACCGTGAATGAT 18

RESULT 37  
 BU442399 710 bp mRNA linear EST 29-NOV-2002  
 LOCUS 604147742F1 CSEQRBN11 Gallus gallus cDNA clone CHEST990d12 5', mRNA  
 DEFINITION  
 sequence.  
 ACCESSION BU442399  
 VERSION BU442399.1 GI:25931710  
 KEYWORDS EST  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 710)  
 Boardman, P.E., Sanz-Ezquerro, J., Overton, I.M., Burt, D.W., Bosch, E.,  
 Fong, W.T., Tickle, C., Brown, W.R.A., Wilson, S.A. and Hubbard, S.J.  
 A Comprehensive Collection of Chicken cDNAs  
 Curr. Biol. 12 (22), 1965-1969 (2002)  
 PUBMED 12445392  
 COMMENT Contact: Simon Hubbard  
 Department of Biomolecular Sciences  
 University of Manchester Institute of Science and Technology  
 (UMIST)  
 PO Box 88, Manchester, M60 1QD, UK  
 Tel: 01612008930  
 Fax: 01612360409  
 Email: Simon.Hubbard@umist.ac.uk.  
 Location/Qualifiers

## FEATURES

## source

1. 710  
 Location/Qualifiers  
 /organism="Gallus gallus"  
 /mol\_type="mRNA"  
 /strain="Layer and broiler"  
 /db\_xref="taxon:9031"  
 /clone="CHEST990d12"  
 /sex="Male and female"  
 /tissue\_type="muscle"  
 /dev\_stage="adult"  
 /lab\_host="DH10B"  
 /clone\_lib="CSEQRBN11"  
 /note="Vector: pBluescript II KS(+); Site 1: EcoRI;  
 Site 2: NotI. This normalized library was constructed from  
 1 million independent clones. cDNA synthesis was initiated  
 using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand  
 reaction, double-stranded cDNA was blunt-ended, ligated to  
 NotI adaptors, digested with EcoRI, size-selected, and  
 cloned into the NotI and EcoRI compatible sites of a  
 custom modified MCS of the pBluescript (KS+) vector. The  
 library was normalized in 2 rounds using conditions  
 adapted from Soares et al., PNAS (1994) 91: 9228-9232 and  
 Bonaldi et al., Genome Research 6 (1996): 791, except that  
 a significantly longer reannealing hybridization was  
 used."

## ORIGIN

Query Match 29.8%; Score 17; DB 5; Length 710;  
 Best Local Similarity 100.0%; Pred. No. 76;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATGGA 38  
 |||||  
 DB 612 ACCGTGACATGATGGA 628

RESULT 38  
 DT063771 742 bp mRNA linear EST 11-AUG-2005  
 LOCUS DT063771  
 DEFINITION AGENCOURT 56126773 NIH\_ZGC\_10 Danio rerio cDNA clone IMAGE:8008418  
 5', mRNA sequence.  
 ACCESSION DT063771  
 VERSION DT063771.1 GI:72363020  
 KEYWORDS EST  
 SOURCE Danio rerio (zebrafish)  
 ORGANISM Danio rerio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 742)  
 NIH-MGC http://mgc.ncl.nih.gov/.  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rml0A07 Bethesda, MD 20892  
 Email: cgapbs-r@mail.nih.gov  
 Tissue Procurement: Len Zon, Harvard  
 cDNA Library Preparation: Open Biosystems  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: L1AM17184 row: e column: 24  
 High quality sequence stop: 675.  
 Location/Qualifiers

## FEATURES

## source

1. 742  
 Location/Qualifiers  
 /organism="Danio rerio"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7955"  
 /clone="IMAGE:8008418"  
 /tissue\_type="Whole Body"  
 /lab\_host="DH10B"  
 /clone\_lib="NIH\_ZGC\_10"  
 /note="Vector: pXpress1; Site 1: NotI; Site 2: EcoRV;  
 bulk tissue was collected from a whole adult individual  
 from the Tuebingen strain. 1st strand cDNA was primed with  
 a Not I - oligo(dT) primer, double-stranded cDNA was  
 cloned into the Not I and EcoRV sites of pXpress-1.  
 library was size-selected for >1 kb fragments. A  
 normalized version of this library is also available  
 (NIH\_ZGC\_7). Library was constructed by Open Biosystems  
 (Huntsville, AL)."

## ORIGIN

Query Match

29.8%; Score 17; DB 8; Length 742;



Best Local Similarity 100.0%; Pred. No. 76;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CAATGATGGAATCCCTG 45  
Db 469 CAATGATGGAATCCCTG 485

## RESULT 39

BU479295

LOCUS 745 bp mRNA linear EST 30-NOV-2002  
DEFINITION 603848693P1 CSEQRBN22 Gallus gallus cDNA clone CHEST841324 5', mRNA

sequence.

ACCESSION

BU479295

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus;

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..745

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST841324"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Vector: pBluescript II KS(+); Site 1: EcoRI;

Site 2: NotI; This normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand

reaction, double-stranded cDNA was blunt-ended, ligated to

NotI adapters, digested with EcoRI, size-selected, and

cloned into the NotI and EcoRI compatible sites of a

custom modified MCS of the pBluescript (KS+) vector. The

library was normalized in 2 rounds using conditions

adapted from Soares et al., PNAS (1994) 91: 9228-9232 and

Bonaldi et al., Genome Research 6 (1996): 791, except that

a significantly longer reannealing hybridization was

used."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 76;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATGGA 38

Db 573 ACCGTGACATGATGGA 589

## RESULT 40

BU484191

LOCUS 746 bp mRNA linear EST 30-NOV-2002  
DEFINITION 603472492P1 CSEQRBN22 Gallus gallus cDNA clone CHEST350h23 5', mRNA

sequence.

ACCESSION

BU484191

VERSION

KEYWORDS

SOURCE

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Archosauria; Aves; Neognathae; Galliformes; Phasianidae;

Phasianinae; Gallus;

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

CONTACT: Simon Hubbard

Department of Biomolecular Sciences

University of Manchester Institute of Science and Technology

(UMIST)

PO Box 88, Manchester, M60 1QD, UK

Tel: 01612008930

Fax: 01612360409

Email: Simon.Hubbard@umist.ac.uk.

Location/Qualifiers

1..746

/organism="Gallus gallus"

/mol\_type="mRNA"

/strain="Layer and broiler"

/db\_xref="taxon:9031"

/clone="CHEST350h23"

/sex="Male and female"

/tissue\_type="Chondrocytes isolated from growth plate cartilage"

/dev\_stage="adult"

/lab\_host="DH10B"

/note="Vector: pBluescript II KS(+); Site 1: EcoRI;

Site 2: NotI; This normalized library was constructed from

1 million independent clones. cDNA synthesis was initiated

using an oligo(dT) primer, using methylated C in the first

strand synthesis reaction. Following this first strand

reaction, double-stranded cDNA was blunt-ended, ligated to

NotI adapters, digested with EcoRI, size-selected, and

cloned into the NotI and EcoRI compatible sites of a

custom modified MCS of the pBluescript (KS+) vector. The

library was normalized in 2 rounds using conditions

adapted from Soares et al., PNAS (1994) 91: 9228-9232 and

Bonaldi et al., Genome Research 6 (1996): 791, except that

a significantly longer reannealing hybridization was

used."

ORIGIN

Query Match

Best Local Similarity 100.0%; Pred. No. 76;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 ACCGTGACATGATGGA 38

Db 573 ACCGTGACATGATGGA 589

Search completed: April 11, 2006, 21:44:14  
Job time : 849.814 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 23.1356 Seconds  
(without alignments)  
4379.433 Million cell updates/sec

Title: US-10-712-654-22

Perfect score: 57

Sequence: 1 cgcacatgcatcattcactacat.....acttgggtgaacaatggg 57

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 1000 summaries

Database : Issued Patents NA:\*

1: /cgn2\_6/ptodata/1/lna/1\_COMB.seq:\*  
2: /cgn2\_6/ptodata/1/lna/5\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A\_COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B\_COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/H\_COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/PCRTUS\_COMB.seq:\*  
7: /cgn2\_6/ptodata/1/lna/PP\_COMB.seq:\*  
8: /cgn2\_6/ptodata/1/lna/RE\_COMB.seq:\*  
9: /cgn2\_6/ptodata/1/lna/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	57	100.0	1710	3	US-09-350-729A-4
2	57	100.0	2160	2	US-08-082-849B-30
3	57	100.0	2160	6	PCR-US94-01624-30
4	57	100.0	2211	3	US-09-350-729A-2
5	57	100.0	2292	3	US-09-350-729A-3
6	57	100.0	2295	3	US-09-350-729A-1
7	57	100.0	2709	2	US-08-021-601-11
8	57	100.0	2709	2	US-08-082-849B-11
9	57	100.0	2709	6	PCR-US94-01624-11
10	57	100.0	4235	2	US-08-021-601-3
11	57	100.0	4235	2	US-08-082-849B-3
12	57	100.0	4235	6	PCR-US94-01624-3
13	20	35.1	1023	3	US-09-107-533A-66
14	18	31.6	79595	3	US-09-949-016-15318
15	18	31.6	148794	3	US-09-949-016-12751
16	17	29.8	327	3	US-09-107-433-1352
17	17	29.8	601	3	US-09-949-016-61177
18	17	29.8	5252	3	US-09-031-563-6
19	17	29.8	5252	3	US-09-392-277-6
20	17	29.8	5252	3	US-09-258-000-6
21	17	29.8	18763	3	US-09-949-016-13524
22	17	29.8	41743	3	US-09-949-016-13796
23	16	28.1	54	2	US-08-883-327-2
24	16	28.1	54	3	US-09-295-336-2
25	16	28.1	54	3	US-09-793-111-2
26	16	28.1	74	3	US-08-256-287B-11
27	16	28.1	74	3	US-08-368-704C-11
28	16	28.1	601	3	US-09-949-016-35263
29	16	28.1	601	3	US-09-949-016-35264
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165	14	24.6	3059	3	US-09-949-016-1144	Sequence 144, App	238	14	24.6	47883	3	US-09-949-016-11886	Sequence 11886, A
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C 247	14	24.6	86213	3	US-09-949-016-17240	Sequence 17240, A	C 320	13	22.8	29	2	US-08-462-646-62	Sequence 62, Appl1
C 248	14	24.6	86213	3	US-09-949-016-17241	Sequence 17241, A	C 321	13	22.8	29	2	US-08-462-646-76	Sequence 76, Appl1
C 249	14	24.6	86213	3	US-09-949-016-17242	Sequence 17242, A	C 322	13	22.8	29	2	US-08-462-646-90	Sequence 90, Appl1
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C 251	14	24.6	87323	3	US-09-949-016-13828	Sequence 13828, A	C 324	13	22.8	29	3	US-09-013-406-62	Sequence 62, Appl1
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C 254	14	24.6	91232	3	US-09-949-016-11926	Sequence 11926, A	C 327	13	22.8	29	3	US-09-168-947-4	Sequence 4, Appl1
C 255	14	24.6	95750	3	US-09-949-016-11926	Sequence 11926, A	C 328	13	22.8	29	3	US-09-766-095-10	Sequence 10, Appl1
C 256	14	24.6	95750	3	US-09-949-016-11926	Sequence 11926, A	C 329	13	22.8	29	3	US-09-766-095-62	Sequence 62, Appl1
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C 258	14	24.6	99370	3	US-09-949-016-17540	Sequence 17540, A	C 331	13	22.8	29	3	US-09-766-095-90	Sequence 90, Appl1
C 259	14	24.6	101300	3	US-09-949-016-16108	Sequence 16108, A	C 332	13	22.8	30	3	US-09-611-627-48	Sequence 48, Appl1
C 260	14	24.6	102053	3	US-09-949-016-13025	Sequence 13025, A	C 333	13	22.8	35	3	US-08-705-4778-56	Sequence 56, Appl1
C 261	14	24.6	111235	3	US-09-949-016-15328	Sequence 15328, A	C 334	13	22.8	48	2	US-08-418-848A-23	Sequence 23, Appl1
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C 263	14	24.6	117410	3	US-09-949-016-12262	Sequence 12262, A	C 336	13	22.8	49	2	US-08-393-888-2	Sequence 2, Appl1
C 264	14	24.6	129778	3	US-09-949-016-12191	Sequence 12191, A	C 337	13	22.8	49	2	US-08-393-888-6	Sequence 6, Appl1
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C 266	14	24.6	131631	3	US-09-949-016-11757	Sequence 11757, A	C 339	13	22.8	49	2	US-08-355-438-2	Sequence 2, Appl1
C 267	14	24.6	139562	3	US-09-949-016-13451	Sequence 13451, A	C 340	13	22.8	49	3	US-09-069-847-3	Sequence 3, Appl1
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C 269	14	24.6	141560	3	US-09-949-016-16476	Sequence 16476, A	C 342	13	22.8	110	3	US-09-066-914B-17	Sequence 17, Appl1
C 270	14	24.6	143644	3	US-09-949-016-15238	Sequence 15238, A	C 343	13	22.8	119	3	US-09-688-980-30	Sequence 30, Appl1
C 271	14	24.6	152070	3	US-09-949-016-15402	Sequence 15402, A	C 344	13	22.8	145	3	US-09-513-999C-16491	Sequence 16491, A
C 272	14	24.6	152132	3	US-09-949-016-13845	Sequence 13845, A	C 345	13	22.8	173	3	US-09-168-947-36	Sequence 36, Appl1
C 273	14	24.6	152145	3	US-09-949-016-12371	Sequence 12371, A	C 346	13	22.8	175	3	US-09-103-359-9	Sequence 9, Appl1
C 274	14	24.6	152331	3	US-09-128-155-16	Sequence 16, Appl1	C 347	13	22.8	192	3	US-09-513-999C-25571	Sequence 25571, A
C 275	14	24.6	156324	3	US-09-949-016-13749	Sequence 13749, A	C 348	13	22.8	200	3	US-09-688-990-14	Sequence 14, Appl1
C 276	14	24.6	162814	3	US-09-949-016-15578	Sequence 15578, A	C 349	13	22.8	201	3	US-09-248-796A-1872	Sequence 1872, Appl1
C 277	14	24.6	176006	3	US-09-949-016-15784	Sequence 16804, A	C 350	13	22.8	207	3	US-09-023-655-439	Sequence 439, Appl1
C 278	14	24.6	176373	3	US-09-128-155-17	Sequence 17, Appl1	C 351	13	22.8	249	3	US-09-248-796A-11028	Sequence 11028, A
C 279	14	24.6	183112	3	US-09-949-016-14184	Sequence 14184, A	C 352	13	22.8	259	3	US-09-103-359-13	Sequence 13, Appl1
C 280	14	24.6	187848	3	US-09-949-016-12111	Sequence 12111, A	C 353	13	22.8	265	3	US-09-313-284A-1099	Sequence 1099, Appl1
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C 282	14	24.6	194790	3	US-09-949-016-13393	Sequence 13393, A	C 355	13	22.8	302	3	US-08-905-223-190	Sequence 190, Appl1
C 283	14	24.6	212449	3	US-09-949-016-15419	Sequence 15419, A	C 356	13	22.8	306	3	US-09-513-999C-24980	Sequence 24980, A
C 284	14	24.6	2218940	3	US-09-949-016-17539	Sequence 17539, A	C 357	13	22.8	315	3	US-09-107-532A-2050	Sequence 2050, Appl1
C 285	14	24.6	227750	3	US-09-949-016-17175	Sequence 17175, A	C 358	13	22.8	321	3	US-09-248-796A-11061	Sequence 11061, A
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C 287	14	24.6	231129	3	US-09-949-016-16110	Sequence 16110, A	C 360	13	22.8	393	3	US-09-513-999C-23293	Sequence 23293, A
C 288	14	24.6	237241	3	US-09-949-016-16101	Sequence 16101, A	C 361	13	22.8	405	3	US-09-621-976-9556	Sequence 9556, Appl1
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C 290	14	24.6	251769	3	US-09-949-016-13186	Sequence 13186, A	C 363	13	22.8	415	3	US-09-621-976-9199	Sequence 9199, Appl1
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C 292	14	24.6	258775	3	US-09-949-016-16435	Sequence 16435, A	C 365	13	22.8	420	3	US-09-328-352-1518	Sequence 1518, Appl1
C 293	14	24.6	265038	3	US-09-949-016-15779	Sequence 15779, A	C 366	13	22.8	423	3	US-09-248-796A-1056	Sequence 1056, Appl1
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C 295	14	24.6	266748	3	US-09-949-016-13187	Sequence 13187, A	C 368	13	22.8	434	3	US-09-620-405B-430	Sequence 430, Appl1
C 296	14	24.6	266748	3	US-09-949-016-13188	Sequence 13188, A	C 369	13	22.8	434	3	US-09-433-826B-430	Sequence 430, Appl1
C 297	14	24.6	271134	3	US-09-949-016-13705	Sequence 12705, A	C 370	13	22.8	434	3	US-09-604-287A-430	Sequence 430, Appl1
C 298	14	24.6	276687	3	US-09-949-016-13840	Sequence 13840, A	C 371	13	22.8	434	3	US-09-834-759-430	Sequence 430, Appl1
C 299	14	24.6	305491	3	US-09-949-016-17550	Sequence 17550, A	C 372	13	22.8	434	3	US-09-590-751A-430	Sequence 430, Appl1
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C 304	14	24.6	1664976	3	US-08-916-421B-1	Sequence 1, Appl1	C 377	13	22.8	448	3	US-09-103-359-912	Sequence 12, Appl1
C 305	14	24.6	1664976	3	US-08-652-570-1	Sequence 1, Appl1	C 378	13	22.8	448	3	US-09-621-976-2930	Sequence 2930, Appl1
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C 307	13	22.8	19	3	US-10-023-649A-18	Sequence 18, Appl1	C 380	13	22.8	480	3	US-09-134-001C-845	Sequence 845, Appl1
C 308	13	22.8	20	3	US-10-023-649A-38	Sequence 38, Appl1	C 381	13	22.8	483	3	US-09-489-039A-3096	Sequence 3096, Appl1
C 309	13	22.8	22	3	US-09-611-627-49	Sequence 49, Appl1	C 382	13	22.8	485	3	US-09-385-982-911	Sequence 31, Appl1
C 310	13	22.8	29	2	US-08-692-610-5	Sequence 5, Appl1	C 383	13	22.8	516	3	US-09-255-991A-1809	Sequence 1809, Appl1
C 311	13	22.8	29	2	US-08-482-428-10	Sequence 10, Appl1	C 384	13	22.8	528	3	US-09-248-796A-7787	Sequence 7787, Appl1
C 312	13	22.8	29	2	US-08-486-705-10	Sequence 10, Appl1	C 385	13	22.8	541	3	US-09-220-132-105	Sequence 105, Appl1
C 313	13	22.8	29	2	US-08-479-852-10	Sequence 10, Appl1	C 386	13	22.8	561	3	US-09-255-991A-14044	Sequence 14044, A
C 314	13	22.8	29	2	US-08-479-852-62	Sequence 62, Appl1	C 387	13	22.8	561	3	US-09-255-991A-14087	Sequence 14087, A
C 315	13	22.8	29	2	US-08-479-852-76	Sequence 76, Appl1	C 388	13	22.8	588	3	US-09-255-991A-1995	Sequence 1995, Appl1
C 316	13	22.8	29	2	US-08-479-852-90	Sequence 90, Appl1	C 389	13	22.8	594	3	US-09-489-039A-1146	Sequence 1146, Appl1



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C 393	13	22.8	601	3	US-09-949-016-32312	Sequence 32312, A	466	13	22.8	601	3	US-09-949-002-8055	Sequence 8055, App
C 394	13	22.8	601	3	US-09-949-016-42398	Sequence 42398, A	467	13	22.8	602	3	US-09-270-767-5378	Sequence 5378, App
C 395	13	22.8	601	3	US-09-949-016-42790	Sequence 42790, A	468	13	22.8	602	3	US-09-270-767-5066	Sequence 20660, A
C 396	13	22.8	601	3	US-09-949-016-47048	Sequence 47048, A	469	13	22.8	609	3	US-09-248-796A-2567	Sequence 2567, App
C 397	13	22.8	601	3	US-09-949-016-47285	Sequence 47285, A	470	13	22.8	612	3	US-09-248-796A-6545	Sequence 6545, App
C 398	13	22.8	601	3	US-09-949-016-47716	Sequence 47716, A	471	13	22.8	614	3	US-10-101-464A-226	Sequence 226, App
C 399	13	22.8	601	3	US-09-949-016-54571	Sequence 54571, A	472	13	22.8	618	3	US-09-328-352-674	Sequence 674, App
C 400	13	22.8	601	3	US-09-949-016-54572	Sequence 54572, A	473	13	22.8	626	3	US-09-270-767-1068	Sequence 1068, App
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C 403	13	22.8	601	3	US-09-949-016-61912	Sequence 61912, A	476	13	22.8	627	3	US-09-270-767-22778	Sequence 22778, A
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C 405	13	22.8	601	3	US-09-949-016-61914	Sequence 61914, A	478	13	22.8	632	3	US-09-533-559-3561	Sequence 3561, App
C 406	13	22.8	601	3	US-09-949-016-65032	Sequence 65032, A	479	13	22.8	642	3	US-09-584-611A-3615	Sequence 3615, App
C 407	13	22.8	601	3	US-09-949-016-66051	Sequence 66051, A	480	13	22.8	672	3	US-09-583-110-542	Sequence 542, App
C 408	13	22.8	601	3	US-09-949-016-66030	Sequence 66030, A	481	13	22.8	672	3	US-09-107-433-926	Sequence 926, App
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C 411	13	22.8	601	3	US-09-949-016-83391	Sequence 83391, A	484	13	22.8	675	3	US-09-533-559-7084	Sequence 7084, App
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C 415	13	22.8	601	3	US-09-949-016-108117	Sequence 108117, A	488	13	22.8	700	3	US-09-735-271-880	Sequence 880, App
C 416	13	22.8	601	3	US-09-949-016-109722	Sequence 109722, A	489	13	22.8	700	3	US-09-735-271-1181	Sequence 1181, App
C 417	13	22.8	601	3	US-09-949-016-121548	Sequence 121548, A	490	13	22.8	700	3	US-09-735-271-1182	Sequence 1182, App
C 418	13	22.8	601	3	US-09-949-016-121549	Sequence 121549, A	491	13	22.8	706	3	US-09-673-335A-47	Sequence 47, App1
C 419	13	22.8	601	3	US-09-949-016-122602	Sequence 122602, A	492	13	22.8	706	3	US-09-533-559-5467	Sequence 5467, App
C 420	13	22.8	601	3	US-09-949-016-122603	Sequence 122603, A	493	13	22.8	723	3	US-08-998-416-604	Sequence 604, App
C 421	13	22.8	601	3	US-09-949-016-127683	Sequence 127683, A	494	13	22.8	728	3	US-07-648-796A-18	Sequence 18, App1
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C 423	13	22.8	601	3	US-09-949-016-132598	Sequence 132598, A	496	13	22.8	749	3	US-09-673-385A-10	Sequence 10, App1
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C 425	13	22.8	601	3	US-09-949-016-139229	Sequence 139229, A	498	13	22.8	766	3	US-09-270-767-17336	Sequence 17336, A
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C 427	13	22.8	601	3	US-09-949-016-142183	Sequence 142183, A	500	13	22.8	771	3	US-09-016-434-1141	Sequence 1141, App
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C 429	13	22.8	601	3	US-09-949-016-142940	Sequence 142940, A	502	13	22.8	784	3	US-09-071-035-139	Sequence 139, App
C 430	13	22.8	601	3	US-09-949-016-144070	Sequence 144070, A	503	13	22.8	784	3	US-10-200-576-139	Sequence 139, App
C 431	13	22.8	601	3	US-09-949-016-149961	Sequence 149961, A	504	13	22.8	798	3	US-08-956-111E-162	Sequence 162, App
C 432	13	22.8	601	3	US-09-949-016-151702	Sequence 151702, A	505	13	22.8	798	3	US-08-781-966A-162	Sequence 162, App
C 433	13	22.8	601	3	US-09-949-016-154292	Sequence 154292, A	506	13	22.8	813	3	US-10-197-220-130	Sequence 130, App
C 434	13	22.8	601	3	US-09-949-016-156920	Sequence 156920, A	507	13	22.8	815	3	US-08-867-381A-53	Sequence 53, App1
C 435	13	22.8	601	3	US-09-949-016-158877	Sequence 158877, A	508	13	22.8	815	3	US-09-521-144-53	Sequence 53, App1
C 436	13	22.8	601	3	US-09-949-016-159844	Sequence 159844, A	509	13	22.8	823	3	US-09-495-050A-73	Sequence 73, App1
C 437	13	22.8	601	3	US-09-949-016-161185	Sequence 161185, A	510	13	22.8	828	3	US-09-543-661A-253	Sequence 253, App
C 438	13	22.8	601	3	US-09-949-016-163552	Sequence 163552, A	511	13	22.8	840	3	US-09-134-000C-1067	Sequence 1067, App
C 439	13	22.8	601	3	US-09-949-016-165290	Sequence 165290, A	512	13	22.8	921	3	US-09-252-991A-5610	Sequence 5610, App
C 440	13	22.8	601	3	US-09-949-016-165291	Sequence 165291, A	513	13	22.8	921	3	US-09-134-000C-1859	Sequence 1859, App
C 441	13	22.8	601	3	US-09-949-016-166736	Sequence 166736, A	514	13	22.8	924	3	US-09-071-035-137	Sequence 137, App
C 442	13	22.8	601	3	US-09-949-016-169476	Sequence 169476, A	515	13	22.8	936	3	US-10-206-576-137	Sequence 137, App
C 443	13	22.8	601	3	US-09-949-016-171910	Sequence 171910, A	516	13	22.8	942	3	US-09-248-796A-1725	Sequence 1725, App
C 444	13	22.8	601	3	US-09-949-016-173576	Sequence 173576, A	517	13	22.8	942	3	US-09-248-796A-1913	Sequence 1913, App
C 445	13	22.8	601	3	US-09-949-016-173577	Sequence 173577, A	518	13	22.8	999	3	US-09-222-998A-41	Sequence 41, App1
C 446	13	22.8	601	3	US-09-949-016-175097	Sequence 175097, A	519	13	22.8	1001	3	US-09-671-317-226	Sequence 226, App
C 447	13	22.8	601	3	US-09-949-016-177245	Sequence 177245, A	520	13	22.8	1002	3	US-09-230-637-9	Sequence 9, App1
C 448	13	22.8	601	3	US-09-949-016-177246	Sequence 177246, A	521	13	22.8	1002	3	US-09-248-796A-11744	Sequence 11744, A
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C 451	13	22.8	601	3	US-09-949-016-179506	Sequence 179506, A	524	13	22.8	1006	3	US-09-521-144-49	Sequence 49, App1
C 452	13	22.8	601	3	US-09-949-016-179653	Sequence 179653, A	525	13	22.8	1053	3	US-09-252-991A-4223	Sequence 4223, A
C 453	13	22.8	601	3	US-09-949-016-183610	Sequence 183610, A	526	13	22.8	1053	3	US-09-602-787A-661	Sequence 661, App
C 454	13	22.8	601	3	US-09-949-016-188527	Sequence 188527, A	527	13	22.8	1131	2	US-07-648-796A-11	Sequence 11, App1
C 455	13	22.8	601	3	US-09-949-016-189872	Sequence 189872, A	528	13	22.8	1138	3	US-10-164-595-33	Sequence 33, App1
C 456	13	22.8	601	3	US-09-949-016-195755	Sequence 195755, A	529	13	22.8	1139	3	US-09-148-545-29	Sequence 29, App1
C 457	13	22.8	601	3	US-09-949-016-200304	Sequence 200304, A	530	13	22.8	1139	3	US-09-621-316-1	Sequence 1, App1
C 458	13	22.8	601	3	US-09-949-016-200995	Sequence 200995, A	531	13	22.8	1142	3	US-09-253-316-1	Sequence 1, App1
C 459	13	22.8	601	3	US-09-949-016-205647	Sequence 205647, A	532	13	22.8	1173	3	US-09-902-540-5559	Sequence 5559, App
C 460	13	22.8	601	3	US-09-949-016-205692	Sequence 205692, A	533	13	22.8	1194	3	US-09-248-796A-4779	Sequence 4779, App
C 461	13	22.8	601	3	US-09-949-001-107	Sequence 107, App	534	13	22.8	1200	2	US-08-356-397-1	Sequence 1, App1
C 462	13	22.8	601	3	US-09-949-001-108	Sequence 108, App	535	13	22.8	1203	3	US-09-248-796A-3748	Sequence 3748, App



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544	13	22.8	1293	3	US-09-489-039A-3199	Sequence 3199, Ap	617	13	22.8	2337	3	US-09-620-412C-185	Sequence 185, App
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547	13	22.8	1338	3	US-09-134-000C-29	Sequence 29, Appl	620	13	22.8	2376	3	US-09-601-198-57	Sequence 57, Appl
548	13	22.8	1341	3	US-09-134-000C-503	Sequence 503, App	621	13	22.8	2381	2	US-08-484-993B-9	Sequence 9, Appl
549	13	22.8	1356	3	US-09-107-532A-2790	Sequence 2790, Ap	622	13	22.8	2381	2	US-08-484-158B-9	Sequence 9, Appl
550	13	22.8	1431	3	US-09-614-221A-601	Sequence 601, App	623	13	22.8	2381	2	US-08-484-158B-9	Sequence 9, Appl
551	13	22.8	1438	3	US-08-928-069-5	Sequence 5, Appl	624	13	22.8	2381	2	US-08-484-158B-9	Sequence 9, Appl
552	13	22.8	1438	3	US-08-828-683A-5	Sequence 5, Appl	625	13	22.8	2381	2	US-08-484-158B-9	Sequence 9, Appl
553	13	22.8	1454	3	US-09-270-767-14168	Sequence 14168, A	626	13	22.8	2381	3	US-08-456-731-9	Sequence 9, Appl
554	13	22.8	1488	3	US-09-949-016-3851	Sequence 3851, A	627	13	22.8	2400	2	US-08-149-223A-9	Sequence 9, Appl
555	13	22.8	1491	3	US-09-774-528-141	Sequence 141, App	628	13	22.8	2404	2	US-07-648-796A-15	Sequence 15, Appl
556	13	22.8	1491	3	US-10-120-988-141	Sequence 141, App	629	13	22.8	2404	2	US-08-866-577-19	Sequence 19, Appl
557	13	22.8	1492	3	US-09-196-520-7	Sequence 7, Appl	630	13	22.8	2406	3	US-09-207-914-23	Sequence 23, Appl
558	13	22.8	1493	3	US-09-149-476-312	Sequence 312, App	631	13	22.8	2419	3	US-09-207-914-23	Sequence 23, Appl
559	13	22.8	1507	3	US-09-949-016-2848	Sequence 2848, Ap	632	13	22.8	2444	3	US-10-104-047-1886	Sequence 1886, Ap
560	13	22.8	1507	3	US-08-867-381A-48	Sequence 48, Appl	633	13	22.8	2454	3	US-08-890-615-1	Sequence 1, Appl
561	13	22.8	1508	3	US-09-521-144-48	Sequence 54, Appl	634	13	22.8	2454	3	US-09-246-220A-1	Sequence 1, Appl
562	13	22.8	1512	3	US-09-107-532A-54	Sequence 54, Appl	635	13	22.8	2475	3	US-09-045-185-1	Sequence 1, Appl
563	13	22.8	1515	3	US-09-489-039A-4795	Sequence 4795, Ap	636	13	22.8	2475	3	US-09-045-185-3	Sequence 3, Appl
564	13	22.8	1516	3	US-09-149-476-188	Sequence 188, App	637	13	22.8	2494	3	US-09-949-002-70	Sequence 70, Appl
565	13	22.8	1518	3	US-09-328-352-3211	Sequence 3211, Ap	638	13	22.8	2507	3	US-09-872-733A-2	Sequence 2, Appl
566	13	22.8	1568	3	US-09-799-451-922	Sequence 922, App	639	13	22.8	2614	3	US-09-004-066-1	Sequence 1, Appl
567	13	22.8	1570	3	US-09-787-583-1	Sequence 1, Appl	640	13	22.8	2739	2	US-07-743-357-16	Sequence 16, Appl
568	13	22.8	1582	3	US-09-210-422-4	Sequence 4, Appl	641	13	22.8	2739	2	US-09-184-418C-22	Sequence 22, Appl
569	13	22.8	1595	3	US-09-328-352-3103	Sequence 3103, Ap	642	13	22.8	2739	3	US-10-290-579A-22	Sequence 22, Appl
570	13	22.8	1609	3	US-09-807-802A-16	Sequence 16, Appl	643	13	22.8	2745	3	US-10-104-047-1533	Sequence 1533, Ap
571	13	22.8	1617	3	US-09-532-594B-19	Sequence 19, Appl	644	13	22.8	2790	3	US-09-254-594-5	Sequence 5, Appl
572	13	22.8	1617	3	US-09-311-021-207	Sequence 207, App	645	13	22.8	2812	3	US-09-620-312D-624	Sequence 624, App
573	13	22.8	1617	3	US-09-966-316-10	Sequence 10, Appl	646	13	22.8	2817	3	US-08-956-111B-295	Sequence 295, App
574	13	22.8	1641	2	US-09-080-887-5	Sequence 5, Appl	647	13	22.8	2817	3	US-08-781-966A-744	Sequence 744, App
575	13	22.8	1641	2	US-09-323-735-5	Sequence 5, Appl	648	13	22.8	2832	3	US-10-104-047-744	Sequence 7, Appl
576	13	22.8	1658	3	US-09-334-938-7	Sequence 7, Appl	649	13	22.8	2931	3	US-09-646-533D-7	Sequence 7, Appl
577	13	22.8	1677	3	US-09-640-211A-219	Sequence 219, App	650	13	22.8	2946	2	US-08-473-122-1	Sequence 1, Appl
578	13	22.8	1685	3	US-09-557-262-1	Sequence 1, Appl	651	13	22.8	2946	2	US-08-472-478-1	Sequence 1, Appl
579	13	22.8	1752	2	US-07-629-104I-1	Sequence 1, Appl	652	13	22.8	2946	2	US-08-463-081B-7	Sequence 7, Appl
580	13	22.8	1756	3	US-09-614-912-117	Sequence 117, App	653	13	22.8	2946	2	US-08-461-319A-7	Sequence 7, Appl
581	13	22.8	1774	3	US-09-949-016-2840	Sequence 2840, Ap	654	13	22.8	2946	2	US-08-462-390B-7	Sequence 7, Appl
582	13	22.8	1800	3	US-09-532-594B-17	Sequence 17, Appl	655	13	22.8	2946	3	US-08-463-074B-7	Sequence 7, Appl
583	13	22.8	1800	3	US-09-807-802A-14	Sequence 14, Appl	656	13	22.8	2946	3	US-08-465-585C-7	Sequence 7, Appl
584	13	22.8	1800	3	US-09-645-337A-3	Sequence 3, Appl	657	13	22.8	2946	3	US-08-652-446-7	Sequence 7, Appl
585	13	22.8	1856	3	US-09-328-352-2139	Sequence 2139, Ap	658	13	22.8	2946	3	US-08-481-639C-1	Sequence 1, Appl
586	13	22.8	1856	3	US-09-280-116-101	Sequence 101, App	659	13	22.8	3000	2	US-08-393-985-3	Sequence 3, Appl
587	13	22.8	1893	3	US-09-269-939A-5	Sequence 5, Appl	660	13	22.8	3000	3	US-09-184-418C-74	Sequence 74, Appl
588	13	22.8	1941	3	US-09-976-594-1047	Sequence 1047, Ap	661	13	22.8	3000	3	US-10-290-579A-92	Sequence 92, Appl
589	13	22.8	2029	3	US-09-949-016-3528	Sequence 3528, Ap	662	13	22.8	3009	3	US-09-184-418C-65	Sequence 65, Appl
590	13	22.8	2040	3	US-09-269-939A-3	Sequence 3, Appl	663	13	22.8	3009	3	US-10-290-579A-57	Sequence 57, Appl
591	13	22.8	2054	3	US-10-104-047-1520	Sequence 1520, Ap	664	13	22.8	3012	3	US-09-184-418C-92	Sequence 92, Appl
592	13	22.8	2097	3	US-09-269-939A-1	Sequence 1, Appl	665	13	22.8	3012	3	US-10-290-579A-92	Sequence 92, Appl
593	13	22.8	2115	3	US-09-614-221A-111	Sequence 111, App	666	13	22.8	3012	3	US-09-393-795-6	Sequence 6, Appl
594	13	22.8	2115	3	US-09-487-558B-217	Sequence 217, App	667	13	22.8	3012	3	US-09-184-418C-83	Sequence 83, Appl
595	13	22.8	2127	2	US-08-833-883-54	Sequence 54, Appl	668	13	22.8	3012	3	US-10-290-579A-83	Sequence 83, Appl
596	13	22.8	2127	2	US-08-833-877-54	Sequence 54, Appl	669	13	22.8	3012	3	US-09-556-877-87	Sequence 87, Appl
597	13	22.8	2131	3	US-08-970-134-2	Sequence 2, Appl	670	13	22.8	3017	3	US-09-620-412C-87	Sequence 87, Appl
598	13	22.8	2208	3	US-09-532-594B-5	Sequence 5, Appl	671	13	22.8	3031	3	US-09-410-568-87	Sequence 87, Appl
599	13	22.8	2211	3	US-09-807-802A-12	Sequence 12, Appl	672	13	22.8	3031	3	US-07-743-357-19	Sequence 19, Appl
600	13	22.8	2229	3	US-10-104-047-424	Sequence 424, App	673	13	22.8	3031	3	US-09-339-159B-31	Sequence 31, Appl
601	13	22.8	2256	2	US-08-896-590A-3	Sequence 3, Appl	674	13	22.8	3031	3	US-09-319-588C-5	Sequence 5, Appl
602	13	22.8	2256	3	US-09-185-832-3	Sequence 3, Appl	675	13	22.8	3033	2	US-09-134-000C-2799	Sequence 2799, Ap
603	13	22.8	2256	3	US-09-540-236-400	Sequence 400, App	676	13	22.8	3058	3	US-09-148-545-94	Sequence 94, Appl
604	13	22.8	2259	2	US-08-896-590A-1	Sequence 1, Appl	677	13	22.8	3058	3	US-09-621-011-94	Sequence 94, Appl
605	13	22.8	2259	3	US-09-185-832-1	Sequence 1, Appl	678	13	22.8				
606	13	22.8	2259	3	US-09-583-110-1566	Sequence 1566, Ap	679	13	22.8				
607	13	22.8	2262	3	US-09-248-796A-4938	Sequence 4938, Ap	680	13	22.8				
608	13	22.8	2289	2	US-08-463-081B-30	Sequence 30, Appl	681	13	22.8				



C 682	13	22.8	3133	3	US-09-509-712B-93	Sequence 93, Appl	755	13	22.8	7277	3	US-09-795-927-5	Sequence 5, Appl1
C 683	13	22.8	3213	2	US-08-633-770A-4	Sequence 4, Appl1	756	13	22.8	7399	2	US-08-418-88A-9	Sequence 9, Appl1
C 684	13	22.8	3213	3	US-09-280-197-8	Sequence 8, Appl1	C 757	13	22.8	7447	3	US-10-216-870-11	Sequence 11, Appl1
C 685	13	22.8	3213	3	US-09-423-126-10	Sequence 10, Appl1	C 758	13	22.8	7518	3	US-09-620-312D-1051	Sequence 1051, Ap
C 686	13	22.8	3220	3	US-09-949-016-981	Sequence 981, App	759	13	22.8	7588	3	US-08-956-111E-142	Sequence 142, App
C 687	13	22.8	3249	3	US-09-343-494-2	Sequence 2, Appl1	760	13	22.8	7588	3	US-08-781-986A-14	Sequence 14, App
C 688	13	22.8	3249	3	US-09-358-383C-3	Sequence 3, Appl1	761	13	22.8	7744	3	US-10-216-870-14	Sequence 14, Appl1
C 689	13	22.8	3249	3	US-10-160-224-2	Sequence 2, Appl1	762	13	22.8	7958	3	US-09-949-016-16531	Sequence 16531, A
C 690	13	22.8	3252	3	US-09-328-352-1367	Sequence 1367, Ap	C 763	13	22.8	8076	3	US-09-532-806-2	Sequence 2, Appl1
C 691	13	22.8	3293	2	US-08-030-076-1	Sequence 1, Appl1	764	13	22.8	8340	3	US-09-874-057-4	Sequence 4, Appl1
C 692	13	22.8	3323	3	US-09-600-776-1	Sequence 1, Appl1	765	13	22.8	8340	3	US-09-874-926-4	Sequence 4, Appl1
C 693	13	22.8	3323	3	US-09-965-830-1	Sequence 1, Appl1	766	13	22.8	8538	3	US-09-774-528-98	Sequence 98, Appl
C 694	13	22.8	3336	3	US-09-949-016-4510	Sequence 4510, Ap	767	13	22.8	8538	3	US-10-120-988-98	Sequence 98, Appl
C 695	13	22.8	3355	3	US-09-358-383C-1	Sequence 1, Appl1	C 768	13	22.8	8831	3	US-09-949-016-15504	Sequence 15504, A
C 696	13	22.8	3416	3	US-09-254-594-4	Sequence 4, Appl1	769	13	22.8	8932	3	US-09-124-900-1	Sequence 1, Appl1
C 697	13	22.8	3512	3	US-09-248-796A-1940	Sequence 1940, Ap	770	13	22.8	8933	3	US-08-463-210-4	Sequence 4, Appl1
C 698	13	22.8	3519	3	US-10-197-220-163	Sequence 163, App	771	13	22.8	8933	3	US-09-620-958A-3	Sequence 3, Appl1
C 699	13	22.8	3523	3	US-09-710-279-4412	Sequence 4412, Ap	772	13	22.8	8933	3	US-09-620-958A-4	Sequence 4, Appl1
C 700	13	22.8	3536	3	US-09-532-806-1	Sequence 1, Appl1	773	13	22.8	8933	3	US-09-620-958A-9	Sequence 9, Appl1
C 701	13	22.8	3549	3	US-09-248-796A-884	Sequence 884, App	774	13	22.8	8933	3	US-08-463-028-4	Sequence 4, Appl1
C 702	13	22.8	3579	3	US-09-134-000C-1439	Sequence 1439, Ap	775	13	22.8	8933	3	US-08-463-209-4	Sequence 4, Appl1
C 703	13	22.8	3600	3	US-09-462-917A-106	Sequence 106, App	776	13	22.8	8933	3	US-09-943-286-3	Sequence 3, Appl1
C 704	13	22.8	3626	3	US-10-104-047-325	Sequence 325, App	777	13	22.8	8933	3	US-09-943-286-4	Sequence 4, Appl1
C 705	13	22.8	3673	3	US-09-602-362E-26	Sequence 26, Appl	778	13	22.8	8933	3	US-09-943-286-9	Sequence 9, Appl1
C 706	13	22.8	3782	3	US-09-799-451-231	Sequence 231, App	779	13	22.8	8953	3	US-09-184-418C-3	Sequence 3, Appl1
C 707	13	22.8	3819	2	US-07-686-322A-3	Sequence 3, Appl1	780	13	22.8	8953	3	US-10-290-579A-3	Sequence 3, Appl1
C 708	13	22.8	3819	2	US-08-002-999-3	Sequence 3, Appl1	781	13	22.8	8954	3	US-09-184-418C-6	Sequence 6, Appl1
C 709	13	22.8	3852	2	US-08-306-546C-1	Sequence 1, Appl1	782	13	22.8	8954	3	US-10-290-579A-6	Sequence 6, Appl1
C 710	13	22.8	3852	2	US-08-530-524A-1	Sequence 1, Appl1	783	13	22.8	8966	3	US-09-184-418C-5	Sequence 5, Appl1
C 711	13	22.8	3856	2	US-07-743-357-20	Sequence 20, Appl	784	13	22.8	8966	3	US-10-290-579A-9	Sequence 9, Appl1
C 712	13	22.8	3856	2	US-08-980-326-75	Sequence 75, Appl	785	13	22.8	8972	3	US-09-184-418C-9	Sequence 9, Appl1
C 713	13	22.8	3857	3	US-09-336-643A-19	Sequence 19, Appl	786	13	22.8	8972	3	US-10-290-579A-9	Sequence 9, Appl1
C 714	13	22.8	3867	3	US-08-762-428A-5	Sequence 5, Appl1	787	13	22.8	8987	3	US-09-184-418C-2	Sequence 2, Appl1
C 715	13	22.8	3919	3	US-08-980-326-1	Sequence 1, Appl1	788	13	22.8	8987	3	US-10-290-579A-2	Sequence 2, Appl1
C 716	13	22.8	3989	3	US-08-956-171E-816	Sequence 816, App	789	13	22.8	8992	3	US-09-184-418C-4	Sequence 4, Appl1
C 717	13	22.8	4016	3	US-08-781-986A-816	Sequence 816, App	790	13	22.8	8992	3	US-10-290-579A-4	Sequence 4, Appl1
C 718	13	22.8	4016	3	US-08-762-428A-7	Sequence 7, Appl1	791	13	22.8	9002	3	US-09-532-806-3	Sequence 3, Appl1
C 719	13	22.8	4055	3	US-09-710-279-3357	Sequence 3357, Ap	792	13	22.8	9010	3	US-09-184-418C-8	Sequence 8, Appl1
C 720	13	22.8	4064	3	US-10-104-047-358	Sequence 358, App	793	13	22.8	9010	3	US-10-290-579A-8	Sequence 8, Appl1
C 721	13	22.8	4113	2	US-07-743-357-21	Sequence 21, Appl	794	13	22.8	9038	3	US-09-949-016-15523	Sequence 15523, A
C 722	13	22.8	4150	3	US-10-023-649A-5	Sequence 5, Appl1	795	13	22.8	9050	3	US-09-184-418C-7	Sequence 7, Appl1
C 723	13	22.8	4213	3	US-09-774-528-24	Sequence 24, Appl	796	13	22.8	9050	3	US-10-290-579A-7	Sequence 7, Appl1
C 724	13	22.8	4213	3	US-10-120-988-24	Sequence 24, Appl	797	13	22.8	9060	3	US-09-184-418C-10	Sequence 10, Appl
C 725	13	22.8	4286	3	US-09-976-594-632	Sequence 632, App	798	13	22.8	9060	3	US-10-290-579A-10	Sequence 10, Appl
C 726	13	22.8	4307	3	US-09-184-418C-48	Sequence 48, Appl	799	13	22.8	9183	3	US-09-319-588C-1	Sequence 1, Appl1
C 727	13	22.8	4307	3	US-09-552-950-1	Sequence 1, Appl1	800	13	22.8	9207	3	US-08-368-353-800	Sequence 800, App
C 728	13	22.8	4307	3	US-09-936-572-1	Sequence 1, Appl1	801	13	22.8	9207	3	US-08-488-551B-800	Sequence 800, App
C 729	13	22.8	4307	3	US-10-290-579A-48	Sequence 48, Appl	802	13	22.8	9350	3	US-09-949-016-16640	Sequence 16640, A
C 730	13	22.8	4313	3	US-09-475-515-3	Sequence 3, Appl1	803	13	22.8	9350	3	US-09-949-016-15965	Sequence 15965, A
C 731	13	22.8	4336	3	US-08-956-171E-546	Sequence 546, App	C 804	13	22.8	9458	3	US-08-956-171E-114	Sequence 114, App
C 732	13	22.8	4336	3	US-08-781-986A-546	Sequence 546, App	C 805	13	22.8	9458	3	US-08-781-986A-114	Sequence 114, App
C 733	13	22.8	4395	3	US-10-023-649A-7	Sequence 7, Appl1	C 806	13	22.8	9458	3	US-08-781-986A-114	Sequence 114, App
C 734	13	22.8	4593	3	US-09-556-877-172	Sequence 172, App	C 807	13	22.8	9555	3	US-09-921-922A-6	Sequence 6, Appl1
C 735	13	22.8	4593	3	US-09-620-412C-172	Sequence 172, App	808	13	22.8	9555	3	US-09-921-922A-6	Sequence 6, Appl1
C 736	13	22.8	4593	3	US-09-598-419-172	Sequence 172, App	809	13	22.8	9709	2	US-08-188-583-5	Sequence 5, Appl1
C 737	13	22.8	4593	3	US-10-197-220-83	Sequence 83, Appl	810	13	22.8	9709	2	US-08-388-353-1	Sequence 1, Appl1
C 738	13	22.8	4617	3	US-08-930-055A-1	Sequence 1, Appl1	811	13	22.8	9709	3	US-08-488-551B-1	Sequence 1, Appl1
C 739	13	22.8	4670	2	US-08-633-770A-12	Sequence 12, Appl	812	13	22.8	9709	3	US-09-309-572-15	Sequence 15, Appl
C 740	13	22.8	4683	3	US-09-807-802A-19	Sequence 19, Appl	813	13	22.8	9719	3	US-09-718-096-15	Sequence 15, Appl
C 741	13	22.8	4718	3	US-09-807-802A-1	Sequence 1, Appl1	814	13	22.8	9719	3	US-09-700-304-1	Sequence 1, Appl1
C 742	13	22.8	4767	3	US-09-532-594A-1	Sequence 1, Appl1	815	13	22.8	9737	2	US-08-944-449-7	Sequence 7, Appl1
C 743	13	22.8	5109	3	US-08-930-055A-2	Sequence 2, Appl1	816	13	22.8	9737	3	US-08-944-449-7	Sequence 7, Appl1
C 744	13	22.8	5362	3	US-08-463-028-5	Sequence 5, Appl1	817	13	22.8	9737	3	US-09-353-363-7	Sequence 3, Appl1
C 745	13	22.8	5362	3	US-08-463-028-5	Sequence 5, Appl1	818	13	22.8	9739	2	US-08-827-688-12	Sequence 12, Appl
C 746	13	22.8	5362	3	US-08-463-209-5	Sequence 5, Appl1	819	13	22.8	9739	2	US-08-388-809-1	Sequence 1, Appl1
C 747	13	22.8	5621	3	US-09-566-921-106	Sequence 106, App	820	13	22.8	9739	2	US-08-647-714-1	Sequence 1, Appl1
C 748	13	22.8	5910	3	US-08-961-527-165	Sequence 165, App	821	13	22.8	9746	2	US-08-022-835-3	Sequence 3, Appl1
C 749	13	22.8	6080	3	US-09-620-512D-327	Sequence 327, App	822	13	22.8	9746	2	US-08-388-809-3	Sequence 3, Appl1
C 750	13	22.8	6151	3	US-09-799-451-528	Sequence 528, App	823	13	22.8	9746	2	US-08-647-714-3	Sequence 3, Appl1
C 751	13	22.8	6741	3	US-09-794-384A-14	Sequence 14, Appl	C 824	13	22.8	9758	3	US-09-392-812A-5	Sequence 5, Appl1
C 752	13	22.8	6743	3	US-08-932-280-1	Sequence 1, Appl1	C 825	13	22.8	9913	3	US-09-827-688-11	Sequence 11, Appl
C 753	13	22.8	6743	3	US-09-357-711A-1	Sequence 1, Appl1	826	13	22.8	10383	3	US-09-949-016-14617	Sequence 14617, A
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## ALIGNMENTS

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RESULT 1
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; Patent No. 6770479
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHER, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WEIKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135
; CURRENT APPLICATION NUMBER: US/09/350,729A
; CURRENT FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1710
; TYPE: DNA
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US-09-350-729A-4
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Best Local Similarity 100.0%; Pred. No. 4.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Patent No. 5677274
; GENERAL INFORMATION:
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atora, Naveen
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; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; TITLE OF INVENTION: Related Methods
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
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; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-161-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 30:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2160 base pairs
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; STRANDEDNESS: single
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; NAME/KEY: CDS
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; OTHER INFORMATION: /product= "PAHIV#2"
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; GENERAL INFORMATION:
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSER: TOWNSEND AND TOWNSEND KHOURIE AND CREW
; STREET: Stewart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
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STATE: CA  
COUNTRY: USA  
ZIP: 94105  
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624  
FILING DATE: June 25, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
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RESULT 4  
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Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PUSHKO, PETER  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350,729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent Ver. 2.1  
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US-09-350-729A-2

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Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PUSHKO, PETER  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350,729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2292  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-350-729A-3

Query Match 100.0%; Score 57; DB 3; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 4.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1080 CGCAATTGATCATCTACTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1136  
1080 CGCAATTGATCATCTACTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1136

RESULT 6  
US-09-350-729A-1  
Sequence 1, Application US/09350729A  
Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PUSHKO, PETER  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350,729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2295  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-350-729A-1

Query Match 100.0%; Score 57; DB 3; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 4.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1083 CGCAATTGATCATCTACTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1139  
1083 CGCAATTGATCATCTACTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1139  
RESULT 7  
US-08-021-601-11  
Sequence 11, Application US/08021601



Patent No. 5591631  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Nichols, Peter J.  
APPLICANT: Arora, Naveen  
APPLICANT: Singh, Yogendra  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 12  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Needle & Rosenberg, P.C.  
STREET: 133 Carnegie Way, Suite 400  
CITY: Atlanta  
STATE: Georgia  
COUNTRY: USA  
ZIP: 30303  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/021,601  
FILING DATE: 19930212  
CLASSIFICATION: 514  
ATTORNEY/AGENT INFORMATION:  
NAME: Spratt, Gwendolyn D.  
REGISTRATION NUMBER: 36,016  
REFERENCE/DOCKET NUMBER: 1414.057  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 404/688-0770  
TELEFAX: 404/688-9880  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2709 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2709  
US-08-021-601-11

Query Match 100.0%; Score 57; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 4.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTATCTTACAGAGGGAAGAACTTGGCTGAAACAATGGG 57  
DB 996 CGCAATTGATCATTCATCTATCTTACAGAGGGAAGAACTTGGCTGAAACAATGGG 1052

RESULT 8  
US-08-082-849B-11  
Sequence 11, Application US/08082849B  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Arora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
TITLE OF INVENTION: Related Methods  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA

ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,849B  
FILING DATE: 25-JUN-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,601  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-161-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2709 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..2709  
OTHER INFORMATION: /product= "PA(1-725)-Human CD4  
residues (1-178)"  
US-08-082-849B-11

Query Match 100.0%; Score 57; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 4.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTATCTTACAGAGGGAAGAACTTGGCTGAAACAATGGG 57  
DB 996 CGCAATTGATCATTCATCTATCTTACAGAGGGAAGAACTTGGCTGAAACAATGGG 1052

RESULT 9  
PCT-US94-01624-11  
Sequence 11, Application PC/TUS9401624  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Arora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND AND TOWNSEND KHOURIE AND CREW  
STREET: Stewart Street Tower, 20th Floor, One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624



```
; FILING DATE: June 25, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2709
; OTHER INFORMATION: /product="PA(1-725)-----Human CD4
; PCT-US94-01624-11

Query Match      100.0%; Score 57; DB 6; Length 2709;
Best Local Similarity 100.0%; Pred. No. 4.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGCAATTGATCATCTATCTCTGACGAGGGAAGAACTGGGCTGAACAATGGG  57
Db      996  CGCAATTGATCATCTATCTCTGACGAGGGAAGAACTGGGCTGAACAATGGG  1052

RESULT 10
US-08-021-601-3
; Sequence 3, Application US/08021601
; Patent No. 5581631
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Nichols, Peter J.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 133 Carnegie Way, Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,601
; FILING DATE: 19930212
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 4235 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1891..4095
; US-08-021-601-3

Query Match      100.0%; Score 57; DB 2; Length 4235;
Best Local Similarity 100.0%; Pred. No. 4.6e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1  CGCAATTGATCATCTATCTCTGACGAGGGAAGAACTGGGCTGAACAATGGG  57
Db      2886  CGCAATTGATCATCTATCTCTGACGAGGGAAGAACTGGGCTGAACAATGGG  2942

RESULT 11
US-08-082-849B-3
; Sequence 3, Application US/08082849B
; Patent No. 5677274
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-161-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
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LOCATION: 1891..4095  
OTHER INFORMATION: /product= "Protective Antigen"  
US-08-082-849B-3

Query Match 100.0%; Score 57; DB 2; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 4.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGAGGAAAGACTGGCTGGAACAATGGG 57  
DB 2886 CGCAATTGATCATCTATCTCTAGCAGGAGGAAAGACTGGCTGGAACAATGGG 2942

## RESULT 12

PCT-US94-01624-3  
Sequence 3, Application PC/TUS9401624  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Atoria, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
NUMBER OF SEQUENCES: 31  
TITLE OF INVENTION: RELATED METHODS  
CORRESPONDENCE ADDRESS:  
ADDRESS: TOWNSEND and TOWNSEND KHOURIE and CREW  
STREET: Stewart Street Tower, 20th Floor, One Market  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624  
FILING DATE: June 25, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4235 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1891..4095  
OTHER INFORMATION: /product= "Protective Antigen"  
PCT-US94-01624-3

Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 4.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGAGGAAAGACTGGCTGGAACAATGGG 57  
DB 2886 CGCAATTGATCATCTATCTCTAGCAGGAGGAAAGACTGGCTGGAACAATGGG 2942

RESULT 13  
US-09-107-532A-66  
Sequence 66, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESS: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Arinello, Pamela Denike  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 66:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1023 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (8) LOCATION 1..1023  
SEQUENCE DESCRIPTION: SEQ ID NO: 66:  
US-09-107-532A-66

Query Match 35.1%; Score 20; DB 3; Length 1023;  
Best Local Similarity 100.0%; Pred. No. 0.13;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AAAGAACTGGGCTGAACA 52  
DB 457 AAAGAACTGGGCTGAACA 476

RESULT 14  
US-09-949-016-15318  
Sequence 15318, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMERPHISMS IN KNOWN GENES ASSOCIATED  
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CL001307



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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15318
; LENGTH: 79595
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-15318

Query Match          31.6%; Score 18; DB 3; Length 79595;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 TTGGGCTGAACAATGGG 57
Db 70974 TTGGGCTGAACAATGGG 70991

RESULT 15
US-09-949-016-12751
; Sequence 12751, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12751
; LENGTH: 148794
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-12751

Query Match          31.6%; Score 18; DB 3; Length 148794;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 TTGGGCTGAACAATGGG 57
Db 92173 TTGGGCTGAACAATGGG 92190

RESULT 16
US-09-107-433-1352/C
; Sequence 1352, Application US/09107433
; Patent No. 6800744
; GENERAL INFORMATION:
; APPLICANT: Lynn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE
; FOR DIAGNOSTIC THERAPEUTICS
; NUMBER OF SEQUENCES: 5206
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham

STATE: Massachusetts
COUNTRY: USA
ZIP: 02354
COMPUTER READABLE FORM:
MEDIUM TYPE: CD-ROM ISO9660
COMPUTER: <Unknown>
OPERATING SYSTEM: <Unknown>
SOFTWARE: <Unknown>
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,433
FILING DATE: 30-Jun-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/ 085131
FILING DATE: May 12, 1998
APPLICATION NUMBER: 60/051553
FILING DATE: July 2, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Deneka
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-011
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
TELEFAX: (781)893-8277
INFORMATION FOR SEQ ID NO: 1352:
SEQUENCE CHARACTERISTICS:
LENGTH: 327 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Streptococcus pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...327
SEQUENCE DESCRIPTION: SEQ ID NO: 1352:
US-09-107-433-1352

Query Match          29.8%; Score 17; DB 3; Length 327;
Best Local Similarity 100.0%; Pred. No. 6;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GAAAGAACTGGGCTG 47
Db 296 GAAAGAACTGGGCTG 280

RESULT 17
US-09-949-016-61177
; Sequence 61177, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 61177
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-61177
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Query Match	29.8%;	Score 17;	DB 3;	Length 601;
Best Local Similarity	100.0%;	Pred. No. 6.1;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	25	AGCAGGGGAAAGAACTT 41		
Db	183	AGCAGGGGAAAGAACTT 199		
RESULT 18				
US-09-031-563-6				
Sequence 6, Application US/09031563A				
Patent No. 6022708				
GENERAL INFORMATION:				
APPLICANT: Arnon Roshenthal				
TITLE OF INVENTION: Fused				
FILE REFERENCE: P1272				
CURRENT APPLICATION NUMBER: US/09/031,563A				
CURRENT FILING DATE: 1998-02-26				
NUMBER OF SEQ ID NOS: 27				
SEQ ID NO 6				
LENGTH: 5252				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-031-563-6				
Query Match	29.8%;	Score 17;	DB 3;	Length 5252;
Best Local Similarity	100.0%;	Pred. No. 6.4;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	18	TATCTTAGCAGGGGAA 34		
Db	3162	TATCTTAGCAGGGGAA 3178		
RESULT 19				
US-09-392-277-6				
Sequence 6, Application US/09392277A				
Patent No. 6451977				
GENERAL INFORMATION:				
APPLICANT: Frederic de Sauvage				
TITLE OF INVENTION: Fused				
FILE REFERENCE: P1272R1P1				
CURRENT APPLICATION NUMBER: US/09/392,277A				
CURRENT FILING DATE: 1999-09-03				
EARLIER APPLICATION NUMBER: US 09/258,000				
EARLIER FILING DATE: 1999-02-25				
EARLIER APPLICATION NUMBER: US 60/076,072				
EARLIER FILING DATE: 1998-02-26				
NUMBER OF SEQ ID NOS: 28				
SEQ ID NO 6				
LENGTH: 5252				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-392-277-6				
Query Match	29.8%;	Score 17;	DB 3;	Length 5252;
Best Local Similarity	100.0%;	Pred. No. 6.4;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	18	TATCTTAGCAGGGGAA 34		
Db	3162	TATCTTAGCAGGGGAA 3178		
RESULT 20				
US-09-258-000-6				
Sequence 6, Application US/09258000				
Patent No. 6531579				
GENERAL INFORMATION:				
APPLICANT: Arnon Roshenthal				
TITLE OF INVENTION: Fused				
FILE REFERENCE: P1272R1				
CURRENT APPLICATION NUMBER: US/09/258,000				
CURRENT FILING DATE: 1999-02-25				
EARLIER APPLICATION NUMBER: US 60/076,072				
EARLIER FILING DATE: 1998-02-26				
NUMBER OF SEQ ID NOS: 28				
SEQ ID NO 6				
LENGTH: 5252				
TYPE: DNA				
ORGANISM: Homo sapiens				
US-09-392-277-6				
Query Match	29.8%;	Score 17;	DB 3;	Length 5252;
Best Local Similarity	100.0%;	Pred. No. 6.4;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	18	TATCTTAGCAGGGGAA 34		
Db	3162	TATCTTAGCAGGGGAA 3178		
RESULT 21				
US-09-949-016-13524/C				
Sequence 13524, Application US/0949016				
Patent No. 6812339				
GENERAL INFORMATION:				
APPLICANT: VENTER, J. Craig et al.				
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF				
FILE REFERENCE: C1001307				
CURRENT APPLICATION NUMBER: US/09/949,016				
CURRENT FILING DATE: 2000-04-14				
PRIOR APPLICATION NUMBER: 60/241,755				
PRIOR FILING DATE: 2000-10-20				
PRIOR APPLICATION NUMBER: 60/237,768				
PRIOR FILING DATE: 2000-10-03				
NUMBER OF SEQ ID NOS: 207012				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO 13524				
LENGTH: 18763				
TYPE: DNA				
ORGANISM: Human				
US-09-949-016-13524				
Query Match	29.8%;	Score 17;	DB 3;	Length 18763;
Best Local Similarity	100.0%;	Pred. No. 6.5;		
Matches 17;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	25	AGCAGGGGAAAGAACTT 41		
Db	15142	AGCAGGGGAAAGAACTT 15126		
RESULT 22				
US-09-949-016-13796				
Sequence 13796, Application US/0949016				
Patent No. 6812339				
GENERAL INFORMATION:				
APPLICANT: VENTER, J. Craig et al.				
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF				
FILE REF				



PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 13796  
LENGTH: 41743  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-13796

Query Match 29.8%; Score 17; DB 3; Length 41743;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GGAAGACTTGGGCTG 47  
Db 10249 GGAAGACTTGGGCTG 10265

RESULT 23  
US-08-883-327-2  
Sequence 2, Application US/08883327A  
Patent No. 5972650  
GENERAL INFORMATION:  
APPLICANT: Yao, Feng  
TITLE OF INVENTION: Tetracycline Repressor Regulated Mammalian Cell  
FILE REFERENCE: Yao application  
CURRENT APPLICATION NUMBER: US/08/883,327A  
CURRENT FILING DATE: 1997-06-26  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 54  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-08-883-327-2

Query Match 28.1%; Score 16; DB 2; Length 54;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TCACTATCTTAGCAG 29  
Db 35 TCACTATCTTAGCAG 50

RESULT 24  
US-09-295-336-2  
Sequence 2, Application US/09295336  
Patent No. 6251640  
GENERAL INFORMATION:  
APPLICANT: Yao, Feng  
TITLE OF INVENTION: Tetracycline Repressor Regulated Mammalian Cell  
FILE REFERENCE: Yao application  
CURRENT APPLICATION NUMBER: US/09/295,336  
CURRENT FILING DATE: 1999-04-21  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 54  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-295-336-2

Query Match 28.1%; Score 16; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TCACTATCTTAGCAG 29  
Db 35 TCACTATCTTAGCAG 50

RESULT 25  
US-09-793-111-2  
Sequence 2, Application US/09793111  
Patent No. 6446871  
GENERAL INFORMATION:  
APPLICANT: Yao, Feng  
TITLE OF INVENTION: Tetracycline Repressor Regulated Mammalian Cell  
FILE REFERENCE: Yao application  
CURRENT APPLICATION NUMBER: US/09/793,111  
CURRENT FILING DATE: 2001-02-27  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 2  
LENGTH: 54  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-793-111-2

Query Match 28.1%; Score 16; DB 3; Length 54;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 TCACTATCTTAGCAG 29  
Db 35 TCACTATCTTAGCAG 50

RESULT 26  
US-08-258-287B-11/c  
Sequence 11, Application US/08258287B  
Patent No. 6083735  
GENERAL INFORMATION:  
APPLICANT: Yuan, Junying  
TITLE OF INVENTION: Programmed Cell Death Genes and Proteins  
NUMBER OF SEQUENCES: 85  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Sterne, Kessler, Goldstein & Fox  
STREET: 1100 New York Avenue, Suite 600  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/258,287B  
FILING DATE: 10-JUN-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/080,850  
FILING DATE: 24-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Bugalsky, Lawrence B.  
REGISTRATION NUMBER: 35,086  
REFERENCE/DOCKET NUMBER: 0609,3920001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 371-2600  
TELEFAX: (202) 371-2540  
TELEX: 248636 SSK  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 74 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: both  
TOPOLOGY: both  
US-08-258-287B-11



Query Match 28.1%; Score 16; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTC A 16  
|||||  
DB 28 CGCAATTGATCATTC A 13

RESULT 27  
US-08-368-704C-11/c  
; Sequence 11, Application US/08368704C  
; Patent No. 6087160

GENERAL INFORMATION:  
; APPLICANT: Yuan, Junying  
; APPLICANT: Miura, Masayuki  
; TITLE OF INVENTION: Programmed Cell Death Genes and Proteins  
; NUMBER OF SEQUENCES: 95  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Sterne, Kessler, Goldstein & Fox  
; STREET: 1100 New York Avenue, Suite 600  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20005

COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/368,704C  
; FILING DATE: 4-JAN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/258,287  
; FILING DATE: 10-JUN-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/080,850  
; FILING DATE: 24-JUN-1993

ATTORNEY/AGENT INFORMATION:  
; NAME: Bugalsky, Lawrence B.  
; REGISTRATION NUMBER: 35,086  
; REFERENCE/DOCKET NUMBER: 0609.3920002  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202) 371-2600  
; TELEFAX: (202) 371-2540

TELEX: 248636 SSK  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 74 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: both  
; TOPOLOGY: both  
; US-08-368-704C-11

Query Match 28.1%; Score 16; DB 3; Length 74;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTC A 16  
|||||  
DB 28 CGCAATTGATCATTC A 13

RESULT 28  
US-09-949-016-35263/c  
; Sequence 35263, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35263  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35263

Query Match 28.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 GAAAGAACTGGGCTG 47  
|||||  
DB 399 GAAAGAACTGGGCTG 384

RESULT 29  
US-09-949-016-35264/c  
; Sequence 35264, Application US/09949016  
; Patent No. 6812339

GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35264  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-35264

Query Match 28.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 GAAAGAACTGGGCTG 47  
|||||  
DB 168 GAAAGAACTGGGCTG 153

RESULT 30  
US-09-949-016-145223/c  
; Sequence 145223, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14



```
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 145223
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-145223
```

```
Query Match          28.1% Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      29 GGGGAAAGAACTTGGG 44
      |||||
Db      127 GCGGAAAGAACTTGGG 112
```

```
RESULT 31
US-09-949-016-156825/c
/ Sequence 156825, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 156825
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-156825
```

```
Query Match          28.1% Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      32 GAAAGACTTGGGCTG 47
      |||||
Db      399 GAAAGAACTTGGGCTG 384
```

```
RESULT 32
US-09-949-016-156826/c
/ Sequence 156826, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
```

```
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 156826
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-156826
```

```
Query Match          28.1% Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      32 GAAAGACTTGGGCTG 47
      |||||
Db      168 GAAAGAACTTGGGCTG 153
```

```
RESULT 33
US-09-949-016-184386
/ Sequence 184386, Application US/09949016
/ Patent No. 6812339
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ FILE REFERENCE: CLO01307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 184386
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
US-09-949-016-184386
```

```
Query Match          28.1% Score 16; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY      23 CTAGCAGGGGAAAGAA 38
      |||||
Db      581 CTAGCAGGGGAAAGAA 596
```

```
RESULT 34
US-09-196-520-1
/ Sequence 1, Application US/09196520
/ Patent No. 6204039
/ GENERAL INFORMATION:
/ APPLICANT: Falco, Carl S.
/ APPLICANT: Allen, Stephen M.
/ TITLE OF INVENTION: Plant Isocitrate Dehydrogenase Homologs
/ FILE REFERENCE: BB-1291
/ CURRENT APPLICATION NUMBER: US/09/196,520
/ EARLIER APPLICATION NUMBER: 60/067,388
/ EARLIER FILING DATE: December 2, 1997
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1501
/ TYPE: DNA
/ ORGANISM: Zea mays
US-09-196-520-1
```



Query Match	28.1%;	Score 16;	DB 3;	Length 1501;
Best Local Similarity	100.0%;	Pred. No. 22;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	31	GGAAGAACTTGGCT	46
Db	462	GGAAGAACTTGGCT	477

RESULT 35  
US-10-104-047-635/c

Query Match	28.1%;	Score 16;	DB 3;	Length 2636;
Best Local Similarity	100.0%;	Pred. No. 22;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	23	CTAGCAGGGGAAGAA	38
Db	2427	CTAGCAGGGGAAGAA	2412

```

RESULT 36
US-09-620-312D-511/C
Sequence 511 Application US/09620312D
Patent No. 6569662
GENERAL INFORMATION:
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Asundi, Vinod
APPLICANT: Zhang, Jie
APPLICANT: Ren, Feiyen
APPLICANT: Chen, Rui-hong
APPLICANT: Zhao, Qing A.
APPLICANT: Wehrman, Tom
APPLICANT: Xue, Aidong J.
APPLICANT: Yang, Yonghong
APPLICANT: Wang, Jian-Rui
APPLICANT: Zhou, Ping
APPLICANT: Ma, Yundong
APPLICANT: Wang, Duntui
APPLICANT: Wang, Zhiwei
APPLICANT: John Tillinghast
APPLICANT: Drmanac, Radoje T.
TITLE OF INVENTION: No. 6569662el Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 784C1P2B
CURRENT APPLICATION NUMBER: US/09/620,312D
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 09/552,317
PRIOR FILING DATE: 2000-04-25
PRIOR APPLICATION NUMBER: 09/488,725
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 1105
SOFTWARE: pc_fl_genes Version 1.0
SEQ ID NO 511
LENGTH: 2907

```

```

? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (359)..(2530)
? FEATURE:
? NAME/KEY: misc feature
? LOCATION: (1)..(297)
? OTHER INFORMATION: n = a,t,c,g
US-09-620-112D-511

```

Query Match	28.1%	Score 16;	DB 3;	Length 2307;
Best Local Similarity	100.0%	Pred. No. 22;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY 23 CTAGCAGGGGAAGAA 38  
|||  
Db 2686 CTAGCAGGGGAAGAA 2671

```

RESULT 37
US-09-949-002-682
; Sequence 682; Application US/099499002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: C1.000790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682
; LENGTH: 10885
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-682

```

Query Match	28.1%;	Score 16;	DB 3;	Length 10885;
Best Local Similarity	100.0%;	Pred. No. 23;		
Matches	16;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0

QY 40 TTGGGCTGAACAATG 55  
|||  
Db 10570 TTGGGCTGAACAATG 10585

```

RESULT 38
US-09-949-002-800
; Sequence 800, Application US/09949002
; Patent No. 690016
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH INFLAMMATORY AUTOIMMUNE DISEASE, METHODS OF DETECTION
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: CLO00790
; CURRENT APPLICATION NUMBER: US/09/949,002
; CURRENT FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: 60/231,401
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 10823
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 800
; LENGTH: 10885
; TYPE: DNA
; ORGANISM: Human
US-09-949-002-800

```



Query Match 28.1%; Score 16; DB 3; Length 10885;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAACTG 55  
Db 10570 TTGGGCTGAACAACTG 10585

## RESULT 39

US-09-949-016-17025  
; Sequence 17025, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 17025  
; LENGTH: 27412  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(27412)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-17025

Query Match 28.1%; Score 16; DB 3; Length 27412;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAGCAGGGGAAGAA 38  
Db 10737 CTAGCAGGGGAAGAA 10752

## RESULT 40

US-09-949-016-13420/C  
; Sequence 13420, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13420  
; LENGTH: 47363  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(47363)

; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-13420

Query Match 28.1%; Score 16; DB 3; Length 47363;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 AGCAGGGGAAGAACT 40  
Db 15982 AGCAGGGGAAGAACT 15967

Search completed: April 11, 2006, 21:50:45  
Job time : 48.1356 secs



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C 248	18	31.6	324926	14	AC127140	Rattus no	C 321	17	29.8	176781	8	AC016732	AC016732 Homo sapi
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C 250	17	29.8	510	6	AX389202	Sequence	C 323	17	29.8	177727	14	AC022178	AC022178 Homo sapi
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C 252	17	29.8	751	10	BV493658	S217P6691	C 325	17	29.8	179117	9	AC106843	AC106843 Mus muscu
C 253	17	29.8	762	15	BT004608	Arabidops	C 326	17	29.8	180795	9	AC110532	AC110532 Mus muscu
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C 257	17	29.8	1452	15	AY740083	Ostreococ	C 330	17	29.8	183584	8	AC012492	AC012492 Homo sapi
C 258	17	29.8	1479	3	AY672531	Unculture	C 331	17	29.8	187423	14	AC034175	AC034175 Homo sapi
C 259	17	29.8	2363	8	HSB801073	AL117548 Homo sapi	C 332	17	29.8	190295	9	AC124445	AC124445 Mus muscu
C 260	17	29.8	3540	6	CQ434057	Sequence	C 333	17	29.8	190298	9	AC121294	AC121294 Mus muscu
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C 263	17	29.8	5252	6	AP491944	Homo sapi	C 336	17	29.8	193425	8	AC015664	AC015664 Homo sapi
C 264	17	29.8	56293	14	AC165692	Bos tauru	C 337	17	29.8	195133	14	AC148635	AC148635 Callithri
C 265	17	29.8	59351	14	AC100656	Mus muscu	C 338	17	29.8	195143	14	AC163218	AC163218 Mus muscu
C 266	17	29.8	60726	14	AC100613	Mus muscu	C 339	17	29.8	196300	9	AC117598	AC117598 Homo sapi
C 267	17	29.8	60726	14	AC100613	Mus muscu	C 340	17	29.8	197063	14	AC159724	AC159724 Bos tauru
C 268	17	29.8	61028	14	AC107658	Mus muscu	C 341	17	29.8	198175	9	AL683800	AL683800 Mouse DNA
C 269	17	29.8	68583	14	AC100087	Mus muscu	C 342	17	29.8	198912	9	AC132580	AC132580 Mus muscu
C 270	17	29.8	69458	8	AC025432	Homo sapi	C 343	17	29.8	199028	9	AC109279	AC109279 Mus muscu
C 271	17	29.8	70326	14	AC068957	Homo sapi	C 344	17	29.8	199412	8	AC005181	AC005181 Homo sapi
C 272	17	29.8	71751	14	AC090222	Homo sapi	C 345	17	29.8	202763	8	AC122342	AC122342 Mus muscu
C 273	17	29.8	74729	8	HS703H14	AL001287 Human DNA	C 346	17	29.8	202879	9	AC005859	AC005859 Homo sapi
C 274	17	29.8	76113	14	AC023453	Homo sapi	C 347	17	29.8	205430	14	AP002756	AP002756 Homo sapi
C 275	17	29.8	78514	14	AL356496	Homo sapi	C 348	17	29.8	206855	8	AC009974	AC009974 Homo sapi
C 276	17	29.8	81638	14	AC155106	Bos tauru	C 349	17	29.8	207664	8	AC157497	AC157497 Pan trogl
C 277	17	29.8	104913	8	HSJ718P11	AL109983 Human DNA	C 350	17	29.8	208483	9	AC107757	AC107757 Mus muscu
C 278	17	29.8	105000	8	BS000599	BS000599 Pan trogl	C 351	17	29.8	208548	14	AC092195	AC092195 Carls fam
C 279	17	29.8	107017	8	AC012510	Homo sapi	C 352	17	29.8	208731	14	AC129037	AC129037 Rattus no
C 280	17	29.8	107868	8	AL445686	Homo sapi	C 353	17	29.8	211375	14	AC141149	AC141149 Rattus no
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C 288	17	29.8	115775	14	AP007841	Lotus cor	C 361	17	29.8	226051	14	AC098525	AC098525 Rattus no
C 289	17	29.8	116067	8	CNS05TF0	AL359662 Human chr	C 362	17	29.8	226251	14	AC111550	AC111550 Rattus no
C 290	17	29.8	118586	8	BX000359	Mouse DNA	C 363	17	29.8	226256	9	AC125082	AC125082 Mus muscu
C 291	17	29.8	12731	14	AC162131	Homo sapi	C 364	17	29.8	226916	8	AC005066	AC005066 Homo sapi
C 292	17	29.8	119387	8	AC108128	Homo sapi	C 365	17	29.8	227705	14	AC152773	AC152773 Bos tauru
C 293	17	29.8	12731	14	AC162131	Loxodontia	C 366	17	29.8	228120	5	CR388002	CR388002 Zebrafish
C 294	17	29.8	139828	8	HS97D16	AL009179 Human DNA	C 367	17	29.8	228870	9	AL808119	AL808119 Mouse DNA
C 295	17	29.8	153645	8	AL929259	Mus muscu	C 368	17	29.8	230829	14	AC105514	AC105514 Rattus no
C 296	17	29.8	153645	8	AL929259	Human DNA	C 369	17	29.8	237532	14	AC162841	AC162841 Bos tauru
C 297	17	29.8	154692	9	AC140327	Mus muscu	C 370	17	29.8	240501	14	AC0998207	AC0998207 Rattus no
C 298	17	29.8	155640	14	AC069263	Homo sapi	C 371	17	29.8	241051	14	AC095846	AC095846 Rattus no
C 299	17	29.8	156933	15	AC125411	Genomic s	C 372	17	29.8	241755	14	AC103414	AC103414 Rattus no
C 300	17	29.8	159709	8	AC008705	Homo sapi	C 373	17	29.8	242705	14	AC027766	AC027766 Mus muscu
C 301	17	29.8	160602	8	AC018972	Homo sapi	C 374	17	29.8	243450	14	AC156705	AC156705 Bos tauru
C 302	17	29.8	161401	14	AC092087	Carls fam	C 375	17	29.8	243687	14	AC096327	AC096327 Rattus no
C 303	17	29.8	161835	9	AC154327	Mus muscu	C 376	17	29.8	248293	14	AC094985	AC094985 Rattus no
C 304	17	29.8	162241	15	AR465811	Oryza sat	C 377	17	29.8	253504	9	AC102602	AC102602 Mus muscu
C 305	17	29.8	162435	8	AL158151	Human DNA	C 378	17	29.8	253617	14	AC123084	AC123084 Rattus no
C 306	17	29.8	163230	14	AC026140	Homo sapi	C 379	17	29.8	254410	14	AC122594	AC122594 Rattus no
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C 308	17	29.8	166370	14	AC076973	Homo sapi	C 381	17	29.8	257094	14	AC113772	AC113772 Rattus no
C 309	17	29.8	166518	8	HS120G22	Human DNA	C 382	17	29.8	258061	14	AC128474	AC128474 Rattus no
C 310	17	29.8	167942	8	AC021654	Homo sapi	C 383	17	29.8	263056	14	AC149733	AC149733 Bos tauru



384	17	29.8	264289	14	AC110353	AC110353 Rattus no	C 457	16	28.1	23885	5	BX537300	BX537300 Zebrafish
C 385	17	29.8	267429	14	AC135654	AC135654 Rattus no	C 458	16	28.1	27615	9	AC0877101	AC0877101 Rattus no
387	17	29.8	307380	1	AE016939	AE016939 Bacteroid	C 459	16	28.1	32661	1	LPN7711	LPN7711 Legionell
388	16	28.1	54	6	AR081884	AR081884 Sequence	C 460	16	28.1	36171	8	HSL1219B	HSL1219B
389	16	28.1	54	6	AR159918	AR159918 Sequence	C 461	16	28.1	38797	8	BS000565	BS000565 Pan trogl
C 390	16	28.1	54	6	AR227727	AR227727 Sequence	C 462	16	28.1	39756	8	HSL113B	HSL113B
C 391	16	28.1	74	6	AR102087	AR102087 Sequence	C 463	16	28.1	40502	8	BX072565	BX072565 Human DNA
C 392	16	28.1	74	6	AR103133	AR103133 Sequence	C 464	16	28.1	40701	2	CBRG42F09	CBRG42F09
C 393	16	28.1	201	10	AR103133	AR103133 Sequence	C 465	16	28.1	43094	2	CBRG44B02	CBRG44B02
C 394	16	28.1	201	10	AR103133	AR103133 Sequence	C 466	16	28.1	44448	9	AC005789	AC005789 Homo sapi
C 395	16	28.1	436	3	AF265261	AF265261 unculture	C 467	16	28.1	48877	9	BX649304	BX649304 Mouse DNA
C 396	16	28.1	531	10	CO678677	CO678677 Sequence	C 468	16	28.1	59999	14	AC131054	AC131054 Homo sapi
C 397	16	28.1	531	10	CO678677	CO678677 Sequence	C 469	16	28.1	59411	8	AC004040	AC004040 Homo sapi
C 398	16	28.1	579	10	CO678677	CO678677 Sequence	C 470	16	28.1	60323	14	AC087334	AC087334 Homo sapi
C 399	16	28.1	582	6	CO769344	CO769344 Sequence	C 471	16	28.1	61425	9	AC120800	AC120800 Rattus no
C 400	16	28.1	595	10	CO769344	CO769344 Sequence	C 472	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 401	16	28.1	600	10	CO769344	CO769344 Sequence	C 473	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 402	16	28.1	615	10	CO769344	CO769344 Sequence	C 474	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 403	16	28.1	622	10	CO769344	CO769344 Sequence	C 475	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 404	16	28.1	624	10	CO769344	CO769344 Sequence	C 476	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 405	16	28.1	650	10	CO769344	CO769344 Sequence	C 477	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 406	16	28.1	651	9	CO769344	CO769344 Sequence	C 478	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 407	16	28.1	659	9	CO769344	CO769344 Sequence	C 479	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 408	16	28.1	685	10	CO769344	CO769344 Sequence	C 480	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 409	16	28.1	744	10	CO769344	CO769344 Sequence	C 481	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 410	16	28.1	787	10	CO769344	CO769344 Sequence	C 482	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 411	16	28.1	790	10	CO769344	CO769344 Sequence	C 483	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 412	16	28.1	820	10	CO769344	CO769344 Sequence	C 484	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 413	16	28.1	830	5	CO769344	CO769344 Sequence	C 485	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 414	16	28.1	900	10	CO769344	CO769344 Sequence	C 486	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 415	16	28.1	918	10	CO769344	CO769344 Sequence	C 487	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 416	16	28.1	949	6	CO769344	CO769344 Sequence	C 488	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 417	16	28.1	1100	6	CO769344	CO769344 Sequence	C 489	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 418	16	28.1	1230	15	CO769344	CO769344 Sequence	C 490	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 419	16	28.1	1301	6	CO769344	CO769344 Sequence	C 491	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 420	16	28.1	1544	6	CO769344	CO769344 Sequence	C 492	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 421	16	28.1	1723	6	CO769344	CO769344 Sequence	C 493	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 422	16	28.1	1733	15	CO769344	CO769344 Sequence	C 494	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 423	16	28.1	1749	15	CO769344	CO769344 Sequence	C 495	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 424	16	28.1	1861	15	CO769344	CO769344 Sequence	C 496	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 425	16	28.1	1883	6	CO769344	CO769344 Sequence	C 497	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 426	16	28.1	2291	6	CO769344	CO769344 Sequence	C 498	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 427	16	28.1	2291	6	CO769344	CO769344 Sequence	C 499	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 428	16	28.1	2456	6	CO769344	CO769344 Sequence	C 500	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 429	16	28.1	2456	6	CO769344	CO769344 Sequence	C 501	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 430	16	28.1	2564	6	CO769344	CO769344 Sequence	C 502	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 431	16	28.1	2589	6	CO769344	CO769344 Sequence	C 503	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 432	16	28.1	2590	6	CO769344	CO769344 Sequence	C 504	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 433	16	28.1	2636	6	CO769344	CO769344 Sequence	C 505	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 434	16	28.1	2636	6	CO769344	CO769344 Sequence	C 506	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 435	16	28.1	2651	8	CO769344	CO769344 Sequence	C 507	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 436	16	28.1	2671	8	CO769344	CO769344 Sequence	C 508	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 437	16	28.1	2736	15	CO769344	CO769344 Sequence	C 509	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 438	16	28.1	2907	6	CO769344	CO769344 Sequence	C 510	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 439	16	28.1	2965	8	CO769344	CO769344 Sequence	C 511	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 440	16	28.1	3345	15	CO769344	CO769344 Sequence	C 512	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 441	16	28.1	3419	2	CO769344	CO769344 Sequence	C 513	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 442	16	28.1	3458	8	CO769344	CO769344 Sequence	C 514	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 443	16	28.1	3458	8	CO769344	CO769344 Sequence	C 515	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 444	16	28.1	3458	8	CO769344	CO769344 Sequence	C 516	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 445	16	28.1	3458	8	CO769344	CO769344 Sequence	C 517	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 446	16	28.1	3458	8	CO769344	CO769344 Sequence	C 518	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 447	16	28.1	3458	8	CO769344	CO769344 Sequence	C 519	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 448	16	28.1	3458	8	CO769344	CO769344 Sequence	C 520	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 449	16	28.1	3458	8	CO769344	CO769344 Sequence	C 521	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 450	16	28.1	3458	8	CO769344	CO769344 Sequence	C 522	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 451	16	28.1	3458	8	CO769344	CO769344 Sequence	C 523	16	28.1	61570	14	AC013506	AC013506 Homo sapi
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C 454	16	28.1	3458	8	CO769344	CO769344 Sequence	C 526	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 455	16	28.1	3458	8	CO769344	CO769344 Sequence	C 527	16	28.1	61570	14	AC013506	AC013506 Homo sapi
C 456	16	28.1	3458	8	CO769344	CO769344 Sequence	C 528	16	28.1	61570	14	AC013506	AC013506 Homo sapi



C 530	16	28.1	122322	15	AT66118	AL022198 Arabidops	603	16	28.1	160738	14	AC161787	AC161787 Cercopit
C 531	16	28.1	123260	9	AC087041	AC087041 Rattus no	C 604	16	28.1	160931	2	AC093498	AC093498 Drosophi1
C 532	16	28.1	125179	15	AC146971	AC146971 Medicago	C 605	16	28.1	161150	9	AC133503	AC133503 Mus muscu
C 533	16	28.1	125750	14	AC092011	AC092011 Felis cat	C 606	16	28.1	161204	8	CNS01R11	AL162811 Human chr
C 534	16	28.1	126736	16	AC044788	AC044788 Homo sapi	607	16	28.1	161241	8	AL390247	AL390247 Human DNA
C 535	16	28.1	129010	8	AL159168	AL159168 Homo sapi	C 608	16	28.1	161266	14	AC148285	AC148285 Rhinoloph
C 536	16	28.1	129517	14	AC016400	AC016400 Homo sapi	C 609	16	28.1	161354	14	AC133374	AC133374 Homo sapi
C 537	16	28.1	129525	14	AC147452	AC147452 Ornithorh	C 610	16	28.1	161872	14	AC015949	AC015949 Homo sapi
C 538	16	28.1	130609	14	AC091798	AC091798 Felis cat	C 611	16	28.1	162289	4	AC097230	AC097230 Sus scrof
C 539	16	28.1	130625	9	AC162615	AC162615 Mus muscu	C 612	16	28.1	162590	14	AC036203	AC036203 Homo sapi
C 540	16	28.1	131042	8	AC073156	AC073156 Homo sapi	C 613	16	28.1	162689	14	AC117145	AC117145 Rattus no
C 541	16	28.1	132301	14	AC129954	AC129954 Bos tauru	C 614	16	28.1	163218	8	AC005837	AC005837 Homo sapi
C 542	16	28.1	133815	14	AC142563	AC142563 Bos tauru	C 615	16	28.1	163805	14	AC114959	AC114959 Homo sapi
C 543	16	28.1	136735	15	AC135604	AC135604 Medicago	C 616	16	28.1	163928	14	AC163266	AC163266 Rhinoloph
C 544	16	28.1	139111	14	AC114281	AC114281 Homo sapi	C 617	16	28.1	164242	9	AC153636	AC153636 Mus muscu
C 545	16	28.1	139627	14	AC146996	AC146996 Arabidac1 p	C 618	16	28.1	164271	14	AC0909571	AC0909571 Homo sapi
C 546	16	28.1	139791	8	AC137673	AC137673 Homo sapi	C 619	16	28.1	164347	14	AC119669	AC119669 Rattus no
C 547	16	28.1	139891	9	AC090647	AC090647 Genomic s	C 620	16	28.1	164423	14	AC026828	AC026828 Homo sapi
C 548	16	28.1	140739	8	AP005432	AP005432 Homo sapi	C 621	16	28.1	164505	14	AL390999	AL390999 Homo sapi
C 549	16	28.1	140984	14	AC023057	AC023057 Homo sapi	C 622	16	28.1	164595	14	AC024501	AC024501 Homo sapi
C 550	16	28.1	142498	14	AC023980	AC023980 Homo sapi	C 623	16	28.1	164652	14	AC021625	AC021625 Homo sapi
C 551	16	28.1	142565	9	AL592545	AL592545 Mouse DNA	C 624	16	28.1	164985	14	AC153585	AC153585 Mus muscu
C 552	16	28.1	143099	14	AC009926	AC009926 Homo sapi	C 625	16	28.1	165069	14	AC149010	AC149010 Papio anu
C 553	16	28.1	143970	8	AC093521	AC093521 Homo sapi	C 626	16	28.1	165098	8	AC145769	AC145769 Pan trogl
C 554	16	28.1	144430	8	AC091155	AC091155 Homo sapi	C 627	16	28.1	166076	8	AC020755	AC020755 Homo sapi
C 555	16	28.1	145250	8	CNS01P78	AL132666 Human chr	C 628	16	28.1	166341	14	AL513486	AL513486 Homo sapi
C 556	16	28.1	145787	8	AC099499	AC099499 Homo sapi	C 629	16	28.1	166692	14	AC023475	AC023475 Homo sapi
C 557	16	28.1	146274	15	AC149542	AC149542 Populus t	C 630	16	28.1	166928	14	AC110905	AC110905 Homo sapi
C 558	16	28.1	147327	8	AC097455	AC097455 Homo sapi	C 631	16	28.1	166966	8	AC016970	AC016970 Homo sapi
C 559	16	28.1	147651	8	AC104716	AC104716 Homo sapi	C 632	16	28.1	166971	8	AL157812	AL157812 Homo sapi
C 560	16	28.1	147798	8	AL390058	AL390058 Human DNA	C 633	16	28.1	167065	14	AC019266	AC019266 Homo sapi
C 561	16	28.1	148204	14	AC069400	AC069400 Homo sapi	C 634	16	28.1	167618	4	AC150577	AC150577 Bos tauru
C 562	16	28.1	148295	8	AC090510	AC090510 Homo sapi	C 635	16	28.1	167735	9	AC122818	AC122818 Mus muscu
C 563	16	28.1	149100	8	AP001881	AP001881 Homo sapi	C 636	16	28.1	167785	14	AC115898	AC115898 Homo sapi
C 564	16	28.1	149289	14	AC137908	AC137908 Carls fam	C 637	16	28.1	167905	8	AC116606	AC116606 Mus muscu
C 565	16	28.1	149572	8	AC004695	AC004695 Homo sapi	C 638	16	28.1	168085	14	AC096867	AC096867 Rattus no
C 566	16	28.1	149854	9	AC117225	AC117225 Mus muscu	C 639	16	28.1	168509	8	AC009837	AC009837 Homo sapi
C 567	16	28.1	150261	9	AC125136	AC125136 Mus muscu	C 640	16	28.1	168997	14	AC021927	AC021927 Homo sapi
C 568	16	28.1	150399	14	AC009369	AC009369 Drosophi1	C 641	16	28.1	169018	14	AC105737	AC105737 Sus scrof
C 569	16	28.1	150598	14	AC158281	AC158281 Loxodonta	C 642	16	28.1	169048	8	AL357935	AL357935 Human DNA
C 570	16	28.1	151044	5	CR788247	CR788247 Zebralfish	C 643	16	28.1	169230	14	AC102275	AC102275 Mus muscu
C 571	16	28.1	151898	14	AC153109	AC153109 Loxodonta	C 644	16	28.1	169261	14	AC154707	AC154707 Mus muscu
C 572	16	28.1	152183	9	AC132899	AC132899 Mus muscu	C 645	16	28.1	169904	8	AC007275	AC007275 Homo sapi
C 573	16	28.1	152414	9	AC129553	AC129553 Mus muscu	C 646	16	28.1	170033	8	AC007679	AC007679 Homo sapi
C 574	16	28.1	152423	14	AC119192	AC119192 Homo sapi	C 647	16	28.1	170400	14	AC048331	AC048331 Homo sapi
C 575	16	28.1	152623	14	AC024530	AC024530 Homo sapi	C 648	16	28.1	170452	8	AP152364	AP152364 Homo sapi
C 576	16	28.1	152723	14	AC140089	AC140089 Ornithorh	C 649	16	28.1	170776	14	AC159961	AC159961 Rhinoloph
C 577	16	28.1	153402	8	HS247E2	AL773569 Homo sapi	C 650	16	28.1	170951	9	AC123552	AC123552 Mus muscu
C 578	16	28.1	153460	14	AC151443	AC151443 Atelerix	C 651	16	28.1	171416	14	AC165340	AC165340 Mus muscu
C 579	16	28.1	153578	8	AC004074	AC004074 Homo Sapi	C 652	16	28.1	171852	8	AL137069	AL137069 Human DNA
C 580	16	28.1	153731	9	AC131995	AC131995 Mus muscu	C 653	16	28.1	172560	14	AC091794	AC091794 Felis cat
C 581	16	28.1	155861	9	AC112272	AC112272 Mus muscu	C 654	16	28.1	172626	8	AC105101	AC105101 Homo sapi
C 582	16	28.1	156165	9	AC158124	AC158124 Mus muscu	C 655	16	28.1	172875	8	AC084301	AC084301 Homo sapi
C 583	16	28.1	156402	8	BS000558	BS000558 Pan trogl	C 656	16	28.1	173370	8	AC024162	AC024162 Homo sapi
C 584	16	28.1	156842	14	BX119928	BX119928 Homo sapi	C 657	16	28.1	173497	14	AC111329	AC111329 Rattus no
C 585	16	28.1	156855	8	AC104000	AC104000 Homo sapi	C 658	16	28.1	173527	9	AC140193	AC140193 Mus muscu
C 586	16	28.1	157079	8	AC010370	AC010370 Homo sapi	C 659	16	28.1	173796	14	AC084788	AC084788 Homo sapi
C 587	16	28.1	157105	9	AC160246	AC160246 Mus muscu	C 660	16	28.1	174147	14	AC148048	AC148048 Otlemur
C 588	16	28.1	157117	9	AC101941	AC101941 Mus muscu	C 661	16	28.1	174521	8	AC131235	AC131235 Homo sapi
C 589	16	28.1	157152	8	AC073427	AC073427 Homo sapi	C 662	16	28.1	174972	8	AC133331	AC133331 Homo sapi
C 590	16	28.1	157384	14	AC162126	AC162126 Atelerix	C 663	16	28.1	174981	8	AC009908	AC009908 Homo sapi
C 591	16	28.1	157510	8	AC087235	AC087235 Homo sapi	C 664	16	28.1	174997	14	AC148207	AC148207 Callicebu
C 592	16	28.1	157624	14	AC087666	AC087666 Homo sapi	C 665	16	28.1	175151	8	AL160152	AL160152 Human DNA
C 593	16	28.1	157740	14	AC166967	AC166967 Mus muscu	C 666	16	28.1	175430	14	AC082646	AC082646 Homo sapi
C 594	16	28.1	157904	8	AC108486	AC108486 Homo sapi	C 667	16	28.1	175463	8	AL591686	AL591686 Human DNA
C 595	16	28.1	158144	14	AC016455	AC016455 Homo sapi	C 668	16	28.1	175517	8	AL162385	AL162385 Human DNA
C 596	16	28.1	158591	9	AC093022	AC093022 Mus Muscu	C 669	16	28.1	175570	8	AL844893	AL844893 Mouse DNA
C 597	16	28.1	158685	14	AC107319	AC107319 Sus scrof	C 670	16	28.1	175968	8	AC018684	AC018684 Homo sapi
C 598	16	28.1	158906	14	AC097003	AC097003 Rattus no	C 671	16	28.1	176107	14	AP002393	AP002393 Homo sapi
C 599	16	28.1	159668	14	AC146288	AC146288 Dantio rex	C 672	16	28.1	176108	8	AC026118	AC026118 Homo sapi
C 600	16	28.1	160310	8	AC010157	AC010157 Homo sapi	C 673	16	28.1	176222	14	AC117138	AC117138 Rattus no
C 601	16	28.1	160396	8	AL592063	AL592063 Human DNA	C 674	16	28.1	176291	8	AC024610	AC024610 Homo sapi
C 602	16	28.1	160452	8	AC110607	AC110607 Homo sapi	C 675	16	28.1	176433	8	AC090246	AC090246 Homo sapi



c 676	16	28.1	176485	8	AC105908	Homo sapi	749	16	28.1	194920	15	ATCRR174	AL161578 Arabidops
c 677	16	28.1	176541	8	AL929325	Homo sapi	c 750	16	28.1	195205	14	AC131416	AC131416 Rattus no
c 678	16	28.1	176609	14	AC160723	Mus muscu	c 751	16	28.1	195544	8	AC024159	AC024159 Homo sapi
c 679	16	28.1	176643	14	AC092407	Papio annu	c 752	16	28.1	195604	14	AC161409	AC161409 Mus muscu
c 680	16	28.1	176669	8	AC026205	Homo sapi	c 753	16	28.1	195913	8	AL954236	AL954236 Pan trogl
c 681	16	28.1	176711	9	AC137969	Mus muscu	c 754	16	28.1	195965	9	AC101727	AC101727 Mus muscu
c 682	16	28.1	176724	14	AL359772	Homo sapi	c 755	16	28.1	197132	14	AL732507	AL732507 Mouse DNA
c 683	16	28.1	176754	14	AP000918	Homo sapi	c 756	16	28.1	197194	9	AL954690	AL954690 Mus muscu
c 684	16	28.1	177726	8	AC145770	Pan trogl	c 757	16	28.1	197200	14	AC009966	AC009966 Homo sapi
c 685	16	28.1	177839	8	AC013603	Homo sapi	c 758	16	28.1	197298	8	PT147K15	PT147K15 Pan trogl
c 686	16	28.1	178229	14	AC010611	Homo sapi	c 759	16	28.1	197346	9	AL731801	AL731801 Mouse DNA
c 687	16	28.1	178234	14	AC149171	Papio annu	c 760	16	28.1	197530	14	AC0099174	AC0099174 Rattus no
c 688	16	28.1	178248	9	AC154233	Mus muscu	c 761	16	28.1	197830	14	CT009696	CT009696 Mus muscu
c 689	16	28.1	178448	14	AC126922	Pan trogl	c 762	16	28.1	197841	14	AC138444	AC138444 Canis fam
c 690	16	28.1	178517	9	AC121905	Mus muscu	c 763	16	28.1	197920	14	AC113281	AC113281 Mus muscu
c 691	16	28.1	178800	14	AC149166	Otolemur	c 764	16	28.1	198134	14	AC024117	AC024117 Homo sapi
c 692	16	28.1	179216	9	AC104832	Mus muscu	c 765	16	28.1	198368	9	AC134303	AC134303 Mus muscu
c 693	16	28.1	180570	14	AC068753	Homo sapi	c 766	16	28.1	198378	14	AC152087	AC152087 Bos tauru
c 694	16	28.1	181283	8	AC131565	Homo sapi	c 767	16	28.1	199251	14	AC105224	AC105224 Homo sapi
c 695	16	28.1	181343	9	AL671882	Mouse DNA	c 768	16	28.1	199284	14	AC107388	AC107388 Homo sapi
c 696	16	28.1	181393	14	AC090811	Homo sapi	c 769	16	28.1	199542	14	AC148120	AC148120 Salimiri b
c 697	16	28.1	181592	14	AC015956	Homo sapi	c 770	16	28.1	199639	14	AC148706	AC148706 Bos tauru
c 698	16	28.1	181922	8	AC098822	Homo sapi	c 771	16	28.1	199785	8	AL355512	AL355512 Homo sapi
c 699	16	28.1	181859	14	AC150406	Branchios	c 772	16	28.1	200214	8	AC103412	AC103412 Homo sapi
c 700	16	28.1	182025	8	AL138900	Homo sapi	c 773	16	28.1	200348	8	AC005516	AC005516 Homo sapi
c 701	16	28.1	182312	14	AP001655	Homo sapi	c 774	16	28.1	200379	8	AL390059	AL390059 Homo sapi
c 702	16	28.1	182538	14	AC019335	Homo sapi	c 775	16	28.1	200393	14	AC151736	AC151736 Mus muscu
c 703	16	28.1	182638	14	AC019335	Homo sapi	c 776	16	28.1	200918	8	AC012360	AC012360 Homo sapi
c 704	16	28.1	182741	14	AC018910	Homo sapi	c 777	16	28.1	201081	14	AC148195	AC148195 Callichr
c 705	16	28.1	183027	8	AF216671	Homo sapi	c 778	16	28.1	201897	9	AC158296	AC158296 Mus muscu
c 706	16	28.1	183176	8	AC106894	Homo sapi	c 779	16	28.1	201897	8	AC026197	AC026197 Homo sapi
c 707	16	28.1	183218	9	AC132440	Mus muscu	c 780	16	28.1	202083	8	AC102860	AC102860 Mus muscu
c 708	16	28.1	183244	14	AC0227188	Homo sapi	c 781	16	28.1	202315	9	AC158360	AC158360 Mus muscu
c 709	16	28.1	183291	2	AC010003	Drosophila	c 782	16	28.1	203187	9	AC124168	AC124168 Mus muscu
c 710	16	28.1	183485	9	AC153560	Mus muscu	c 783	16	28.1	203330	9	AL589670	AL589670 Mouse DNA
c 711	16	28.1	184037	8	AC047369	Mus muscu	c 784	16	28.1	203336	9	AL591433	AL591433 Mouse DNA
c 712	16	28.1	184113	9	AC024270	Homo sapi	c 785	16	28.1	203937	14	AL831776	AL831776 Bos tauru
c 713	16	28.1	184362	8	AC079305	Homo sapi	c 786	16	28.1	204136	14	AL831776	AL831776 Bos tauru
c 714	16	28.1	184503	8	AL356476	Human DNA	c 787	16	28.1	204608	14	AC148790	AC148790 Otolemur
c 715	16	28.1	184510	8	AL356476	Human DNA	c 788	16	28.1	204658	14	AC148790	AC148790 Otolemur
c 716	16	28.1	184548	14	AC023551	Homo sapi	c 789	16	28.1	204696	14	AP001654	AP001654 Homo sapi
c 717	16	28.1	184589	8	AC008716	Homo sapi	c 790	16	28.1	204727	9	AC147020	AC147020 Mus muscu
c 718	16	28.1	185564	14	AC152014	Otolemur	c 791	16	28.1	205648	14	AC122026	AC122026 Bos tauru
c 719	16	28.1	185741	8	AC006203	Homo sapi	c 792	16	28.1	205648	14	AC163366	AC163366 Bos tauru
c 720	16	28.1	185798	14	AC148265	Callichr	c 793	16	28.1	205809	14	AC161359	AC161359 Mus muscu
c 721	16	28.1	186256	14	AC012079	Homo sapi	c 794	16	28.1	206016	14	AC138263	AC138263 Mus muscu
c 722	16	28.1	186548	8	CNS0182	Human chr	c 795	16	28.1	206472	14	AC131874	AC131874 Rattus no
c 723	16	28.1	186739	8	AC072028	Homo sapi	c 796	16	28.1	206643	9	AC125162	AC125162 Mus muscu
c 724	16	28.1	186994	14	AC143399	Macaca mu	c 797	16	28.1	206784	8	HS9317	HS9317 Human DNA
c 725	16	28.1	187248	14	AC121471	Rattus no	c 798	16	28.1	206940	9	AC113001	AC113001 Mus muscu
c 726	16	28.1	187394	14	AC104573	Homo sapi	c 799	16	28.1	207295	8	AL353572	AL353572 Human DNA
c 727	16	28.1	187523	14	AC151181	Bos tauru	c 800	16	28.1	207845	14	AC108507	AC108507 Mus muscu
c 728	16	28.1	187816	9	AL606919	Mouse DNA	c 801	16	28.1	209258	14	AC151027	AC151027 Mus muscu
c 729	16	28.1	188137	14	AC148796	Otolemur	c 802	16	28.1	209434	8	AC026227	AC026227 Homo sapi
c 730	16	28.1	188247	9	HS570H19	Human sapi	c 803	16	28.1	209789	14	AC158220	AC158220 Mus muscu
c 731	16	28.1	188853	9	AC102105	Mus muscu	c 804	16	28.1	210193	9	AC125210	AC125210 Mus muscu
c 732	16	28.1	188980	14	AC090087	Homo sapi	c 805	16	28.1	210952	14	AC128082	AC128082 Rattus no
c 733	16	28.1	189016	8	AC008422	Homo sapi	c 806	16	28.1	211423	14	AC163690	AC163690 Mus muscu
c 734	16	28.1	189031	8	AC096733	Homo sapi	c 807	16	28.1	211533	8	AC098482	AC098482 Homo sapi
c 735	16	28.1	189041	14	AC152312	Bos tauru	c 808	16	28.1	211600	14	AC013266	AC013266 Homo sapi
c 736	16	28.1	189287	14	AC068362	Homo sapi	c 809	16	28.1	213077	8	AC109585	AC109585 Homo sapi
c 737	16	28.1	189608	8	AL359253	Human sapi	c 810	16	28.1	213591	14	AC141759	AC141759 Aps me11
c 738	16	28.1	189893	14	AC013254	Drosophila	c 811	16	28.1	214128	14	AC160307	AC160307 Bos tauru
c 739	16	28.1	189991	9	AL831750	Mouse DNA	c 812	16	28.1	214425	14	AC099091	AC099091 Canis fam
c 740	16	28.1	190089	8	BS000576	Pan trogl	c 813	16	28.1	214835	14	AC161363	AC161363 Bos tauru
c 741	16	28.1	190156	9	AC147612	Mus muscu	c 814	16	28.1	215042	14	AC162395	AC162395 Bos tauru
c 742	16	28.1	192683	14	AC020741	Homo sapi	c 815	16	28.1	216363	14	AC156867	AC156867 Bos tauru
c 743	16	28.1	192683	14	AC138805	Homo sapi	c 816	16	28.1	216400	14	AC125934	AC125934 Rattus no
c 744	16	28.1	192712	14	AL592442	Homo sapi	c 817	16	28.1	217124	9	AC151228	AC151228 Bos tauru
c 745	16	28.1	193424	8	AC005690	Homo sapi	c 818	16	28.1	218747	9	AC093339	AC093339 Mus muscu
c 746	16	28.1	193793	8	AC099780	Homo sapi	c 819	16	28.1	219047	14	AC136822	AC136822 Rattus no
c 747	16	28.1	193973	14	AC16747	Mus muscu	c 820	16	28.1	221455	9	AL606831	AL606831 Mouse DNA
c 748	16	28.1	194405	14	AC021122	Homo sapi	c 821	16	28.1	222051	14	AC132783	AC132783 Rattus no



822	16	28.1	222138	14	AC093961	AC093961 Rattus no	C 895	16	28.1	281085	14	AC166979	AC166979 Mus muscu
C 823	16	28.1	222679	14	AC124844	AC124844 Rattus no	886	16	28.1	283388	14	AC012285	AC012285 Homo sapi
C 824	16	28.1	222860	6	AX474783	Sequence	897	16	28.1	288889	14	AC162601	AC162601 Bos tauru
C 825	16	28.1	223387	14	AC147800	Mus muscu	898	16	28.1	295400	14	AC103344	AC103344 Rattus no
C 826	16	28.1	224603	9	AL672240	Mouse DNA	C 899	16	28.1	299974	14	AC079512	AC079512 Mus muscu
C 827	16	28.1	224638	9	AC133099	Mus muscu	900	16	28.1	300140	14	AC129109	AC129109 Homo sapi
C 828	16	28.1	225677	14	AC098032	Rattus no	901	16	28.1	303314	2	AE003538	AE003538 Drosophila
C 829	16	28.1	225684	14	AC156203	Bos tauru	C 902	16	28.1	304250	1	BX294152	BX294152 Pirellula
830	16	28.1	227857	9	AC094975	Rattus no	903	16	28.1	305735	14	AC14916	AC14916 Mus muscu
C 831	16	28.1	228147	9	AC090652	Mus muscu	C 904	16	28.1	306309	14	AC105494	AC105494 Rattus no
832	16	28.1	228185	8	AC146175	Pan trogl	905	16	28.1	315654	14	AC108159	AC108159 Rattus no
833	16	28.1	228931	14	AC073355	AC073355 Rattus no	C 906	16	28.1	321708	14	AC087142	AC087142 Mus muscu
834	16	28.1	229010	14	AC073686	Mus muscu	C 907	16	28.1	328822	14	AC125301	AC125301 Rattus no
835	16	28.1	230020	14	AC106534	Rattus no	908	16	28.1	337203	2	CR382401	CR382401 Plasmid
836	16	28.1	230930	14	AC130854	Rattus no	C 909	16	28.1	338116	14	AC087159	AC087159 Mus muscu
837	16	28.1	231332	9	AC096070	Rattus no	C 910	16	28.1	340000	6	AX282122	AX282122 Sequence
C 838	16	28.1	231763	14	AC101847	AC101847 Rattus no	C 911	16	28.1	349980	6	AX282714	AX282714 Sequence
C 839	16	28.1	232491	9	AC093043	Mus Muscu	C 912	16	28.1	349980	8	AY517111	AY517111 Homo sapi
C 840	16	28.1	232984	14	AC115597	Rattus no	913	16	26.3	183	10	BV199652	BV199652 sqm20196
841	16	28.1	233392	14	AC150504	Bos tauru	C 914	16	26.3	201	10	BV202657	BV202657 sqm20965
842	16	28.1	234065	14	AC140765	Rattus no	C 915	16	26.3	201	10	BV202658	BV202658 sqm20965
C 843	16	28.1	234489	5	BX004983	Zebrafish	C 916	16	26.3	201	10	BV202659	BV202659 sqm20965
C 844	16	28.1	237720	14	AC094774	Rattus no	C 917	16	26.3	201	10	BV202660	BV202660 sqm20965
845	16	28.1	239106	14	AC135373	AC135373 Rattus no	C 918	16	26.3	256	6	BD032515	BD032515 Sequence
C 846	16	28.1	239353	14	AC128996	Rattus no	919	16	26.3	256	6	AX896982	AX896982 Sequence
C 847	16	28.1	240039	14	AC111926	Rattus no	920	16	26.3	256	6	G65920	G65920 6Y972 M1sce
C 848	16	28.1	240216	14	AC117121	Rattus no	921	16	26.3	300	10	BD071453	BD071453 Sequence
C 849	16	28.1	241023	14	AC110433	Rattus no	C 922	16	26.3	308	6	BD071453	BD071453 Sequence
C 850	16	28.1	242729	14	AC125861	Rattus no	C 923	16	26.3	310	6	BD071453	BD071453 Sequence
851	16	28.1	242745	14	AC109521	Rattus no	924	16	26.3	337	6	BD071453	BD071453 Sequence
C 852	16	28.1	244047	14	AC152583	Bos tauru	925	16	26.3	338	6	BD071453	BD071453 Sequence
C 853	16	28.1	244441	14	AC098180	Rattus no	C 926	16	26.3	338	6	BD071453	BD071453 Sequence
854	16	28.1	244749	14	AC098444	Rattus no	C 927	16	26.3	339	6	BD071453	BD071453 Sequence
855	16	28.1	244859	14	CR974428	Mus muscu	C 928	16	26.3	339	6	BD071453	BD071453 Sequence
856	16	28.1	245021	14	AC140769	Rattus no	929	16	26.3	339	6	BD071453	BD071453 Sequence
857	16	28.1	246615	14	AC094056	Bos tauru	C 930	16	26.3	339	6	BD071453	BD071453 Sequence
858	16	28.1	246832	14	AC094056	Rattus no	931	16	26.3	339	6	BD071453	BD071453 Sequence
859	16	28.1	248489	14	AC160570	Pan trogl	932	16	26.3	340	6	BD071453	BD071453 Sequence
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C 862	16	28.1	251176	14	AC131434	Rattus no	935	16	26.3	341	6	BD071453	BD071453 Sequence
863	16	28.1	252985	14	AC130744	Rattus no	936	16	26.3	341	6	BD071453	BD071453 Sequence
C 864	16	28.1	254116	14	AC118902	Rattus no	C 937	16	26.3	348	10	AL954807	AL954807 Arbidops
865	16	28.1	254701	14	AC131019	Rattus no	938	16	26.3	357	6	BD071453	BD071453 Sequence
866	16	28.1	254762	14	AC154483	Mus muscu	C 939	16	26.3	374	10	G62162	G62162 Bst972 Foet
C 867	16	28.1	254762	14	AC154483	Mus muscu	940	16	26.3	395	6	BD071453	BD071453 Sequence
C 868	16	28.1	255158	14	AC156836	Mus muscu	941	16	26.3	406	6	BD071453	BD071453 Sequence
869	16	28.1	256608	14	AC021040	Homo sapi	942	16	26.3	411	9	MUSIGHLINE	M27020 Mus muscu
870	16	28.1	257036	9	AC115910	Mus muscu	943	16	26.3	419	6	BD071453	BD071453 Sequence
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C 872	16	28.1	258594	14	AC115393	Rattus no	945	16	26.3	438	6	BD071453	BD071453 Sequence
873	16	28.1	259403	14	AC118091	Rattus no	C 946	16	26.3	443	6	BD071453	BD071453 Sequence
C 874	16	28.1	260290	14	AC094332	Rattus no	C 947	16	26.3	443	6	BD071453	BD071453 Sequence
C 875	16	28.1	261088	14	AC131166	Rattus no	C 948	16	26.3	443	6	BD071453	BD071453 Sequence
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C 877	16	28.1	261659	14	AC109683	Rattus no	C 950	16	26.3	450	6	BD071453	BD071453 Sequence
878	16	28.1	261709	14	AC154385	Mus muscu	C 951	16	26.3	450	6	BD071453	BD071453 Sequence
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884	16	28.1	268313	14	AC094642	Rattus no	C 957	16	26.3	450	6	BD071453	BD071453 Sequence
C 885	16	28.1	270023	14	AC094829	Rattus no	958	16	26.3	453	10	BV144965	BV144965 Arbidops
886	16	28.1	271237	2	AE003521	Drosophila	959	16	26.3	459	2	AY961568	AY961568 Lysiphle
C 887	16	28.1	272669	14	AC135936	Rattus no	960	16	26.3	460	10	BV144963	BV144963 P2A02478-
C 888	16	28.1	273812	14	AC095725	Rattus no	C 961	16	26.3	469	15	AP429278	AP429278 Pscopann
889	16	28.1	275501	14	AC152190	Bos tauru	962	16	26.3	472	10	BV144955	BV144955 P2A02478-
C 890	16	28.1	276568	14	AC079423	Mus muscu	963	16	26.3	475	10	BV144956	BV144956 P2A02478-
891	16	28.1	277408	14	AC160210	Bos tauru	964	16	26.3	479	10	BV144960	BV144960 P2A02478-
C 892	16	28.1	275878	14	AC107519	Rattus no	965	16	26.3	479	10	BV144966	BV144966 P2A02478-
C 893	16	28.1	276492	14	AC111574	Rattus no	966	16	26.3	480	10	BV144964	BV144964 P2A02478-
894	16	28.1	280473	14	AC068823	Homo sapi	967	16	26.3	484	10	BV144957	BV144957 P2A02478-



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978 15 26.3 531 2 ASSSUMU X9813 Ammonia BP.  
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C 991 15 26.3 565 6 CQ509375 Sequence CQ509375 Sequence  
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C 997 15 26.3 584 15 ATH526786 ATH526786 Arabidops  
C 998 15 26.3 584 15 ATH526814 ATH526814 Arabidops  
C 999 15 26.3 586 10 BV237088 BV237088 S23P6475  
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## ALIGNMENTS

RESULT 1  
AB125961/c 721 bp DNA linear BCT 02-APR-2004  
LOCUS AB125961  
DEFINITION Bacillus anthracis plasmid pXOI pagA gene, partial cds.  
ACCESSION AB125961  
VERSION AB125961.1 GI:46093482  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 Inoue, S., Noguchi, A., Tanabayashi, K. and Yamada, A.  
AUTHORS Preparation of a positive control DNA for molecular diagnosis of  
TITLE Bacillus anthracis  
JOURNAL Unpublished  
REFERENCES 2 (bases 1 to 721)  
AUTHORS Inoue, S. and Noguchi, A.  
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Zoonosis, Department of Veterinary Science, 1-23-1 Toyama,  
Shinjuku-ku, Tokyo 162-8640, Japan (E-mail: sinoue@nih.go.jp,  
Tel:81-3-5285-1111 (ex.2620), Fax:81-3-5285-1179)  
FEATURES  
source 1..721  
/organism="Bacillus anthracis"  
/mol\_type="Genomic DNA"  
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/db\_xref="taxon:1392"  
/plasmid="pXOI"  
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extension PCR"  
complement(1..721)

gene

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NIIISKNDOSTQNTDQTRISKRTSRRHTSEVGNARVHASFPIGGVAGFS  
NSNSTVAIDHSLSLAGERTVAETMGTLNADTARLNADIRVYNTGTAPIVAVLPPTSL  
VLGNQTLATIKAKENQLSQTL"

## ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 721;  
Best Local Similarity 100.0%; Pred. No. 3.6e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGAGAAAGAACTTGGCTGAACAATGGG 57  
Db 221 CGCAATTGATCATTCATCTCTAGCAGGGAGAAAGAACTTGGCTGAACAATGGG 165

## RESULT 2

AX353777 954 bp DNA linear PAT 06-FEB-2002  
LOCUS AX353777  
DEFINITION Sequence 8 from Patent WO0204646.  
ACCESSION AX353777  
VERSION AX353777.1 GI:18618828

KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.

REFERENCE 1 Williamson, E.D., Miller, J., Walker, N.J., Ballile, L.W., Holden, P.T.,  
AUTHORS Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 8 17-JAN-2002;  
The Secretary of State for Defense (GB)

## FEATURES

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/organism="synthetic construct"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:32630"  
/note="DNA sequence used to encode SEQ ID NO: 7"

## ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 954;  
Best Local Similarity 100.0%; Pred. No. 3.5e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGAGAAAGAACTTGGCTGAACAATGGG 57  
Db 489 CGCAATTGATCATTCATCTCTAGCAGGGAGAAAGAACTTGGCTGAACAATGGG 545

RESULT 3  
AX353779 1278 bp DNA linear PAT 06-FEB-2002  
LOCUS AX353779  
DEFINITION Sequence 10 from Patent WO0204646.  
ACCESSION AX353779  
VERSION AX353779.1 GI:18618829  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
OTHER other sequences; artificial sequences.

REFERENCE 1 Williamson, E.D., Miller, J., Walker, N.J., Ballile, L.W., Holden, P.T.,  
AUTHORS Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 10 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES Location/Qualifiers



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/note="DNA sequence used to encode SEQ ID NO: 9"

ORIGIN

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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
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489 CGCAATTGATCATTCATCTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 545

RESULT 4
CS135645 1281 bp DNA linear PAT 09-AUG-2005
LOCUS
DEFINITION Sequence 10 from Patent WO2005068493.
ACCESSION CS135645
VERSION CS135645.1 GI:72056311
KEYWORDS
SOURCE Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 Cutting,S.M.
AUTHORS Anthrax vaccine in the form of a spore
TITLE Patent: WO 2005068493-A 10 28-JUL-2005;
JOURNAL Royal Holloway and Bedford New College (GB)
FEATURES
source
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/organism="Bacillus anthracis"
/mol_type="unassigned DNA"
/db_xref="taxon:1392"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 57; DB 6; Length 1281;
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Qy
1 CGCAATTGATCATTCATCTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 57
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495 CGCAATTGATCATTCATCTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 551

RESULT 5
AX353775 1461 bp DNA linear PAT 06-FEB-2002
LOCUS
DEFINITION Sequence 6 from Patent WO204646.
ACCESSION AX353775
VERSION AX353775.1 GI:18618827
KEYWORDS
SOURCE synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,
AUTHORS Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.
TITLE Expression system
JOURNAL Patent: WO 0204646-A 6 17-JAN-2002;
The Secretary of State for Defense (GB)
FEATURES
source
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/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="DNA sequence used to encode SEQ ID NO: 5"

ORIGIN

Query Match
Best Local Similarity 100.0%; Score 57; DB 6; Length 1461;
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Best Local Similarity 100.0%; Pred. No. 3.2e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy
1 CGCAATTGATCATTCATCTATCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 57
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996 CGCAATTGATCATTCATCTATCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 1052

RESULT 6
AY921578 1694 bp DNA linear BCT 16-APR-2005
LOCUS
DEFINITION Bacillus anthracis isolate 34F2 plasmid pXOI protective antigen
(pai) gene, partial cds.
ACCESSION AY921578
VERSION AY921578.1 GI:62467684
KEYWORDS
SOURCE Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 (bases 1 to 1694)
AUTHORS Vahedi,F., Moazeni Dula,G. and Mahmoudi,M.
TITLE Humoral immunity in mice induced by vaccination with a plasmid
encoding anthrax protective antigen
JOURNAL Unpublished
2 (bases 1 to 1694)
AUTHORS Vahedi,F., Moazeni Dula,G. and Mahmoudi,M.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2005) Immunology Research Center, BuAli Research
Institute, Mashhad University of Medical Sciences, BuAli Sq.,
Mashhad, Iran
FEATURES
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DHSLSLNGERTWARTWGLNTADVTARLVNANIRVYVGTAPIVNLPTTSLVAGKQTLA
TIKAKENQLSQILAPNNYVPSKNIAPIALNADPFSSPTIYNNQPLFELKTKQLRA
DTPDVGNIATVYFNENGRVVDTSNNSVLPJOETTARIIFNGKDLNVERRLAAV
NPSDPLETTKEDMTLKEALKIAPGFENPENGLOVOGKDIETDFNPDQTSQNIKNOL
AEKLNATVITLIDKIKINAKNNILIRKRPYVDNNIIVAGADESVVVEAHREVINNST
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ORIGIN

Query Match
Best Local Similarity 100.0%; Score 57; DB 1; Length 1694;
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RESULT 7
CS135643 1707 bp DNA linear PAT 09-AUG-2005
LOCUS
DEFINITION Sequence 8 from Patent WO2005068493.
ACCESSION CS135643
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VERSION CS135643.1 GI:72056309  
KEYWORDS Bacillus anthracis  
SOURCE Bacillus anthracis  
ORGANISM Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 8 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
source 1.1707  
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DB 495 CGCAATTGATCATCTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACATGGG 551  
RESULT 8  
AR570597 1710 bp DNA linear PAT 14-DEC-2004  
LOCUS AR570597  
DEFINITION Sequence 4 from patent US 6770479.  
ACCESSION AR570597  
VERSION AR570597.1 GI:56571410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1710)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 4 03-AUG-2004;  
The United States of America as represented by the Secretary of the Army; Washington, DC;  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 57; DB 6; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 3.1e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 498 CGCAATTGATCATCTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACATGGG 554  
RESULT 9  
AX353781 1785 bp DNA linear PAT 06-FEB-2002  
LOCUS AX353781  
DEFINITION Sequence 12 from Patent WO0204646.  
ACCESSION AX353781  
VERSION AX353781.1 GI:18618830  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1  
AUTHORS Williamson, E.D., Miller, J., Walker, N.J., Baillie, L.W., Holden, P.T.,  
Plick-Smith, H.C., Bullifent, H.L., Titball, R.W. and Topping, A.W.  
TITLE Expression system

JOURNAL Patent: WO 0204646-A 12 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3.1e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CGCAATTGATCATCTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACATGGG 57  
DB 996 CGCAATTGATCATCTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACATGGG 1052  
RESULT 10  
I69387 2160 bp DNA linear PAT 04-FEB-1998  
LOCUS I69387  
DEFINITION Sequence 30 from patent US 5677274.  
ACCESSION I69387  
VERSION I69387.1 GI:2831509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 2160)  
AUTHORS Leppla, S.H., Kimpel, K.R., Arora, N., Singh, Y. and Nichols, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 30 14-OCT-1997;  
FEATURES  
source Location/Qualifiers  
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Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1008 CGCAATTGATCATCTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACATGGG 1064  
RESULT 11  
CS135652 2208 bp DNA linear PAT 09-AUG-2005  
LOCUS CS135652  
DEFINITION Sequence 17 from Patent WO2005068493.  
ACCESSION CS135652  
VERSION CS135652.1 GI:72056316  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 17 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
source 1.2208  
/organism="Bacillus anthracis"  
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/db\_xref="taxon:1392"  
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Best Local Similarity 100.0%; Pred. No. 3e-21;



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Db 996 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 1052

RESULT 12
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LOCUS AX353783 2208 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 14 from Patent WO204646.
ACCESSION AX353783
VERSION AX353783.1 GI:18618831
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
other sequences; artificial sequences.
REFERENCE
1 Williamson,E.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,
AUTHORS Flick-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.
TITLE Expression system
JOURNAL Patent: WO 0204646-A 14 17-JAN-2002;
The Secretary of State for Defense (GB)
FEATURES
source 1..2208
Location/Qualifiers
/organism="synthetic construct"
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/note="DNA sequence used to encode SEQ ID NO: 13"

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Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 57
Db 996 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 1052

RESULT 13
CS061689
LOCUS CS061689 2211 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 9 from Patent WO2005026203.
ACCESSION CS061689
VERSION CS061689.1 GI:62553664
KEYWORDS
SOURCE Bacillus anthracis
ORGANISM Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 Kopecko,D.J., Osorio,M., Bhattacharyya,S., Giri,C.P. and Blake,M.
AUTHORS DNA promoters and anthrax vaccines
JOURNAL Patent: WO 2005026203-A 9 24-MAR-2005;
Department of Health and Human Services (US)
FEATURES
source 1..2211
Location/Qualifiers
/organism="Bacillus anthracis"
/mol_type="unassigned DNA"
/db_xref="taxon:1392"

ORIGIN
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Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 999 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 1055

RESULT 14
AR570595
LOCUS AR570595 2211 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 2 from patent US 6770479.
ACCESSION AR570595
VERSION AR570595.1 GI:56571408
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE
1 (bases 1 to 2211)
AUTHORS Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.
TITLE Anthrax vaccine
JOURNAL Patent: US 6770479-A 2 03-AUG-2004;
The United States of America as represented by the Secretary of the
Army; Washington, DC;
MOX;
FEATURES
source 1..2211
Location/Qualifiers
/organism="unknown"
/mol_type="genomic DNA"

ORIGIN
Query Match 100.0%; Score 57; DB 6; Length 2211;
Best Local Similarity 100.0%; Pred. No. 3e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 57
Db 999 CGCAATTGATCATCTCTCTCTGACAGGGGAAAGAACTTGCGCTGAACAATGGG 1055

RESULT 15
BAN413937
LOCUS BAN413937 2225 bp DNA linear BCT 22-MAY-2002
DEFINITION Bacillus anthracis partial pag gene, isolate IT-Cardi-6241.
ACCESSION A0413937
VERSION A0413937.1 GI:16031494
KEYWORDS
SOURCE pag gene.
ORGANISM Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1 Adone,R., Paeguali,P., La Rosa,G., Marianelli,C., Muscillo,M.,
AUTHORS Pisanella,A., Frasca,M. and Cluchini,F.
TITLE Sequence analysis of the gene encoding for the major virulence
JOURNAL factors of bacillus anthracis vaccine strain 'Carbosap
REFERENCE J. Appl. Microbiol. 92, 1-5 (2002)
2 (bases 1 to 2225)
AUTHORS Muscillo,M.
TITLE Direct Submission
JOURNAL Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199,
Italy
FEATURES
source 1..2225
Location/Qualifiers
/organism="Bacillus anthracis"
/mol_type="genomic DNA"
/strain="Ferrara"
/isolate="IT-Cardi-6241"
/db_xref="taxon:1392"
/plasmid="pXOI"
/country="Italy"
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IYNVLPITSLVGRKQTLATIKAKENQSLALPNNTYPSKRLAPIALNADDPSS
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2225;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
Db 1053 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1109

RESULT 16  
AY700758 2227 bp DNA linear BCT 18-AUG-2004  
LOCUS Anthracis strain Sterne plasmid px01 protective antigen  
DEFINITION gene, complete cds.  
ACCESSION AY700758  
VERSION AY700758.1 GI:51235129  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2227)  
AUTHORS Aziz, M.A. and Bhattachar, R.  
TITLE Mature protective antigen gene with prokaryotic ribosomal binding  
site  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2227)  
AUTHORS Aziz, M.A. and Bhattachar, R.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUN-2004) Centre for Biotechnology, Jawaharlal Nehru  
University, New Mehrauli Road, New Delhi 110067, India  
FEATURES  
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KKEVVSIDNLQLEBELKOKSSNSRKRSTASDPVDRNDGIPSLSEVGYTVVKNK  
RTPASPMISINIEKKGLTKYKSPKSTASDPVDFEKVTGRIDKNSPEARHVLVA  
APIVHVMENIILSKNEDOSTONTOSRTISKNTSTRTSTSEVGNAEVHASF  
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IYNVLPITSLVGRKQTLATIKAKENQSLALPNNTYPSKRLAPIALNADDPSS  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2227;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
Db 1015 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1071

RESULT 17  
BAN413936 2231 bp DNA linear BCT 22-MAY-2002  
LOCUS Bacillus anthracis partial pag gene, isolate IT-Carb3-6254.  
DEFINITION A0413936  
ACCESSION A0413936.1 GI:16031492  
VERSION A0413936.1 GI:16031492  
KEYWORDS pag gene.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1  
AUTHORS Adone, R., Pasquali, P., La Rosa, G., Martanello, C., Muscillo, M.,  
Fasanella, A., Francia, M. and Ciuchini, F.  
TITLE Sequence analysis of the gene encoding for the major virulence  
factors of bacillus anthracis vaccine strain 'Carbospap  
J. Appl. Microbiol. 92, 1-5 (2002)  
2 (bases 1 to 2231)  
Muscillo, M.  
TITLE Direct Submission  
JOURNAL Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,  
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00159,  
Italy  
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ORIGIN



Query Match 100.0%; Score 57; DB 1; Length 2231;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
Db 1060 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1116

RESULT 18  
LOCUS AR570596 2292 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3 from patent US 6770479.  
ACCESSION AR570596  
VERSION AR570596.1 GI:56571409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2292)  
AUTHORS Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 3 03-AUG-2004;  
The United States of America as represented by the Secretary of the Army; Washington, DC;  
WOX;

FEATURES  
source location/Qualifiers  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
Db 1080 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1136

RESULT 19  
LOCUS AY997299 2295 bp DNA linear BCT 26-APR-2005  
DEFINITION Bacillus anthracis strain A16r protective antigen (pag) gene,  
complete cds.  
ACCESSION AY997299  
VERSION AY997299.1 GI:62823103  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2295)  
AUTHORS Xu,J., Dong,D. and Chen,W.  
TITLE Protective antigen gene of Bacillus anthracis strain A16r  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 2295)  
AUTHORS Xu,J., Dong,D. and Chen,W.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-2005) Department of Molecular Biology, Beijing  
Institute of Microbiology and Epidemiology, 20 Dongdajie, Fengtai,  
Beijing 100071, China  
location/Qualifiers  
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/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
/strain="A16r"  
/db\_xref="taxon:1392"

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FKLYWDSQNKKEVISSDNLQLPKOKSSNSRKRSSTAGPYVDRDNDGI PDSLEV  
EGYVDVKNKRTFLSPWISNHEKKGLTKYKSSPEKSTASDPYSDPEKTVGRIDKNV  
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ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
Db 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1139

RESULT 20  
LOCUS CS135651 2295 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 16 from Patent WO2005068493.  
ACCESSION CS135651  
VERSION CS135651.1 GI:72056315  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1  
AUTHORS Cutting,S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 16 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 57; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
Db 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1139

RESULT 21  
LOCUS AR570594 2295 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6770479.  
ACCESSION AR570594  
VERSION AR570594.1 GI:56571407  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.



REFERENCE 1 (bases 1 to 2295)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 1 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
MOX;

FEATURES  
source Location/Qualifiers  
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ORIGIN  
Query Match 100.0%; Score 57; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1083 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1139

RESULT 22  
AF306778 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306778  
VERSION AF306778.1 GI:10880942  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2369)  
Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
J. Bacteriol. 181 (8), 2358-2362 (1999)  
10197996  
2 (bases 1 to 2369)  
Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
Direct Submission  
Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
Location/Qualifiers  
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/organism="Bacillus anthracis"  
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FKLYTDSQNKKEVSISSDNLOLPELKQKSSRSRSTASGPTVPDRDNDGIPSLBY  
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ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1131 CGCAATTGATCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1187

RESULT 23  
AF306779 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate 28 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306779  
VERSION AF306779.1 GI:10880944  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2369)  
Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
J. Bacteriol. 181 (8), 2358-2362 (1999)  
10197996  
2 (bases 1 to 2369)  
Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
Direct Submission  
Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
Location/Qualifiers  
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Db 1131 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1187

RESULT 24  
AF306780 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate BA1035 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306780  
VERSION AF306780.1 GI:10880946  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
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Db 1131 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1187  
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RESULT 25  
AF306781 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate 33 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306781

VERSION AF306781.1 GI:10880948  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
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Db 1131 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1187  
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RESULT 26  
AF306782 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306782  
VERSION AF306782.1 GI:10880950  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus



JOURNAL anthracis  
PUBMED J. Bacteriol. 181 (8), 2358-2362 (1999)  
10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
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SPEARHPVLAAPYIVHVDMENTIISKNEPOSQNTDSQTRTISKNSTSRHTSEVHG  
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IRYVNTGAPINVLPTTSLVKGKQTLATIKAKNOLSLAIPNNYPSKLIAPIAL  
NAODPFSSPTITMNYNOLPELEKTKQLLDYDYGNIATYFNGRVVDTGSNWS  
VLPOIETTARIIFNGKDLNVERIAVNSDPLETTKPMPTLEAKLIAFGNESN  
GNLQYQKGDITFDPNPDQTSQNIKNQIAELNVNTIYVLDKIKLANAMNLIIDKR  
PHYDRNNIAGVADSEVVEKAHREVINSSTEGILLNIDKIRIKILSGYVLEIDTEGLK  
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ENGDTSTNGIKILIFSKKGYEIG"

ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
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Db 1131 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1187

RESULT 27  
AF306783 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate BA1024 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306783  
VERSION AF306783.1 GI:10880952  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2369)  
Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
source  
1..2369  
Location/Qualifiers

/organism="Bacillus anthracis"  
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/db\_xref="taxon:1392"  
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1..2369  
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49..2343  
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/codon\_start=1  
/transl\_table=1  
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SOGILGYFSDLPFOAPMNVVTSSTTGDISPSESELENIPSENOYFOBAIWSGFIKVK  
SDEYTPATSDNHVTMWDDEIVINKASNSKRIEKGRLVQIKIQRREPTLEGLD  
FKLYTDSQNKKEVSSDNLQPELKOKSSNRKRSAGPTVPDRNDGIPDSLEV  
EGYTDVGNKRTPLSPWISNIEHKKGLTKYKSPKRWSTASDPYSDPEKVTGRIDKNV  
SPEARHPVLAAPYIVHVDMENTIISKNEPOSQNTDSQTRTISKNSTSRHTSEVHG  
NAEVAHSPFDIGSVSAGFSNSSTVAIDHSLAGERTMAETGLNTADTARLAN  
IRYVNTGAPINVLPTTSLVKGKQTLATIKAKNOLSLAIPNNYPSKLIAPIAL  
NAODPFSSPTITMNYNOLPELEKTKQLLDYDYGNIATYFNGRVVDTGSNWS  
VLPOIETTARIIFNGKDLNVERIAVNSDPLETTKPMPTLEAKLIAFGNESN  
GNLQYQKGDITFDPNPDQTSQNIKNQIAELNVNTIYVLDKIKLANAMNLIIDKR  
PHYDRNNIAGVADSEVVEKAHREVINSSTEGILLNIDKIRIKILSGYVLEIDTEGLK  
EVIINDRYMNLSSLRQDKTEIFDKKYNDKLPLYISNPNKVNVAVTKENTIIIPS  
ENGDTSTNGIKILIFSKKGYEIG"

ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 3e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
|||||  
Db 1131 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1187

RESULT 28  
AF268967 2549 bp DNA linear BCT 31-JUL-2000  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (paga) gene,  
DEFINITION complete cds.  
ACCESSION AF268967  
VERSION AF268967.1 GI:9280532  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2549)  
Cohen, S., Mendelson, I., Alboum, Z., Kobiler, D., Elhanany, B.,  
Bino, T., Leitner, M., Imbar, I., Roseenberg, H., Gozes, Y., Barak, R.,  
Fisher, M., Kromann, C., Velan, B. and Shaffer, A.  
Attenuated nontoxicogenic and nonencapsulated recombinant Bacillus  
anthracis spore vaccines protect against anthrax  
JOURNAL Infect. Immun. 68 (8), 4549-4558 (2000)  
PUBMED 10899854  
REFERENCE 2 (bases 1 to 2549)  
AUTHORS Cohen, S., Mendelson, I. and Shaffer, A.  
TITLE Direct Submission  
JOURNAL Submitted (18-MAY-2000) Department of Biochemistry, Israel  
Institute for Biological Research, P.O. Box 19, Ness Ziona 74100,  
Israel  
FEATURES  
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/organism="Bacillus anthracis"  
/mol\_type="genomic DNA"  
/strain="V770-NP1-R; ATCC14185"  
/db\_xref="ATCC:14185"  
/db\_xref="taxon:1392"  
/plasmid="pX01"



gene 152..2446  
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152..2446  
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/codon\_start=1  
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FKLWTDQNKKEVISDNLQPELKQKSSNRKRSTAGVPDRDNDGIPSLSEY  
EGYVDVKNKRTPLSPWISNIHEKGLTKYKSPKWSADPSDFEKTGRIDKNV  
SPEARPLVAAYPIVHVMENIILSKNEDOSTONTDTRTISKQTSRTHSEVHG  
NAVHASFDIGGSVSGAFSNSSTVAIDHSLSAGERTAAETMGATATALAN  
IRVNTGTAPIYNNVLPITTSILVGRKQTLATIKAKENQSLAPNNYPSKULATL  
NAQDDFSPITVMNNOPLLEKTKQLRLDTQVGNLATYVFNKGRVVDIGSNWSE  
VLPOIETTARIIFNGKDLNVERIAAVNSDPLETKPMTLKAALKIAFGNEPN  
GNLQYQKDIETEPNPDQTSQNIKNQALNATNTIYTVLDKIKLAKNAILRDKR  
FHYDRNNIAGVADSVKEAREVINSSTEGILINDIDIKIISGYIVLEDEEGLK  
EVINDRYMNLNSSLRODGKTFIDFKKNDKLPYISNPYKVVAVYATKENTTIINS  
ENGDTSTNGIKILIFSKGYEIG"

ORIGIN

Query Match 100.0%; Score 57; DB 1; Length 2549;  
Best Local Similarity 100.0%; Pred. No. 2.9e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 57  
Db 1234 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 1230

RESULT 29  
AX933603 2605 bp DNA linear PAT 22-DEC-2003  
LOCUS  
DEFINITION Sequence 3 from Patent WO03087378.  
ACCESSION AX933603  
VERSION AX933603.1 GI:40312826  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1 Schmaljohn,C.U. and Fuller,J.  
AUTHORS  
TITLE Nucleic acid immunization  
JOURNAL Patent: WO 03087378-A 3 23-OCT-2003;  
PowderJect Research Limited (GB)  
FEATURES  
Source  
Location/Qualifiers  
1..2605  
/organism="Bacillus anthracis"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:1392"  
174..2468  
/note="unnamed protein product"  
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/protein\_id="CAF03989.1"  
/db\_xref="GI:40312827"  
/translation="MKKKVLIPIIMALSTIIIVSSNGNLEVIQAEVKQNRRLNSESSE  
SGLIGYFSPILNFOAPMVVTSSTTGDISPSELENIPESEKQFQSHATWGFIVKK  
SDEYTFATSDNHVTWVDDVEVINKASNSKRILEKRLVQIKIQYQREPMTEKGLV  
FKLWTDQNKKEVISDNLQPELKQKSSNRKRSTAGVPDRDNDGIPSLSEY  
EGYVDVKNKRTPLSPWISNIHEKGLTKYKSPKWSADPSDFEKTGRIDKNV  
SPEARPLVAAYPIVHVMENIILSKNEDOSTONTDTRTISKQTSRTHSEVHG  
NAVHASFDIGGSVSGAFSNSSTVAIDHSLSAGERTAAETMGATATALAN  
IRVNTGTAPIYNNVLPITTSILVGRKQTLATIKAKENQSLAPNNYPSKULATL

CDS

152..2446  
/gene="paga"  
152..2446  
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/note="common internalizing receptor binding protein of the two binary exotoxins; similar to protective antigen precursor product encoded by GenBank Accession Number M22589"  
/codon\_start=1  
/transl\_table=11  
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SGLIGYFSPILNFOAPMVVTSSTTGDISPSELENIPESEKQFQSHATWGFIVKK  
SDEYTFATSDNHVTWVDDVEVINKASNSKRILEKRLVQIKIQYQREPMTEKGLV  
FKLWTDQNKKEVISDNLQPELKQKSSNRKRSTAGVPDRDNDGIPSLSEY  
EGYVDVKNKRTPLSPWISNIHEKGLTKYKSPKWSADPSDFEKTGRIDKNV  
SPEARPLVAAYPIVHVMENIILSKNEDOSTONTDTRTISKQTSRTHSEVHG  
NAVHASFDIGGSVSGAFSNSSTVAIDHSLSAGERTAAETMGATATALAN  
IRVNTGTAPIYNNVLPITTSILVGRKQTLATIKAKENQSLAPNNYPSKULATL

NAQDDFSPITVMNNOPLLEKTKQLRLDTQVGNLATYVFNKGRVVDIGSNWSE  
VLPOIETTARIIFNGKDLNVERIAAVNSDPLETKPMTLKAALKIAFGNEPN  
GNLQYQKDIETEPNPDQTSQNIKNQALNATNTIYTVLDKIKLAKNAILRDKR  
FHYDRNNIAGVADSVKEAREVINSSTEGILINDIDIKIISGYIVLEDEEGLK  
EVINDRYMNLNSSLRODGKTFIDFKKNDKLPYISNPYKVVAVYATKENTTIINS  
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misc\_feature 1241..1246  
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ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 2.9e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 57  
Db 1256 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 1312

RESULT 30  
I33400 133400 2709 bp DNA linear PAT 06-FEB-1997  
LOCUS  
DEFINITION Sequence 11 from patent US 5591631.  
ACCESSION I33400  
VERSION I33400.1 GI:1824191  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 2709)  
AUTHORS Leppila,S.H., Klimpel,K.R., Arora,N., Singh,Y. and Nichols,P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 11 07-JAN-1997;  
FEATURES  
Source  
Location/Qualifiers  
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/organism="unknown"  
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ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 2.9e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 57  
Db 996 CGCAATTGATCATTCACTATCTCTAGCAGGGGAAAGAACTTGGCTGAACAATGGG 1052

RESULT 31  
I69378 169378 2709 bp DNA linear PAT 04-FEB-1998  
LOCUS  
DEFINITION Sequence 11 from patent US 5677274.  
ACCESSION I69378  
VERSION I69378.1 GI:2831500  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 2709)  
AUTHORS Leppila,S.H., Klimpel,K.R., Arora,N., Singh,Y. and Nichols,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 11 14-OCT-1997;  
FEATURES  
Source  
Location/Qualifiers  
1..2709  
/organism="unknown"  
/mol\_type="unassigned DNA"

ORIGIN

Query Match 100.0%; Score 57; DB 6; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 2.9e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 57  
DB 996 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 1052

RESULT 32  
BACPG 4235 bp DNA linear BCT 02-AUG-1999  
DEFINITION Bacillus anthracis cryptic protein and protective antigen precursor  
(paga) genes, complete cds.  
ACCESSION M22589  
VERSION M22589.1 GI:143280

KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 (bases 1 to 4235)  
Welkos, S.L., Lowe, J.R., Eden-McCutchan, F., Vodkin, M., Leppla, S.H. and Schmidt, J.J.  
Sequence and analysis of the DNA encoding protective antigen of Bacillus anthracis  
JOURNAL Gene 69 (2), 287-300 (1988)  
PUBMED 3148491  
REFERENCE 2 (bases 1 to 4235)  
Welkos, S.  
Direct Submission  
TITLE Submitted (15-JUN-1989) Bacteriology, USAMRIID, Ft. Detrick, Frederick, MD 21702, USA  
JOURNAL Location/Qualifiers  
FEATURES  
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416..994  
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1804..4098  
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/translation="MKRRVLIPLMALSTIIIVSSGNLEAVTAQVKGQNRLLNSESSE SGGILGYTFSDLNFAQPMVVTISSTIGDLSISESEANTPSENOIFQSAIWSGFTYKK SDEYFATPSADNHWVMVDDEVINKASNSNRIKLEKGLYQIKI QYORENTEKGLD FCLVWDSQNKKEVISDNLOPELKQKSNSRKRKSTAGTPVDRDQDGLPDLLEV EGYTVDKKRTFELSPWISNIHEKKGLTKYKSPKMSSTADSPYDPEVTRIDKNV SPEARHPLVAAPIVHVMENITLSKNEOSQONTDSETRTISKNTSRTSTSVHG NAEVHASFDDIGSVSAGRSNSNSTVAIDHLSLAGERTAEFTMGANTADPRLANAN IRVNTGAPITVNLPTTSLVAGKQVLTATIAKENQSLIAPNNVYPSKLAFLAL NAODFSSPTITMANNQFLBETKQRLDTPQVGNATVNPENGRVAVDQFMSR VLPQIOETFAIRIFNGKDLIVERLIAVNPEDPLETTEDMTLEKALIAQFMSR GNLOYOGKDIETEDFNFDQOSTONIKOULANVTIYVLDKIKLMAAMNLLIDRK RHYDRNNTAVGADSVYGAHREVINSSREGILANTIDQIRKILSGYIYEIDTEGLK EYINDRYMLNLSLRQDKRTIDRFKINDKLPITISNPYVNVYAVYAKENTIIIPS ENGDTSTNGIKILIFSKKYBIG"

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mat\_peptide

/gene="paga"  
/product="protective antigen"

ORIGIN  
Query Match 100.0%; Score 57; DB 1; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 2.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 57  
DB 2886 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 2942

RESULT 33  
LOCUS 133396 4235 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5591631.  
ACCESSION 133396  
VERSION 133396.1 GI:1824187  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4235)  
Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholas, P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 3 07-JAN-1997;  
FEATURES  
source  
1..4235  
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ORIGIN  
Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 2.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 57  
DB 2886 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 2942

RESULT 34  
LOCUS 169374 4235 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 3 from patent US 5677274.  
ACCESSION 169374  
VERSION 169374.1 GI:2831496  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4235)  
Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholas, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 3 14-OCT-1997;  
FEATURES  
source  
1..4235  
/organism="unknown"  
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ORIGIN  
Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 2.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 57  
DB 2886 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAAGAACTTGCGCTGAAACAATGGG 2942

RESULT 35  
AF065404/c



LOCUS	AF065404	181654 bp	DNA	circular BCT 01-OCT-2003
DEFINITION	Bacillus anthracis virulence plasmid PX01, complete sequence.			
ACCESSION	AF065404			
VERSION	AF065404.1	GI:4894216		
KEYWORDS	.			
SOURCE	Bacillus anthracis			
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus			
REFERENCE	Bacteria group.			
AUTHORS	1 (bases 1 to 181654)			
TITLE	Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A.R., Hill,K.K.,			
JOURNAL	Kelm,P., Koehler,T.M., Lamke,G., Kumano,S., Mahillon,J., Manter,D.,			
PUBMED	Martinez,Y., Rice,D., Svensson,R. and Jackson,P.J.			
REFERENCE	Sequence and organization of PX01, the large Bacillus anthracis			
AUTHORS	plasmid harboring the anthrax toxin genes			
TITLE	J. Bacteriol. 181 (20), 6509-6515 (1999)			
JOURNAL	10515943			
PUBMED	2 (bases 1 to 181654)			
REFERENCE	Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A., Hill,K., Kelm,P.,			
AUTHORS	Koehler,T., Kumano,S., Lamke,G., Manter,D., Martinez,Y.,			
TITLE	Rice,D.O., Svensson,R. and Jackson,P.			
JOURNAL	Direct Submission			
PUBMED	Submitted (14-MAY-1998) Life Sciences Division, Los Alamos National			
REFERENCE	Laboratory, T4A3, LS-6, HR-11, MS M88, Los Alamos, NM 87545, USA			
AUTHORS	Location/Qualifiers			
TITLE	1..181654			
JOURNAL	/organism="Bacillus anthracis"			
PUBMED	/mol_type="genomic DNA"			
REFERENCE	/strain="Sterne"			
AUTHORS	/db_xref="taxon:1392"			
TITLE	/plasmid="virulence plasmid PX01"			
JOURNAL	complement(1127..1630)			
PUBMED	/note="Hypothetical protein, Methanobacterium			
REFERENCE	thermoautotrophicum, (AE000631)"			
AUTHORS	/codon_start=1			
TITLE	/transl_table=1			
JOURNAL	/product="PX01-01"			
PUBMED	/protein_id="AAD32305.1"			
REFERENCE	/db_xref="gi:4894217"			
AUTHORS	/translation="MEVLIPELILIAVLIPLVSVKKHVPMKKGAGKGLVKRWLSL			
TITLE	DRKSYVLAHNTVTYETGGDTTQIDHIYAIEGVAVETKNYEGRITGSEKRAATQGI			
JOURNAL	FRKSSFONPHONYKHIKALEWLIBQLPCTISAAFPKCSLRNVNHSKERVKYL			
PUBMED	HMKFAKO"			
REFERENCE	complement(1639..1644)			
AUTHORS	2751..2755			
TITLE	2760..3338			
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AUTHORS	/protein_id="AAD32306.1"			
TITLE	/db_xref="gi:4894218"			
JOURNAL	/translation="MLSHHTILFSLVQVPLIVSGIITYILLDTDEMTKWTFSEIGIF			
PUBMED	AIPIETRPQVFONKRSIISLNQHEKFSKINTPLVSIPLVFNASIFPLKLIAFILOM			
REFERENCE	TVIIPLLELYCLYDRLRPIHNLVYVKKIICDKQKLIKRIIPNNBEHGTTIKTRDOO			
AUTHORS	YFLTYAVLSGISLIPISIEEVEFEERYNNLMGR"			
TITLE	complement(3389..4024)			
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PUBMED	/transl_table=1			
REFERENCE	/product="PX01-03"			
AUTHORS	/protein_id="AAD32307.1"			
TITLE	/db_xref="gi:4894219"			
JOURNAL	/translation="MKREKMGIVLCITLVMIILLVPLQAOASVKVDPNKLGENDVS			
PUBMED	SSPFQDGINPRKTEDKSDRGSSIIOKEIGIYARAFYGVNIISISVLVYNVALI			
REFERENCE	ITKNGOMKKAATGSMTSPISMSMRSLSVYFLBSDFSPRNITFDLDLPFKATALIF			
AUTHORS	TPFWLAGIRLRRIHESHTKQPEYFRMANRVITGSCLLCMALVAPLWLFANN"			
TITLE	complement(4024..4653)			
JOURNAL	/codon_start=1			
PUBMED	/transl_table=1			
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AUTHORS	/protein_id="AAD32308.1"			
TITLE	/db_xref="gi:4894220"			
JOURNAL	/translation="MNINSISNNVVEKLGQTTRYEKQOVOLAVSKSSNIHAHYMP			
PUBMED	BFSEVKSINTELDIEYENLTSTVCVIDRKTSQOEIERONSFMITEVEDVDVIDE			

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RBS  
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Query Match 100.0%; Score 57; DB 1; Length 181654;  
Best Local Similarity 100.0%; Pred. No. 1.5e-21;  
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VERSION AB011190.1 GI:20520075  
KEYWORDS  
SOURCE Bacillus anthracis str. A2012  
ORGANISM Bacillus anthracis str. A2012  
REFERENCE  
AUTHORS 1 (bases 1 to 181677)  
Read,T.D., Salzberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapfle,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Comparative genome sequencing for discovery of novel polymorphisms  
in Bacillus anthracis  
JOURNAL Science 296 (5575), 2028-2033 (2002)  
PUBMED 12004073  
2 (bases 1 to 181677)  
Read,T.D., Salzberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapfle,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2002) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
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Best Local Similarity 100.0%; Pred. No. 1.5e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 CGCAATGATCATTCATCTCTAGACGGGGAAGAAGACTTGGGCTGAACAATGGG 57
Db 144861 CGCAATGATCATTCATCTCTAGACGGGGAAGAAGACTTGGGCTGAACAATGGG 144917

RESULT 37
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SEQUENCE
ACCESSION
AE017336
VERSION
AE017336.2
KEYWORDS
GI:47552137
SOURCE
ORGANISM
Bacillus anthracis str. 'Ames Ancestor'
Bacillus anthracis str. 'Ames Ancestor'
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
1 (bases 1 to 181677)
REFERENCE
1 Ravel,J., Raekov,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,
Salzberg,S. and Fraser,C.M.

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TITLE Bacillus anthracis comparative genomics  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 181677)  
AUTHORS Ravel,J., Raako,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,  
Federova,N.B., Salzman,S. and Fraser,C.M.  
TITLE Direct Submission  
JOURNAL Submitted (17-MAY-2004) The Institute for Genomic Research, 9712  
Medical Center Dr., Rockville, MD 20850, USA  
COMMENT On May 21, 2004 this sequence version replaced gi.47499967.  
This sequence is to be utilized as the reference strain for  
Bacillus anthracis research - all other sequences should be  
compared to this sequence.  
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LOCUS AR345455  
DEFINITION Sequence 66 from patent US 6583275.  
ACCESSION AR345455  
VERSION AR345455.1 GI:33742500  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1023)  
AUTHORS Doucette-Stamm, L.A. and Bush, D.  
TITLE Nucleic acid sequences and expression system relating to  
JOURNAL Enterococcus faecium for diagnostics and therapeutics  
Genome Patent: US 6583275-A 66 24-JUN-2003;  
Genome Therapeutics Corporation; Waltham, MA  
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ACCESSION CS061690  
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SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Kopecko, D.J., Osorio, M., Bhattacharyya, S., Giri, C.P. and Blake, M.  
TITLE DNA promoters and anthrax vaccines  
JOURNAL Patent: WO 2005026203-A 10 24-MAR-2005;  
Department of Health and Human Services (US)  
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ORGANISM Caenorhabditis briggsae  
REFERENCE 1 (bases 1 to 38685)  
AUTHORS Washington University Genome Sequencing Center.  
TITLE The C. briggsae Genome Sequencing Project  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 38685)  
AUTHORS Waterston, R.  
TITLE Direct Submission  
JOURNAL Submitted (04-NOV-2000) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT Submitted by:  
Genome Sequencing Center  
Department of Genetics, Washington University,  
St. Louis, MO 63110, USA  
e-mail: jpeich@watson.wustl.edu  
NOTICE: This sequence may not be the entire insert of this clone.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we provide a small overlap between  
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FEATURES  
Location/Qualifiers



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Job time : 422.151 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:17 ; Search time 79.4164 Seconds  
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Title: US-10-712-654-22

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Scoring table: OLIGO NUC  
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Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0  
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Post-processing: Listing first 1000 summaries

Database :

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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c 251	15	26.3	2236	2	AAQ65610	Aaq65610 Feline zo	324	15	26.3	127602	14	AEA61155	Aea61155 Human GLU
c 252	15	26.3	2236	2	AAV64792	Aav64792 Feline zp	325	15	26.3	127722	12	ADQ97301	Adq97301 Human can
c 253	15	26.3	2236	2	AAZ22715	Aaz22715 Feline zo	326	15	26.3	136328	6	ABZ35015	Abz35015 Human gen
c 254	15	26.3	2236	3	AAZ33249	Aaz33249 Feline zo	327	15	26.3	143899	6	AAU38336	Aau38336 Genomic s
c 255	15	26.3	2236	3	AAZ95652	Aaz95652 Feline zo	328	15	26.3	160921	11	ACN44962	Acn44962 Human gen
c 256	15	26.3	2236	3	AAZ46260	Aaz46260 Feline co	329	15	26.3	177531	8	ACF62732	Acf62732 Cancer ba
c 257	15	26.3	2236	3	AAZ37804	Aaz37804 Feline zo	330	15	26.3	177531	8	ADB20847	Adb20847 MRPl base
c 258	15	26.3	2429	2	AAK86759	Aak86759 CDNA enco	331	15	26.3	177531	10	ADB87936	Adb87936 Human UGT
c 259	15	26.3	2518	13	ADX13884	Adx13884 Plant ful	332	15	26.3	177531	10	ADB86919	Adb86919 Human MDR
c 260	15	26.3	2624	2	AAI89886	Aai89886 Mouse fir	333	15	26.3	177531	10	ADB92110	Adb92110 Human MDR
c 261	15	26.3	2624	12	ADO30174	Ado30174 Mouse GPC	334	15	26.3	177531	10	ADH74617	Adh74617 Human BAC
c 262	15	26.3	2735	4	AAH16242	Aah16242 Human CDN	335	15	26.3	203020	14	ADZ12576	Adz12576 Human can
c 263	15	26.3	2889	12	ADK65985	Adk65985 Tobacco N	336	15	26.3	212231	11	ACN44598	Acn44598 Human gen
c 264	15	26.3	3081	13	ADRO7065	Adr07065 Full leng	337	15	26.3	215980	6	AAU38337	Aau38337 Complemen
c 265	15	26.3	3316	12	ADK65989	Adk65989 Tomato NA	338	15	26.3	218802	14	ADW98820	Adw98820 Human her
c 266	15	26.3	3375	8	ABZ34820	Abz34820 Coding se	339	15	26.3	220224	11	ACN444702	Acn444702 Human gen
c 267	15	26.3	3375	8	ABZ34849	Abz34849 Coding se	340	15	26.3	229354	6	ABQ74179	Abq74179 Human cyt
c 268	15	26.3	3375	8	ABX75323	Abx75323 Human CDN	341	15	26.3	247682	12	ADL08109	Adl08109 Human gen
c 269	15	26.3	3375	8	ABD52550	Abd52550 FZB3 DNA	342	15	26.3	319608	3	AAH51601	Aah51601 Human chr
c 270	15	26.3	3375	8	ABZ81822	Abz81822 Receptor	343	15	26.3	319608	5	AAH05301	Aah05301 Human chr
c 271	15	26.3	3442	12	ADOL5852	Adol5852 4 synthes	344	15	26.3	319608	5	AAH05301	Aah05301 Human chr
c 272	15	26.3	3733	12	ADK65987	Adk65987 Potato NA	345	15	26.3	229354	20	ABK92282	Abk92282 Human tum
c 273	15	26.3	3746	4	AAH18222	Aah18222 Human CDN	346	15	26.3	229354	6	ABK92281	Abk92281 Human tum
c 274	15	26.3	3774	12	ADQ25334	Adq25334 Human sof	347	15	26.3	229354	21	ADU42260	Adu42260 Human sof
c 275	15	26.3	3933	12	ADQ23257	Adq23257 Human pzd	348	15	26.3	229354	21	AAA94588	Aaa94588 Oligonuc1
c 276	15	26.3	3977	11	ACN89360	Acn89360 Breast ca	349	15	26.3	229354	34	AAK83203	Aak83203 Oligonuc1
c 277	15	26.3	3981	12	ADL35700	Adl35700 Human ang	350	15	26.3	229354	49	ABZ22691	Abz22691 Oligonuc1
c 278	15	26.3	4570	10	ADDE5732	Adde5732 Human gen	351	15	26.3	229354	8	ABZ22688	Abz22688 Oligonuc1
c 279	15	26.3	4885	13	ADRO7829	Adr07829 Full leng	352	15	26.3	229354	49	ABZ22693	Abz22693 Oligonuc1
c 280	15	26.3	6062	4	AAAD20729	Aad20729 Human gly	353	15	26.3	229354	50	AAH90282	Aah90282 Human cto
c 281	15	26.3	6065	4	AAAD20680	Aad20680 Human gly	354	15	26.3	229354	51	AAH90279	Aah90279 Human cto
c 282	15	26.3	7787	6	ABQ71070	Abq71070 Listeria	355	15	26.3	229354	51	AAH90280	Aah90280 Human cto
c 283	15	26.3	8297	12	ADQ21281	Adq21281 Human sof	356	15	26.3	229354	51	AAH90281	Aah90281 Human cto
c 284	15	26.3	8297	13	ADU06138	Adu06138 Novel bro	357	15	26.3	229354	6	ADL16112	Adl16112 Single st
c 285	15	26.3	11029	4	ABU20444	Abu20444 Drosoph11	358	15	26.3	229354	51	ABZ37426	Abz37426 CDR1/2 di
c 286	15	26.3	12879	6	ABK92230	Abk92230 Prostate	359	15	26.3	229354	65	ADP97510	Adp97510 C. albica
c 287	15	26.3	12879	6	ABK92230	Abk92230 Prostate	360	15	26.3	229354	87	ADP97510	Adp97510 C. albica
c 288	15	26.3	12880	11	ADN39609	Adn39609 Cancer/an	361	15	26.3	229354	94	ABZ37393	Abz37393 Synthetic
c 289	15	26.3	12880	11	ADN39609	Adn39609 Cancer/an	362	15	26.3	229354	133	ADR30309	Adr30309 Mouse gen
c 290	15	26.3	13202	4	AAK51828	Aak51828 Human pol	363	15	26.3	229354	173	ABZ40178	Abz40178 Human 1lv
c 291	15	26.3	13202	4	AAK51828	Aak51828 Human pol	364	15	26.3	229354	192	ABV44107	Abv44107 Human pro
c 292	15	26.3	13833	6	ABK47910	Abk47910 Human B-F	365	15	26.3	229354	242	AAV35270	Av35270 Human pro
c 293	15	26.3	18379	13	ADS36502	Ads36502 Human aut	366	15	26.3	229354	212	AAK78509	Aak78509 Human Nkx
c 294	15	26.3	19079	13	ADS36471	Ads36471 Human aut	367	15	26.3	229354	219	ADT75449	Adt75449 Human ova
c 295	15	26.3	19399	4	ABL06008	Ab106008 Drosoph11	368	15	26.3	229354	5	ADT75449	Adt75449 Human ova
c 296	15	26.3	24741	11	ACN44542	Acn44542 Human gen	369	15	26.3	229354	242	AAV35270	Av35270 Human pro
c 297	15	26.3	26555	4	AAK68605	Aak68605 Human imm	370	15	26.3	229354	242	AAV35270	Av35270 Human pro
c 298	15	26.3	26555	4	AAK68605	Aak68605 Human imm	371	15	26.3	229354	242	AAV35270	Av35270 Human pro
c 299	15	26.3	26555	4	AAK68605	Aak68605 Human imm	372	15	26.3	229354	242	AAV35270	Av35270 Human pro
c 300	15	26.3	32152	4	ABA08132	Ab08132 Human gen	373	15	26.3	229354	288	ABX66066	Abx66066 Corn ear-
c 301	15	26.3	42347	12	ADP84152	Adp84152 Human ova	374	15	26.3	229354	292	ABE64185	Ab64185 Stomach c
c 302	15	26.3	42347	12	ADP84152	Adp84152 Human ova	375	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 303	15	26.3	56583	3	AAA35003	Aaa35003 Human ade	376	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 304	15	26.3	56583	10	ABZ96819	Abz96819 Human low	377	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 305	15	26.3	56583	11	ABD20668	Abd20668 Human nuc	378	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 306	15	26.3	57296	4	AAK78847	Aak78847 Human imm	379	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 307	15	26.3	57296	4	AAK78847	Aak78847 Human imm	380	15	26.3	229354	295	AAV35270	Av35270 Human pro
c 308	15	26.3	57296	4	AAK78847	Aak78847 Human imm	381	15	26.3	229354	300	AAZ13403	Aaz13403 Human gen
c 309	15	26.3	57296	4	AAK78847	Aak78847 Human imm	382	15	26.3	229354	305	AAZ13403	Aaz13403 Human gen
c 310	15	26.3	60500	11	ACN44530	Acn44530 Human gen	383	15	26.3	229354	308	AAZ13403	Aaz13403 Human gen
c 311	15	26.3	65621	11	ACN44402	Acn44402 Human gen	384	15	26.3	229354	317	ABN21262	Abn21262 Human ORF



C	385	14	24.6	328	10	ACD94450	Ac9d9450 Human col	458	14	24.6	382	14	ADY50103	ADY50103 Endotheli
	386	14	24.6	329	2	AA060575	AA060575 Human bra	459	14	24.6	382	14	ADY50111	ADY50111 Endotheli
	387	14	24.6	332	12	ADY50135	ADY50135 Endotheli	460	14	24.6	382	14	ADY50119	ADY50119 Endotheli
	388	14	24.6	335	12	ADP6414	ADP6414 Human CDN	461	14	24.6	382	14	ADY50115	ADY50115 Endotheli
	389	14	24.6	339	5	ADL40685	ADL40685 Human ova	462	14	24.6	382	14	ADY50107	ADY50107 Endotheli
	390	14	24.6	339	5	ADL61910	ADL61910 Human ova	463	14	24.6	383	14	ADY33986	ADY33986 Anti-Tie
	391	14	24.6	339	14	ADY34028	ADY34028 Anti-Tie	464	14	24.6	384	6	ABL62461	ABL62461 Colon ade
	392	14	24.6	339	14	AEA45002	AEA45002 Apolipop	465	14	24.6	384	6	ABL66917	ABL66917 Lung can
	393	14	24.6	339	14	AEA44992	AEA44992 Apolipop	466	14	24.6	384	10	ADFO3594	ADFO3594 Bacteri
	394	14	24.6	339	14	AEA44984	AEA44984 Apolipop	467	14	24.6	384	14	ADW04740	ADW04740 PAPP-A im
	395	14	24.6	341	14	ADY50139	ADY50139 Endotheli	468	14	24.6	384	14	AEA53311	AEA53311 Novel hum
	396	14	24.6	341	14	ADY50143	ADY50143 Endotheli	469	14	24.6	384	14	AEA53275	AEA53275 Novel hum
	397	14	24.6	341	14	ADY50127	ADY50127 Endotheli	470	14	24.6	384	14	AEA44974	AEA44974 Apolipop
	398	14	24.6	341	14	ADY50131	ADY50131 Endotheli	471	14	24.6	386	14	ADY34024	ADY34024 Anti-Tie
	399	14	24.6	341	14	ADY50123	ADY50123 Endotheli	472	14	24.6	386	14	ADY33998	ADY33998 Anti-Tie
	400	14	24.6	342	12	ADL93577	ADL93577 Human CD4	473	14	24.6	387	14	ADW04722	ADW04722 PAPP-A im
	401	14	24.6	342	14	ADY50095	ADY50095 Endotheli	474	14	24.6	387	14	ADW04715	ADW04715 Novel hum
	402	14	24.6	342	14	ADY50083	ADY50083 Endotheli	475	14	24.6	387	14	AEA53231	AEA53231 Novel hum
	403	14	24.6	342	14	ADY50091	ADY50091 Endotheli	476	14	24.6	387	14	AEA53359	AEA53359 Novel hum
	404	14	24.6	344	14	ADY50087	ADY50087 Endotheli	477	14	24.6	387	14	AEA53211	AEA53211 Novel hum
	405	14	24.6	344	14	ADY50099	ADY50099 Endotheli	478	14	24.6	387	14	AEA53235	AEA53235 Novel hum
	406	14	24.6	344	14	ADY50079	ADY50079 Endotheli	479	14	24.6	387	14	AEA53363	AEA53363 Novel hum
	407	14	24.6	345	14	AEA44978	AEA44978 Apolipop	480	14	24.6	387	14	AEA53383	AEA53383 Novel hum
	408	14	24.6	345	14	AEA44976	AEA44976 Apolipop	481	14	24.6	387	14	AEA44994	AEA44994 Apolipop
	409	14	24.6	348	12	ADL93565	ADL93565 Human CD4	482	14	24.6	389	2	AA061215	AA061215 Human bra
	410	14	24.6	348	12	ADL93597	ADL93597 Human CD4	483	14	24.6	389	14	ADY50075	ADY50075 Endotheli
	411	14	24.6	348	12	ADL93593	ADL93593 Human CD4	484	14	24.6	390	6	ADJ36784	ADJ36784 Human pur
	412	14	24.6	351	12	ADL93581	ADL93581 Human CD4	485	14	24.6	390	14	ADW04732	ADW04732 PAPP-A im
	413	14	24.6	351	14	ADW04733	ADW04733 PAPP-A im	486	14	24.6	390	14	ADW04722	ADW04722 PAPP-A im
	414	14	24.6	351	14	ADW04752	ADW04752 PAPP-A im	487	14	24.6	390	14	AEA53219	AEA53219 Novel hum
	415	14	24.6	351	14	ADW04737	ADW04737 PAPP-A im	488	14	24.6	390	14	AEA53223	AEA53223 Novel hum
	416	14	24.6	353	3	AA00847	AA00847 Human sec	489	14	24.6	390	14	AEA53259	AEA53259 Novel hum
	417	14	24.6	354	5	ABV56197	ABV56197 Human pro	490	14	24.6	390	14	AEA53347	AEA53347 Novel hum
	418	14	24.6	354	10	ADD26886	ADD26886 Human adi	491	14	24.6	390	14	ADW04749	ADW04749 PAPP-A im
	419	14	24.6	354	12	ADL93573	ADL93573 Human CD4	492	14	24.6	393	14	ADW04749	ADW04749 PAPP-A im
	420	14	24.6	354	12	ADL93569	ADL93569 Human CD4	493	14	24.6	393	14	ADW04724	ADW04724 PAPP-A im
	421	14	24.6	354	14	AEA45000	AEA45000 Apolipop	494	14	24.6	393	14	ADW04721	ADW04721 PAPP-A im
	422	14	24.6	354	14	AEA45008	AEA45008 Apolipop	495	14	24.6	393	14	ADW04742	ADW04742 PAPP-A im
	423	14	24.6	354	14	AEA44982	AEA44982 Apolipop	496	14	24.6	393	14	ADW04741	ADW04741 PAPP-A im
	424	14	24.6	354	14	AEA44990	AEA44990 Apolipop	497	14	24.6	393	14	ADW05024	ADW05024 PAPP-A im
	425	14	24.6	355	5	ABV47718	ABV47718 Human pro	498	14	24.6	393	14	ADW04739	ADW04739 PAPP-A im
	426	14	24.6	357	12	ADL93511	ADL93511 Human CD4	499	14	24.6	393	14	ADY33946	ADY33946 Anti-Tie
	427	14	24.6	357	14	AEA44986	AEA44986 Apolipop	500	14	24.6	393	14	AEA53283	AEA53283 Novel hum
	428	14	24.6	357	14	AEA44998	AEA44998 Apolipop	501	14	24.6	393	14	AEA53291	AEA53291 Novel hum
	429	14	24.6	357	14	AEA45006	AEA45006 Apolipop	502	14	24.6	393	14	AEA53307	AEA53307 Novel hum
	430	14	24.6	360	12	ADL93515	ADL93515 Human CD4	503	14	24.6	393	14	AEA53251	AEA53251 Novel hum
	431	14	24.6	360	12	ADL93589	ADL93589 Human CD4	504	14	24.6	393	14	AEA53319	AEA53319 Novel hum
	432	14	24.6	363	14	ADY34020	ADY34020 Anti-Tie	505	14	24.6	393	14	AEA53343	AEA53343 Novel hum
	433	14	24.6	364	9	ACH46412	ACH46412 Human inf	506	14	24.6	395	14	ADY34006	ADY34006 Anti-Tie
	434	14	24.6	366	12	ADL93585	ADL93585 Human CD4	507	14	24.6	395	14	ADY34014	ADY34014 Anti-Tie
	435	14	24.6	366	12	AEA45004	AEA45004 Apolipop	508	14	24.6	395	14	ABJ30386	ABJ30386 Human liv
	436	14	24.6	369	12	ADL93501	ADL93501 Human CD4	509	14	24.6	396	4	ADW04736	ADW04736 PAPP-A im
	437	14	24.6	369	12	ADL93519	ADL93519 Human CD4	510	14	24.6	396	14	ADW04729	ADW04729 PAPP-A im
	438	14	24.6	369	14	ADW04717	ADW04717 PAPP-A im	511	14	24.6	396	14	ADW04748	ADW04748 PAPP-A im
	439	14	24.6	369	14	ADW04719	ADW04719 PAPP-A im	512	14	24.6	396	14	ADW04735	ADW04735 PAPP-A im
	440	14	24.6	369	14	ADW04718	ADW04718 PAPP-A im	513	14	24.6	396	14	ADW04745	ADW04745 PAPP-A im
	441	14	24.6	369	14	ADW04720	ADW04720 PAPP-A im	514	14	24.6	396	14	ADW04731	ADW04731 PAPP-A im
	442	14	24.6	369	14	ADW04734	ADW04734 PAPP-A im	515	14	24.6	396	14	ADW04730	ADW04730 PAPP-A im
	443	14	24.6	369	14	ADW04725	ADW04725 PAPP-A im	516	14	24.6	396	14	ADY33926	ADY33926 Human rec
	444	14	24.6	369	14	ADW04716	ADW04716 PAPP-A im	517	14	24.6	396	14	ADY33954	ADY33954 Anti-Tie
	445	14	24.6	369	14	ADY33982	ADY33982 Anti-Tie	518	14	24.6	396	14	ADY33930	ADY33930 Anti-Tie
	446	14	24.6	369	14	AEA53395	AEA53395 Novel hum	519	14	24.6	396	14	AEA53351	AEA53351 Novel hum
	447	14	24.6	369	14	AEA53315	AEA53315 Novel hum	520	14	24.6	396	14	AEA53355	AEA53355 Novel hum
	448	14	24.6	369	14	AEA44980	AEA44980 Apolipop	521	14	24.6	396	14	AEA53287	AEA53287 Novel hum
	449	14	24.6	375	4	AA191404	AA191404 Human pol	522	14	24.6	396	14	AEA53215	AEA53215 Novel hum
	450	14	24.6	375	14	ADY33966	ADY33966 Anti-Tie	523	14	24.6	398	14	ADY50057	ADY50057 Endotheli
	451	14	24.6	375	14	AEA53371	AEA53371 Novel hum	524	14	24.6	398	14	ADY50065	ADY50065 Endotheli
	452	14	24.6	378	8	ABZ22680	ABZ22680 Human ant	525	14	24.6	398	14	ADY50061	ADY50061 Endotheli
	453	14	24.6	378	14	AEA53299	AEA53299 Novel hum	526	14	24.6	398	14	ADY50072	ADY50072 Novel hum
	454	14	24.6	378	14	AEA44996	AEA44996 Apolipop	527	14	24.6	398	14	AEA53379	AEA53379 Novel hum
	455	14	24.6	378	14	AEA44988	AEA44988 Apolipop	528	14	24.6	399	14	AEA53327	AEA53327 Novel hum
	456	14	24.6	381	14	AEA53367	AEA53367 Novel hum	529	14	24.6	399	14	AEA53387	AEA53387 Novel hum
	457	14	24.6	382	8	ABX42902	ABX42902 Bovine ES	530	14	24.6	399	14	AEA53207	AEA53207 Novel hum



531	14	24.6	402	14	ADM05026	Adg05026 PAPP-A im	604	14	24.6	576	12	ADQ09940	Adq09940 Human NK-
532	14	24.6	402	14	AEAS3227	Aeas3227 Novel hum	605	14	24.6	576	12	ADQ09866	Adq09866 Human NK-
533	14	24.6	402	14	AEAS3243	Aeas3243 Novel hum	606	14	24.6	582	12	ACH87124	Ach87124 Human gen
534	14	24.6	402	14	AEAS3339	Aeas3339 Novel hum	607	14	24.6	594	10	ADC93335	Adc93335 E. faeciu
535	14	24.6	405	14	AEAS3375	Aeas3375 Novel hum	608	14	24.6	596	5	ABVS2263	Abvs2263 Human pro
536	14	24.6	405	14	ADM04750	Adm04750 PAPP-A im	609	14	24.6	596	13	ACN51009	Acn51009 Corton an
537	14	24.6	405	14	AEAS3247	Aeas3247 Novel hum	610	14	24.6	601	14	AEBS3392	Aeb33392 Human DNA
538	14	24.6	405	14	AEAS3267	Aeas3267 Novel hum	611	14	24.6	601	14	AEBS3393	Aeb33393 Human DNA
539	14	24.6	405	14	AEAS3323	Aeas3323 Novel hum	612	14	24.6	601	14	AEBS32926	Aeb32927 Human DNA
540	14	24.6	405	14	AEAS3263	Aeas3263 Novel hum	613	14	24.6	601	14	AEBS3391	Aeb33391 Human DNA
541	14	24.6	408	14	ADM04746	Adm04746 PAPP-A im	614	14	24.6	601	14	AEBS32928	Aeb32928 Human DNA
542	14	24.6	408	14	ADM04751	Adm04751 PAPP-A im	615	14	24.6	609	5	AAAS91644	Aas91644 DNA encod
543	14	24.6	411	14	ADM04727	Adm04727 PAPP-A im	616	14	24.6	609	5	AAAS91644	Aas91644 DNA encod
544	14	24.6	411	14	ADM04727	Adm04727 PAPP-A im	617	14	24.6	611	4	AAK68486	Aak68486 Human imm
545	14	24.6	411	14	AEAS3279	Aeas3279 Novel hum	618	14	24.6	610	4	AAH060456	Aah060456 Human can
546	14	24.6	411	14	AEAS3303	Aeas3303 Novel hum	619	14	24.6	612	4	AAH08686	Aah08686 Human can
547	14	24.6	412	14	ADY33958	Ady33958 Ant-i-tie	620	14	24.6	679	3	AAFI1995	Aafi1995 Aspergill
548	14	24.6	413	14	ADY33978	Ady33978 Ant-i-tie	621	14	24.6	679	13	ADU56036	Adu56036 Aspergill
549	14	24.6	413	14	ADY34002	Ady34002 Ant-i-tie	622	14	24.6	679	14	ADZ94039	Adz94039 Aspergill
550	14	24.6	413	14	ADY33994	Ady33994 Ant-i-tie	623	14	24.6	685	6	ABN89431	Abn89431 Mouse Ztn
551	14	24.6	413	14	ADY33990	Ady33990 Ant-i-tie	624	14	24.6	695	6	AAAS62895	Aas62895 Human G p
552	14	24.6	413	14	ADY34010	Ady34010 Ant-i-tie	625	14	24.6	696	6	ABK80363	Abk80363 Bacillus
553	14	24.6	414	8	ABX39930	Abx39930 Bovine ES	626	14	24.6	705	6	ABO68768	Abog68768 Listeria
554	14	24.6	414	14	ADM04738	Adm04738 PAPP-A im	627	14	24.6	710	3	AAFI5582	Aafi5582 Human pro
555	14	24.6	414	14	ADM04747	Adm04747 PAPP-A im	628	14	24.6	725	12	ADJ42050	Adj42050 Plant cDN
556	14	24.6	414	14	ADM04744	Adm04744 PAPP-A im	629	14	24.6	743	10	ADK56796	Adk56796 Plant DNA
557	14	24.6	414	14	ADM04743	Adm04743 PAPP-A im	630	14	24.6	744	4	AAI95543	Aai95543 Human neu
558	14	24.6	417	10	ABT41102	Abt41102 Toxicity	631	14	24.6	749	4	AAI24932	Aai24932 Human bre
559	14	24.6	417	12	ADP72073	Adp72073 Renal tox	632	14	24.6	763	2	AAI26204	Aai26204 Human gen
560	14	24.6	419	6	AD245737	Ad245737 Single st	633	14	24.6	784	4	AAAC43810	Aac43810 Arabidops
561	14	24.6	419	10	ABZ37388	Abz37388 Synthetic	634	14	24.6	799	2	AAVS9781	Aav59781 Human sec
562	14	24.6	420	12	ADQ21534	Adq21534 Human bot	635	14	24.6	799	2	ABSV73775	Abv73775 Human cDN
563	14	24.6	420	14	ADM04726	Adm04726 PAPP-A im	636	14	24.6	799	8	ABX05374	Abx05374 Human nov
564	14	24.6	422	14	AEAS3255	Aeas3255 Novel hum	637	14	24.6	799	10	ACD82918	Acd82918 CDNA seq
565	14	24.6	425	14	ADY34036	Ady34036 Ant-i-tie	638	14	24.6	799	10	ADI23003	Adi23003 CDNA enc
566	14	24.6	426	14	ABSS27166	Abss27166 Human liv	639	14	24.6	799	12	ADH74005	Adh74005 Human sec
567	14	24.6	426	14	AEAS3335	Aeas3335 Novel hum	640	14	24.6	812	4	ABEL14419	Abel14419 Drosophil
568	14	24.6	429	14	ADY33970	Ady33970 Ant-i-tie	641	14	24.6	812	4	AAKS6634	Aaks6634 Human imm
569	14	24.6	429	14	ADY33950	Ady33950 Ant-i-tie	642	14	24.6	821	2	AAQ12851	Aaq12851 A. niger p
570	14	24.6	432	4	AAK85264	Aak85264 Human imm	643	14	24.6	825	4	AAAS40894	Aas40894 CDNA enc
571	14	24.6	432	4	AAK85265	Aak85265 Human imm	644	14	24.6	825	5	ABAO6448	Abao6448 Human cDN
572	14	24.6	432	4	AAI91532	Aai91532 Human pol	645	14	24.6	825	5	AAAS29687	Aas29687 Human cDN
573	14	24.6	439	3	MAAC01594	Mac01594 Human sec	646	14	24.6	825	6	ABVS3785	Abv3785 Human pol
574	14	24.6	439	14	ADY33934	Ady33934 Ant-i-tie	647	14	24.6	842	5	AAAS73610	Aas73610 DNA encod
575	14	24.6	439	14	ADY33938	Ady33938 Ant-i-tie	648	14	24.6	847	4	AAH04759	Aah04759 Human cDN
576	14	24.6	441	6	ABK33012	Abk33012 DNA encod	649	14	24.6	857	3	AACT7277	Aac77277 Human ORF
577	14	24.6	441	14	ADY33974	Ady33974 Ant-i-tie	650	14	24.6	857	4	ABA08773	Abao8773 Human sec
578	14	24.6	442	13	ACFP90330	Acfp90330 Human SIR	651	14	24.6	857	4	AAI60292	Aai60292 Human pol
579	14	24.6	443	11	ACN86468	Acn86468 Breatb. ca	652	14	24.6	858	5	AAAS91744	Aas91744 DNA encod
580	14	24.6	444	14	ADY33962	Ady33962 Ant-i-tie	653	14	24.6	861	6	ABZ12203	Abz12203 Arabidops
581	14	24.6	446	14	ADY33942	Ady33942 Ant-i-tie	654	14	24.6	894	9	ADDA29986	Ada29986 DNA encod
582	14	24.6	448	6	ABV98594	Abv98594 Human pan	655	14	24.6	911	4	AAK75939	Aak75939 Human imm
583	14	24.6	448	8	ABQ82961	Abq82961 Human lun	656	14	24.6	930	3	AAAC4938	Aac4938 Human cDN
584	14	24.6	454	5	AAAS91745	Aas91745 DNA encod	657	14	24.6	938	13	ADY133287	Ady13287 Arabidops
585	14	24.6	455	9	ACH25479	Ach25479 Human adu	658	14	24.6	963	10	ADK60024	Adk60024 plant DNA
586	14	24.6	459	10	ADFO3048	Adfo3048 Bacterial	659	14	24.6	969	4	AAH43567	Aah43567 Human DHD
587	14	24.6	471	14	ADY34032	Ady34032 Ant-i-tie	660	14	24.6	975	6	AAH74541	Aah74541 Bacillus
588	14	24.6	472	6	ABL93383	Ab193383 Arabidops	661	14	24.6	1004	13	ADSA48691	Ads48691 Bacterial
589	14	24.6	474	5	ABV14176	Abv14176 Human pro	662	14	24.6	1032	13	ADXS59233	Adxs59233 Plant ful
590	14	24.6	475	14	ADY73379	Ady73379 Human col	663	14	24.6	1038	12	ADJ40557	Adj40557 Plant cDN
591	14	24.6	487	3	AACT4884	Aac74884 Human ORF	664	14	24.6	1049	6	ABK93141	Abk93141 Human pro
592	14	24.6	487	6	ABN15972	Abn15972 Human ORF	665	14	24.6	1053	6	ABZ32033	Abz32033 Candida a
593	14	24.6	490	9	ACH25728	Ach25728 Human adu	666	14	24.6	1058	3	AAAC48710	Aac48710 Arabidops
594	14	24.6	497	14	ADV75278	Adv75278 Human col	667	14	24.6	1062	3	AAAC40392	Aac40392 Arabidops
595	14	24.6	498	3	AAAC01577	Aac01577 Human nec	668	14	24.6	1141	3	AAAC33606	Aac33606 Arabidops
596	14	24.6	510	5	ABAI3822	Abai3822 Human ner	669	14	24.6	1158	8	ABZ36352	Abz36352 Arabidops
597	14	24.6	525	6	ABQ55893	Abq55893 Human ova	670	14	24.6	1190	5	ABV29010	Abv29010 Human pro
598	14	24.6	529	13	ADQ52478	Adq52478 Novel can	671	14	24.6	1190	5	ABV23170	Abv23170 Human pro
599	14	24.6	530	6	ABN65638	Abn65638 Human can	672	14	24.6	1197	13	ADK43732	Adk43732 Streptoco
600	14	24.6	543	4	AAH13014	Aah13014 Human cDN	673	14	24.6	1198	10	ADDA6524	Ada6524 Human gen
601	14	24.6	566	13	ADX35541	Adx35541 Plant ful	674	14	24.6	1206	3	AAA81654	Aaa81654 N. mening
602	14	24.6	570	4	AAH09054	Aah09054 Human cDN	675	14	24.6	1209	4	AAH43563	Aah43563 Human DHD



C 677	14	24.6	1210	3	AAA12992	Aaa12992	CDNA	enco	C 750	14	24.6	1847	9	ACD82779	AcC82779	CDNA	sequ
C 678	14	24.6	1210	10	ADH88958	Adh88958	Human	fat	C 751	14	24.6	1847	10	AD123002	Ad123002	CDNA	enco
C 679	14	24.6	1210	12	ADP12109	Adp12109	Human	fat	C 752	14	24.6	1847	10	AD123864	Ad123864	CDNA	enco
C 680	14	24.6	1221	13	ADR92779	Adr92779	Novel	S.	C 753	14	24.6	1847	12	ADH73866	Adh73866	Human	sec
C 681	14	24.6	1221	13	AA556649	Aa556649	Streptococ		C 754	14	24.6	1847	12	ADH74004	Adh74004	Human	sec
C 682	14	24.6	1263	8	ACA36468	Ac36468	Prokaryot		C 755	14	24.6	1847	14	ADW21299	Adw21299	Mouse	Bly
C 683	14	24.6	1282	10	ADBO9925	Adbo9925	Novel	DNA	C 756	14	24.6	1882	14	AB268876	Ab268876	Nucleotid	
C 684	14	24.6	1282	13	ADSI1648	Adsi1648	Human	the	C 757	14	24.6	1882	14	ADM03441	Adm03441	Murine	BR
C 685	14	24.6	1290	6	ABK75031	Abk75031	Bacillus		C 758	14	24.6	1887	4	AAH18090	Aah18090	Human	CDN
C 686	14	24.6	1293	14	ADY65611	Ady65611	S. manson		C 759	14	24.6	1902	12	AD126200	Ad126200	Human	CDN
C 687	14	24.6	1299	11	ACN89634	Acn89634	Breast	ca	C 760	14	24.6	1911	11	ACL27225	ACL27225	Rice	abio
C 688	14	24.6	1301	4	AAK80258	Aak80258	Human	imm	C 761	14	24.6	1922	13	ADQ80271	Adq80271	Peroxisom	
C 689	14	24.6	1302	4	AAKS1580	Aak1580	Human	pol	C 762	14	24.6	1941	4	AA158129	Aa158129	Human	pol
C 690	14	24.6	1319	6	ADXA9533	Adxa9533	Plant	ful	C 763	14	24.6	1941	5	ADQ98335	Adq98335	DNA	enco
C 691	14	24.6	1324	13	ABO60944	Ab060944	Springos		C 764	14	24.6	1941	9	ADBA8095	Adba8095	Novel	hum
C 692	14	24.6	1328	13	ADX52599	Adx52599	Plant	ful	C 765	14	24.6	1943	6	ADD35411	Add35411	Murine	BA
C 693	14	24.6	1340	8	ADA68077	Ada68077	Arabidops		C 766	14	24.6	1967	10	ADC10107	Adc10107	Human	NOV
C 694	14	24.6	1341	6	AB213590	Ab213590	Arabidops		C 767	14	24.6	1975	12	ADN60430	Adn60430	B. lichen	
C 695	14	24.6	1344	2	AAK97716	Aax97716	Extended		C 768	14	24.6	1982	3	AAK76997	Aac76997	Human	ORF
C 696	14	24.6	1348	8	ADP18983	Adp18983	Human	sec	C 769	14	24.6	2000	6	AB217239	Ab217239	Human	ORF
C 697	14	24.6	1350	14	ACCA3077	Acc43077	DNA	seque	C 770	14	24.6	2000	10	ACC61838	Acc61838	Gene	sequ
C 698	14	24.6	1350	14	ABE67541	Aeb67541	Rice	geno	C 771	14	24.6	2000	10	ADK63771	Adk63771	Disease	
C 699	14	24.6	1356	14	ADX84852	Adx84852	Inositol		C 772	14	24.6	2000	11	ACL83353	ACL83353	Rice	etre
C 700	14	24.6	1404	14	ADW17019	Adw17019	Pinus	rad	C 773	14	24.6	2006	2	AAV39297	Aav39297	Human	RAD
C 701	14	24.6	1409	13	ADS48336	Ad48336	Bacterial		C 774	14	24.6	2008	2	AAV39297	Aav39297	Human	RAD
C 702	14	24.6	1410	9	ADSA0863	Ad30863	DNA	enco	C 775	14	24.6	2015	13	ADP25042	Adp25042	PRO	polyp
C 703	14	24.6	1420	6	ABK93142	Abk93142	Human	pro	C 776	14	24.6	2019	13	ADSE6703	Adse6703	Bacterial	
C 704	14	24.6	1424	4	AA159915	Aa159915	Human	pol	C 777	14	24.6	2019	13	ADSE63186	Adse63186	Bacterial	
C 705	14	24.6	1428	11	ACH96011	Ach96011	Klebsleil		C 778	14	24.6	2073	8	ABT18893	Abt18893	Aspergill	
C 706	14	24.6	1443	11	ACN44279	Acn44279	Human	mrn	C 779	14	24.6	2073	8	ABT18299	Abt18299	Aspergill	
C 707	14	24.6	1448	13	ADC36341	Adc36341	Arabidops		C 780	14	24.6	2076	3	AAZ92763	Aaz92763	Bacterial	
C 708	14	24.6	1449	13	ADA48478	Ada48478	Bacterial		C 781	14	24.6	2079	13	ADSA45305	Adsa45305	Bacterial	
C 709	14	24.6	1456	13	ACN39852	Acn39852	Tumour-as		C 782	14	24.6	2109	13	ADSS95521	Adss95521	Bacterial	
C 710	14	24.6	1459	14	ADY64945	Ady64945	S. manson		C 783	14	24.6	2112	3	AAZ92760	Aaz92760	Artemista	
C 711	14	24.6	1482	6	AB232040	Ab232040	Candida	a	C 784	14	24.6	2117	11	ADM03565	Adm03565	Human	CDN
C 712	14	24.6	1512	10	ADC93615	Adc93615	E. faeciu		C 785	14	24.6	2129	2	AAV52849	Aav52849	Human	eya
C 713	14	24.6	1512	13	ADX49834	Adx49834	Plant	ful	C 786	14	24.6	2155	12	ADQ63989	Adq63989	Novel	hum
C 714	14	24.6	1515	13	ADX13348	Adx13348	Plant	ful	C 787	14	24.6	2190	13	ADX14830	Adx14830	Plant	ful
C 715	14	24.6	1515	13	ADX32889	Adx32889	Plant	ful	C 788	14	24.6	2224	4	ADD05653	Add05653	Human	sec
C 716	14	24.6	1576	4	AAH99120	Aah99120	Human	BST	C 789	14	24.6	2229	10	ADBO7555	Adbo7555	Novel	cod
C 717	14	24.6	1594	14	ADM95296	Adm95296	DNA	seque	C 790	14	24.6	2277	11	ADL72872	Adl72872	Anthrax	v
C 718	14	24.6	1622	2	AAV40299	Aav40299	Splnach	c	C 791	14	24.6	2287	11	ADL30779	Adl30779	Human	CDN
C 719	14	24.6	1627	11	ACN44501	Acn44501	Mouse	mrn	C 792	14	24.6	2287	12	ADSL82846	Adsl82846	Human	lym
C 720	14	24.6	1629	8	ACA50724	Ac50724	Prokaryot		C 793	14	24.6	2295	12	ADL22888	Adl22888	Anthrax	v
C 721	14	24.6	1632	13	ADR83814	Adr83814	S. pyogen		C 794	14	24.6	2302	2	AAK02971	Aak02971	Human	li-
C 722	14	24.6	1632	6	ABW66073	Abw66073	Streptococ		C 795	14	24.6	2324	11	ACN44265	Acn44265	Mouse	mrn
C 723	14	24.6	1642	6	ABL42394	Ab142394	Histidyl-		C 796	14	24.6	2334	2	AAK78523	Aak78523	Human	NKx
C 724	14	24.6	1649	3	AAZ92754	Aaz92754	Artemista		C 797	14	24.6	2358	12	ADP98673	Adp98673	C. albica	
C 725	14	24.6	1668	9	ACF57420	Ac57420	Saccharom		C 798	14	24.6	2375	12	ADL12363	Adl12363	Human	ste
C 726	14	24.6	1686	12	ADJ72014	Adj72014	Human	PMN	C 799	14	24.6	2382	8	ABT20713	Abt20713	Aspergill	
C 727	14	24.6	1690	13	ADR26149	Adr26149	Breast	ca	C 800	14	24.6	2382	8	ABT20115	Abt20115	Aspergill	
C 728	14	24.6	1691	14	ADM17003	Adm17003	Pinus	rad	C 801	14	24.6	2385	11	ACL27517	ACL27517	Rice	abio
C 729	14	24.6	1700	4	AAKS2564	Aak52564	Human	pol	C 802	14	24.6	2394	6	AB280664	Ab280664	Human	his
C 730	14	24.6	1734	8	ACA48422	Ac48422	Prokaryot		C 803	14	24.6	2394	6	ABQ78740	Abq78740	Nucleotid	
C 731	14	24.6	1751	2	AAV40300	Aav40300	Sugarbeet		C 804	14	24.6	2394	14	ADY86901	Ady86901	Human	his
C 732	14	24.6	1751	12	ADJ72013	Adj72013	Human	PMN	C 805	14	24.6	2406	5	AA590807	Aa590807	DNA	enco
C 733	14	24.6	1752	10	ABX06229	Abx06229	S. pneumo		C 806	14	24.6	2432	6	AA594971	Aa594971	Human	DNA
C 734	14	24.6	1755	12	ADQ00913	Adq00913	Mouse	hom	C 807	14	24.6	2471	13	ADX30447	Adx30447	Plant	ful
C 735	14	24.6	1769	13	ADX54382	Adx54382	Plant	ful	C 808	14	24.6	2506	4	AAH15133	Aah15133	Human	CDN
C 736	14	24.6	1782	12	ADL72870	Adl72870	Anthrax	v	C 809	14	24.6	2506	10	ADP76350	Adp76350	Novel	hum
C 737	14	24.6	1784	14	ADL21993	Adl21993	Murine	ca	C 810	14	24.6	2543	13	ADZ61852	Adz61852	Murine	cd
C 738	14	24.6	1786	10	ADBG1975	Adbg1975	Human	CDN	C 811	14	24.6	2559	11	ACL27684	ACL27684	Rice	abio
C 739	14	24.6	1788	12	ADL72866	Adl72866	Anthrax	v	C 812	14	24.6	2564	6	AB199414	Ab199414	Mouse	lac
C 740	14	24.6	1788	12	ADL72882	Adl72882	Anthrax	v	C 813	14	24.6	2567	4	ABL07972	Ab107972	Drosophill	
C 741	14	24.6	1793	4	AAH13752	Aah13752	Human	CDN	C 814	14	24.6	2659	12	ADN05121	Adn05121	Antipepti	
C 742	14	24.6	1830	6	ABN85310	Abn85310	Human	cyt	C 815	14	24.6	2669	12	ADQ64160	Adq64160	Novel	hum
C 743	14	24.6	1842	12	AD142997	Ad142997	Plant	tira	C 816	14	24.6	2797	4	AAH18686	Aah18686	Human	CDN
C 744	14	24.6	1842	12	ADQ62401	Adq62401	Transcrip		C 817	14	24.6	2800	11	ADQ05366	Adq05366	Human	PK2
C 745	14	24.6	1843	5	AA529563	Aa529563	Human	end	C 818	14	24.6	2800	12	ADN43272	Adn43272	Nucleotid	
C 746	14	24.6	1847	2	AAV59649	Aav59649	Human	sec	C 819	14	24.6	2804	6	ABK35928	Abk35928	CDNA	sequ
C 747	14	24.6	1847	6	AB573774	Ab573774	Human	CDN	C 820	14	24.6	3031	2	AAQ11272	Aaq11272	Prepro-po	
C 748	14	24.6	1847	6	AB573636	Ab573636	Human	CDN	C 821	14	24.6	3043	4	ABL14418	Ab114418	Drosophill	
C 749	14	24.6	1847	9	ACD82917	AcD82917	CDNA	sequ	C 822	14	24.6	3057	13	ACN39165	Acn39165	Tumour-as	



C 823	14	24.6	3074	8	ACA03947	cDNA down	C 896	14	24.6	6138	4	ABL10249	ABL10249 Drosophila
C 824	14	24.6	3075	11	AD132043	Human cDN	897	14	24.6	6183	6	ABK24357	ABK24357 DNA encod
C 825	14	24.6	3075	13	AD884110	Human lym	898	14	24.6	6183	10	ADP19269	ADP19269 Human ins
C 826	14	24.6	3076	10	AD864751	Human cDN	899	14	24.6	6183	13	ADP23962	ADP23962 PRO polyP
C 827	14	24.6	3083	2	AAV59086	Human rib	C 900	14	24.6	6310	8	ACC49518	ACC49518 Tumour-as
C 828	14	24.6	3095	4	ABL08158	Abi108158 Drosophi	C 901	14	24.6	6310	11	ADN38943	ADN38943 Cancer/an
C 829	14	24.6	3117	10	ADG32881	ADG32881 Human DNA	C 902	14	24.6	6310	12	AD031195	AD031195 Human neu
C 830	14	24.6	3117	12	ADN03734	ADN03734 Antipori	C 903	14	24.6	6349	10	AD869220	AD869220 C. neofo
C 831	14	24.6	3117	12	AD018187	AD018187 Human PRO	904	14	24.6	6628	6	AD146116	AD146116 Single st
C 832	14	24.6	3117	12	ADQ09287	ADQ09287 Human RRM	905	14	24.6	6645	12	AD127143	AD127143 Pain regu
C 833	14	24.6	3117	14	ADY14535	ADY14535 DNA encod	906	14	24.6	6648	6	ABL88419	ABL88419 Pain regu
C 834	14	24.6	3117	14	ADY14537	ADY14537 DNA encod	907	14	24.6	6840	6	ABL88419	ABL88419 Pain regu
C 835	14	24.6	3153	12	ADQ24098	ADQ24098 Human sof	908	14	24.6	6840	6	ABK84742	ABK84742 Human cDN
C 836	14	24.6	3206	4	AAFS8337	AAFS8337 Human GTP	909	14	24.6	6840	10	ADK60979	ADK60979 Overian c
C 837	14	24.6	3225	13	ADT45089	ADT45089 Bacterial	910	14	24.6	6843	2	AAH84509	AAH84509 Human LDL
C 838	14	24.6	3270	6	ABN69089	ABN69089 Streptoco	911	14	24.6	6868	10	AD102598	AD102598 Human cDN
C 839	14	24.6	3295	10	ACC78161	ACC78161 B. subtil	912	14	24.6	6868	12	AD876874	AD876874 Human cDN
C 840	14	24.6	3344	10	AD122666	AD122666 Human liv	913	14	24.6	6872	10	AD862195	AD862195 Human gen
C 841	14	24.6	3383	4	ABL24200	ABL24200 Drosophi	914	14	24.6	6872	10	AD862199	AD862199 Human gen
C 842	14	24.6	3402	6	ABN70514	ABN70514 Streptoco	915	14	24.6	6902	5	AAH98724	AAH98724 Human lat
C 843	14	24.6	3402	12	AD010472	AD010472 DNA encod	916	14	24.6	6906	8	ACC50992	ACC50992 Human bla
C 844	14	24.6	3402	14	AD202906	AD202906 Streptoco	917	14	24.6	6906	12	AD019387	AD019387 Human PRO
C 845	14	24.6	3453	13	ADU69394	ADU69394 S. agalact	918	14	24.6	6906	13	ADP54445	ADP54445 Human PRO
C 846	14	24.6	3453	13	ADV84265	ADV84265 Streptoco	919	14	24.6	6906	13	ADP23553	ADP23553 PRO polyP
C 847	14	24.6	3492	13	ADSS7783	ADSS7783 Bacterial	920	14	24.6	6906	14	ADY15093	ADY15093 DNA encod
C 848	14	24.6	3540	2	AAK06875	AAK06875 Yeast NPC	921	14	24.6	6908	10	ADL24746	ADL24746 Intestina
C 849	14	24.6	3546	6	ABN66454	ABN66454 Streptoco	922	14	24.6	6921	5	ABAI6675	ABAI6675 Human ner
C 850	14	24.6	3546	13	ADR84817	ADR84817 S. pyogen	C 923	14	24.6	6923	10	ADP81689	ADP81689 Human che
C 851	14	24.6	3601	13	ADRO6500	ADRO6500 Full leng	924	14	24.6	6961	2	AAH84508	AAH84508 Rabbit LD
C 852	14	24.6	3660	12	ADQ63479	ADQ63479 Novel hum	925	14	24.6	6981	6	ABK76520	ABK76520 cDNA enco
C 853	14	24.6	3689	8	ABK242573	ABK242573 Human his	926	14	24.6	6981	6	ABL68557	ABL68557 Kidney ca
C 854	14	24.6	3689	12	ADQ05719	ADQ05719 Human his	927	14	24.6	6981	6	ABK64741	ABK64741 Human den
C 855	14	24.6	3689	12	ADQ29967	ADQ29967 Human GPC	928	14	24.6	6981	10	ADL24745	ADL24745 Intestina
C 856	14	24.6	3822	10	ADDE60108	ADDE60108 Human gen	C 929	14	24.6	7151	6	AAH70693	AAH70693 M. sativa
C 857	14	24.6	3822	10	ADDA8729	ADDA8729 Human gen	C 930	14	24.6	7175	8	ABX13439	ABX13439 M. sativa
C 858	14	24.6	3855	10	ADCC37639	ADCC37639 Human nuc	C 931	14	24.6	7188	12	ADU71226	ADU71226 Mouse eth
C 859	14	24.6	3883	4	ABL15834	ABL15834 Drosophi	C 932	14	24.6	7188	12	ADU71220	ADU71220 Mouse eth
C 860	14	24.6	4038	11	ADQ05365	ADQ05365 Human PK2	C 933	14	24.6	7321	13	AD844424	AD844424 Aspergill
C 861	14	24.6	4038	12	ADNA43271	ADNA43271 Nucleotid	C 934	14	24.6	7374	6	ABK40035	ABK40035 Human che
C 862	14	24.6	4073	8	ABT117705	ABT117705 Aspergill	C 935	14	24.6	7374	6	ABL70601	ABL70601 Chemical
C 863	14	24.6	4148	5	AA571815	AA571815 DNA encod	936	14	24.6	7503	10	ABT31940	ABT31940 Human bre
C 864	14	24.6	4148	12	ADQ64904	ADQ64904 Novel hum	C 937	14	24.6	7503	3	AAA70206	AAA70206 Plasmodu
C 865	14	24.6	4178	12	ADQ036310	ADQ036310 Intracell	938	14	24.6	8078	4	AA542095	AA542095 Genomic s
C 866	14	24.6	4254	5	ABK71276	ABK71276 Human bra	939	14	24.6	8078	4	AA542094	AA542094 Genomic s
C 867	14	24.6	4254	12	ADN05923	ADN05923 Antipori	940	14	24.6	8078	4	AA526804	AA526804 Human gen
C 868	14	24.6	4290	3	ADP90750	ADP90750 Human hep	941	14	24.6	8078	4	AA526805	AA526805 Human gen
C 869	14	24.6	4298	3	AAZ48248	AAZ48248 Human oxi	942	14	24.6	8078	8	ABX74153	ABX74153 Human nov
C 870	14	24.6	4298	11	ADJ56287	ADJ56287 Fruit fly	943	14	24.6	8078	8	ABX74154	ABX74154 Human nov
C 871	14	24.6	4305	11	ADM66782	ADM66782 Human cDN	944	14	24.6	8125	3	AAZ29606	AAZ29606 Basic fra
C 872	14	24.6	4382	6	ABK51617	ABK51617 DNA encod	945	14	24.6	8578	2	AAK84351	AAK84351 Stealt h v
C 873	14	24.6	4382	8	ABT19519	ABT19519 Aspergill	946	14	24.6	8960	3	AAFS7929	AAFS7929 HIV-1 non
C 874	14	24.6	4382	10	ADP30404	ADP30404 Human cel	947	14	24.6	8968	3	AAFS7919	AAFS7919 HIV-1 non
C 875	14	24.6	4382	13	ADR25717	ADR25717 Breast ca	C 948	14	24.6	9126	13	ADR84349	ADR84349 Aspergill
C 876	14	24.6	4491	8	ACA30151	ACA30151 Prokaryo	949	14	24.6	9245	4	ABL10248	ABL10248 Drosophi
C 877	14	24.6	4597	2	AAV52308	AAV52308 Streptoco	950	14	24.6	9473	1	AAAN2768	AAAN2768 HIV-2 var
C 878	14	24.6	4650	12	ADQ18554	ADQ18554 Human sof	951	14	24.6	9532	6	ADT46290	ADT46290 Single st
C 879	14	24.6	4667	14	ADZ12941	ADZ12941 Murine ca	952	14	24.6	9532	10	ABZ37360	ABZ37360 MLIa3 nu
C 880	14	24.6	4712	6	ABK51618	ABK51618 DNA encod	C 953	14	24.6	9924	6	ABK77350	ABK77350 cDNA enco
C 881	14	24.6	4712	10	ADP30403	ADP30403 Human bra	954	14	24.6	10199	6	ABO71072	ABO71072 cDNA enco
C 882	14	24.6	4712	11	ADN95242	ADN95242 Human BCC	955	14	24.6	10251	10	ABZ37478	ABZ37478 Drosophi
C 883	14	24.6	4712	14	ADX44472	ADX44472 Human col	C 956	14	24.6	10497	2	AAK30048	AAK30048 Human IL-
C 884	14	24.6	4712	14	ADY33983	ADY33983 Human col	957	14	24.6	11043	12	AD019890	AD019890 Human PRO
C 885	14	24.6	4718	13	ABD32741	ABD32741 Human can	958	14	24.6	11043	13	ADP55013	ADP55013 Human PRO
C 886	14	24.6	4725	14	ACL64156	ACL64156 M. xanthu	959	14	24.6	11043	13	ADP24549	ADP24549 PRO polyP
C 887	14	24.6	4726	13	ABD32738	ABD32738 Human can	960	14	24.6	11043	13	ADY16808	ADY16808 DNA encod
C 888	14	24.6	4735	13	ABD32740	ABD32740 Human can	961	14	24.6	11122	12	ADQ23994	ADQ23994 Human sof
C 889	14	24.6	4748	5	AA594823	AA594823 Human DNA	C 962	14	24.6	11208	6	ABO69245	ABO69245 (31 o
C 890	14	24.6	4794	5	AA594071	AA594071 DNA encod	C 963	14	24.6	11617	13	ADV87698	ADV87698 Streptoco
C 891	14	24.6	4808	6	ABZ21063	ABZ21063 4fe-4S re	C 964	14	24.6	11617	13	ADV78951	ADV78951 Streptoco
C 892	14	24.6	4930	6	AAH18226	AAH18226 Human cDN	C 965	14	24.6	12586	4	AAK67076	AAK67076 Human imm
C 893	14	24.6	5520	6	ABT03038	ABT03038 Human bre	966	14	24.6	12799	4	AAK73835	AAK73835 Human imm
C 894	14	24.6	5877	10	ADP74184	ADP74184 Human nov	967	14	24.6	13499	4	ABL15566	ABL15566 Drosophi
C 895	14	24.6	5955	12	ADH22268	ADH22268 Rice PONG	C 968	14	24.6	13572	9	AAH58743	AAH58743 Human tra



C 969	1	24.6	13749	14	AEA39447	Escherich
C 970	1	24.6	13855	4	ABL15289	Dirosophi
C 971	14	24.6	13908	8	ABX16379	High grow
C 972	14	24.6	14657	14	AEA31026	Shigella
C 973	14	24.6	13328	2	ADQ81139	Adq81139
C 974	14	24.6	15390	14	AEA33353	HELA2-8-9
C 975	14	24.6	15428	4	ABK42726	Genomic s
C 976	14	24.6	16428	4	AAK81010	Human imm
C 977	14	24.6	16428	4	ADBB60882	Connectiv
C 978	14	24.6	16869	3	ABN797976	Human ret
C 979	14	24.6	16929	4	AAK72509	Human imm
C 980	14	24.6	15929	12	ADJ12871	DNA, fragm
C 981	14	24.6	16998	4	AAK67949	Human imm
C 982	14	24.6	20001	13	ACN37239	Human per
C 983	14	24.6	20001	14	ADZ59524	Secondary
C 984	14	24.6	21043	14	ADZ592383	Human gen
C 985	14	24.6	21044	14	AE832390	Human gen
C 986	14	24.6	22473	4	AAK71400	Human imm
C 987	14	24.6	22567	11	ACN445500	Mouse gen
C 988	14	24.6	22613	14	ADZ12992	Murine ca
C 989	14	24.6	22885	11	ACM44576	Adn44576
C 990	14	24.6	22916	4	AAK65305	Human imm
C 991	14	24.6	23324	4	AAI56668	Human G-C
C 992	14	24.6	24348	4	ABL15288	Drosophi
C 993	14	24.6	24333	12	ADU12497	DNA, fragm
C 994	14	24.6	24333	12	ADU12606	DNA, fragm
C 995	14	24.6	25944	11	ADL27125	Mouse gen
C 996	14	24.6	26317	9	ADA66531	Mouse IgG
C 997	14	24.6	26320	9	ADA03047	Mouse IgG
C 998	14	24.6	26320	10	ADB72785	Mouse IgG
C 999	14	24.6	27409	11	ACN44592	Mouse gen
C1000	14	24.6	28313	10	ADG36369	Human chr9

## ALIGNMENTS

RESULT 1  
 ADDR48524  
 ID ADDR48524 standard; DNA; 57 BP.  
 XX ADDR48524;  
 AC  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 DE paga target sequence #2.  
 XX  
 KW Bacillus anthracis; cutaneous; respiratory anthrax infection; paga; capB;  
 KW px01; px02; target sequence; ds.  
 XX  
 OS Bacillus anthracis.  
 XX  
 PN WO2004070001-A2.  
 XX  
 PD 19-AUG-2004.  
 XX  
 PF 12-NOV-2003; 2003WO-US036240.  
 XX  
 PR 15-NOV-2002; 2002US-0426552P.  
 PR 16-MAY-2003; 2003US-0471082P.  
 XX  
 PA (GENP-) GEN-PROBE INC.  
 XX  
 PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;  
 XX  
 WI; 2004-604428/58.  
 XX  
 PT New oligonucleotides that hybridize specifically to a Bacillus anthracis  
 PT sequence, useful for detecting cutaneous and respiratory Bacillus anthracis  
 PT infections.  
 XX  
 PS Claim 1; SEQ ID NO 22; 61pp; English.  
 XX

CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridises to a sequence contained in a *Bacillus*  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from *paga* and *capB* gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids *pXO1* and *pXO2*, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a *paga*  
CC target sequence.

Query Match	100.0%	Score 57	DB 13	Length 57
Best Local Similarity	100.0%	Pred. No.	5, 8e-21	
Matches 57	Conservative 0	Mismatches 0	Indels 0	Gaps 0

```

Oy 1 CGCAATTGATCATTTCACTATCTTAGACAGGGGAAAGAACTTGGGCTGAACATATGGG 57
Db 1 CGCAATTGATCATTTCACTATCTTAGACAGGGGAAAGAACTTGGGCTGAACATATGGG 57

```

RESULT 2  
ACC85232  
ID ACC85232 standard; DNA; 77 BP.

DT	18-SEP-2003	(first entry)
XX		
DE	Anthrax toxin protective antigen PA mutagenic primer #18	

KW Anthrax; anthrax toxin; vaccine; protective antigen; lethal factor;  
 KM oedema factor; EF; LF; PA; PCR; mutagenic; primer; antibacterial; ss

OS	Bacillus anthracis.
OS	Synthetic.

XX 12-JUN-2003 .

PF 20-MAR-2002; 2002WO-IN0000048.

PR 05-DEC-2001; 2001IN-DE001222.

PA (BHAT/) BHATNAGAR R.  
VV

PI	Bhatnagar R,	Gupta P,	Batra S,	Singh A,	Ahuja N,
PI	Kumar P,				

DR WPI; 2003-505303/47.

PT New recombinant DNA construct comprising an expression vector and a DNA fragment including genes for wild or mutant type Protective Antigen, PT lethal Factor or Edema Factor, useful for preventing or treating anthrax infection.

PS Disclosure; Page 20; 42pp; English

CC The present invention relates to a recombinant DNA construct comprising  
CC an expression vector and a DNA fragment including genes for wild type or  
CC mutant type Protective Antigen (PA), Lethal Factor (LF) or Oedema Factor  
CC (EF) from *Bacillus anthracis* anthrax toxin. The recombinant DNA construct  
CC is useful for preparing a composition for preventing or treating anthrax  
CC infection, for example in a vaccine. The present sequence is a mutagenic  
CC primer used to create a mutant part of the anthrax toxin

Sequence 77 BP; 23 A; 16 C; 20 G; 18 T; 0 U; 0 Other;

Query Match	100.0%;	Score 57;	DB 10;	Length 77;
Best Local Similarity	100.0%;	Pred. No. 5.8e-21;		



Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 57  
DB 5 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 61

## RESULT 3

AD29118  
ID AD29118 standard; DNA, 954 BP.

AC AD29118;

DT 07-MAY-2002 (first entry)

DE Bacillus subtilis protective antigen (PA) domain 1b+2 DNA.

KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;

XX Bacillus anthracis infection; antibacterial; ds.

OS Bacillus subtilis.

XX Key Location/Qualifiers

FT CDS 1..954

FT /product= "Domain 1b+2"

FT /note= "CDS does not include start and stop codon"

FT /partial

XX WO200204646-A1.

XX 17-JAN-2002.

XX 06-JUL-2001; 2001WO-GB003065.

XX 08-JUL-2000; 2000GB-00016702.

XX (MINA ) UK SEC FOR DEFENCE.

XX Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;

XX Flick-Smith HC, Bullifent HL, Tlball RM, Topping AW;

XX WPI; 2002-171720/22.

XX P-PSDB; AAE16286.

XX New immunogenic reagent having a polypeptide of the full length

PT Protective Antigen of Bacillus anthracis, useful for treating B.

PT anthracis infection or in preparing a medicament for the prophylaxis or

PT treatment of the infection.

XX Example 5; Fig 3; 40pp; English.

XX The present invention relates to an immunogenic reagent, which produces

CC an immune response that is protective against Bacillus anthracis. The

CC reagent comprises one or more polypeptides which together represent up to

CC three domains of the full length Protective Antigen (PA) of Bacillus

CC anthracis or variants of these, and at least one of the domains comprises

CC domain 1 or domain 4 of PA or its variant. The invention is used as a

CC vaccine. The immunogenic reagent is useful in the preparation of a

CC medicament for the prophylaxis or treatment of B. anthracis infection.

CC The present sequence is Bacillus subtilis protective antigen domain 1b+2

CC DNA

XX Sequence 954 BP; 351 A; 163 C; 192 G; 248 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 57; DB 6; Length 954;

XX Best Local Similarity 100.0%; Pred. No. 5.7e-21;

XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 57

DB 489 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 545

## RESULT 4

ADR48535  
ID ADR48535 standard; DNA, 1108 BP.

XX ADR48535;

XX 04-NOV-2004 (first entry)

XX pagA target sequence #5.

XX pagA target sequence #5.

XX Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;

XX px01; px02; target sequence; ds.

OS Bacillus anthracis.

XX WO2004070001-A2.

XX 19-AUG-2004.

XX 12-NOV-2003; 2003WO-US036240.

XX 15-NOV-2002; 2002US-0426552P.

XX 16-MAY-2003; 2003US-0471082P.

XX (GENP-) GEN-PROBE INC.

XX Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;

XX WPI; 2004-604428/58.

XX New oligonucleotides that hybridize specifically to a Bacillus anthracis

PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax

PT infections.

XX Claim 21; SEQ ID NO 33; 61pp; English.

XX The present invention relates to an oligonucleotide of 20-40 nucleotides

CC that specifically hybridizes to a sequence contained in a Bacillus

CC anthracis target sequence. The methods and compositions of the present

CC invention are useful for detecting the presence of Bacillus anthracis

CC nucleic acid in a sample, in particular for detecting cutaneous and

CC respiratory anthrax infections. Two synthetic genetic target sequences,

CC derived from pagA and capB gene sequences, were synthesized to provide

CC known standards for testing oligonucleotides for detection of the genes

CC carried by the plasmids px01 and px02, without requiring handling of

CC virulent Bacillus anthracis. The present sequence represents a pagA

CC target sequence.

XX Sequence 1108 BP; 409 A; 188 C; 224 G; 287 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 57; DB 13; Length 1108;

XX Best Local Similarity 100.0%; Pred. No. 5.7e-21;

XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 57

DB 494 CGCAATTGATCATCTATCTCTAGCGAGGAAAGAACTTGGCTGAACAATGGG 550

## RESULT 5

ADL16358  
ID ADL16358 standard; DNA, 1272 BP.

XX ADL16358;

XX 06-MAY-2004 (first entry)

XX pBP113 vector DNA for expression of 47kDa PA deletion mutant (PA47).

XX Immunogenic; vaccine; lethal infection; protective antigen; PA;

XX lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.



```

OS Bacillus anthracis.
OS Synthetic.
FH Key Location/Qualifiers
FT CDS 1..1272
FT /*tag= a
FT /product= "PA deletion mutant protein (PA47)"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168665/16.
XX P-PSDB; ADL16359.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 23; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is pBR13 vector DNA for the
XX expression of Bacillus anthracis 47 Kda N-terminal PA deletion mutant
XX (PA47). This sequence is used in the invention.
XX
XX Sequence 1272 BP; 507 A; 172 C; 238 G; 355 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 57; DB 12; Length 1272;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 60 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 116

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FT FT /note= "CDS does not include start and stop codon"
FT FT /partial
XX
XX WO200204646-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-GB003065.
XX
XX 08-JUL-2000; 2000GB-00016702.
XX
XX (MINA ) UK SEC FOR DEFENCE.
XX
XX Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
XX Flick-Smith HC, Bullifent HL, Tibball RW, Topping AW;
XX
XX WPI; 2002-171720/22.
XX P-PSDB; AAE18287.
XX
XX New immunogenic reagent having a polypeptide of the full length
XX protective antigen of Bacillus anthracis, useful for treating B
XX anthracis infection or in preparing a medicament for the prophylaxis or
XX treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
XX an immune response that is protective against Bacillus anthracis. The
XX reagent comprises one or more polypeptides which together represent up to
XX three domains of the full length Protective Antigen (PA) of Bacillus
XX anthracis or variants of these, and at least one of the domains comprises
XX domain 1 or domain 4 of PA or its variant. The invention is used as a
XX vaccine. The immunogenic reagent is useful in the preparation of a
XX medicament for the prophylaxis or treatment of B. anthracis infection.
XX The present sequence is Bacillus subtilis protective antigen domain
XX 1b+2+3 DNA
SQ
Sequence 1278 BP; 489 A; 210 C; 245 G; 334 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 6; Length 1278;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 100; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 489 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 545

```

```

RESULT 6
AAB29119
ID AAB29119 standard; DNA; 1278 BP.
XX
XX AAB29119;
XX
XX 07-MAY-2002 (first entry)
XX
XX Bacillus subtilis protective antigen (PA) domain 1b+2+3 DNA.
XX
XX Immunogenic reagent; immune response; protective antigen; PA; vaccine;
XX Bacillus anthracis infection; antibacterial; ds.
XX
XX Bacillus subtilis.
XX
XX Key Location/Qualifiers
XX CDS 1..1278
XX /*tag= a
XX /product= "Domain 1b+2+3"

```

```

RESULT 7
AEB63722
ID AEB63722 standard; DNA; 1281 BP.
XX
XX AEB63722;
XX
XX 06-OCT-2005 (first entry)
XX
XX DNA encoding anthrax protective antigen domain D1b23.
XX
XX Antigen; bacillus anthracis infection; antibacterial; vaccine;
XX protective antigen; PA; ds.
XX
XX Bacillus anthracis.
XX
XX WO2005068493-A1.
XX
XX 28-JUL-2005.
XX
XX 17-JAN-2005; 2005WO-GB000170.
XX
XX 17-JAN-2004; 2004GB-00001036.
XX
XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.

```



PI Cutting SM;  
XX  
XX WPI; 2005-563956/57.  
PT New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
XX Claim 5; SEQ ID NO 10; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus baduui; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen domain D1b23.  
XX  
SQ Sequence 1281 BP; 492 A; 210 C; 244 G; 335 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 14; Length 1281;  
Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTGGGCTGAACAATGGG 57  
DB 495 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTGGGCTGAACAATGGG 551  
RESULT 8  
AAD29117  
ID AAD29117 standard; DNA; 1461 BP.  
XX  
XX AAD29117;  
AC  
XX  
DT 07-MAY-2002 (first entry)  
XX  
DE Bacillus subtilis protective antigen (PA) domain 1-2 DNA.  
XX  
KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;  
KW Bacillus anthracis infection; antibacterial; ds.  
XX  
OS Bacillus subtilis.  
XX  
XX Key Location/Qualifiers  
FH 1..1461  
FT CDS  
FT /tag= a  
FT /product= "Domain 1+2"  
FT /note= "CDS does not include start and stop codon"  
FT /partial  
XX  
XX WO200204646-A1.  
XX  
XX 17-JAN-2002.

PF 06-JUL-2001; 2001WO-GB003065.  
XX  
XX 08-JUL-2000; 2000GB-00016702.  
XX  
XX (M1NA ) UK SEC FOR DEFENCE.  
XX  
XX  
PI Williamson ED, Miller J, Walker NJ, Baillie LMW, Holden PT;  
PI Flick-Smith HC, Bullifent HL, Titball RW, Topping AW;  
XX  
XX WPI; 2002-171720/22.  
DR P-PSDB; AAE18285.  
XX  
XX New immunogenic reagent having a polypeptide of the full length  
PT Protective Antigen of Bacillus anthracis, useful for treating B  
PT anthracis infection or in preparing a medicament for the prophylaxis or  
PT treatment of the infection.  
XX  
XX Example 5; Fig 3; 40pp; English.  
XX  
XX The present invention relates to an immunogenic reagent, which produces  
CC an immune response that is protective against Bacillus anthracis. The  
CC reagent comprises one or more polypeptides which together represent up to  
CC three domains of the full length Protective Antigen (PA) of Bacillus  
CC anthracis or variants of these, and at least one of the domains comprises  
CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
CC vaccine. The immunogenic reagent is useful in the preparation of a  
CC medicament for the prophylaxis or treatment of B. anthracis infection.  
CC The present sequence is Bacillus subtilis protective antigen domain 1+2  
CC DNA  
XX  
SQ Sequence 1461 BP; 548 A; 238 C; 280 G; 395 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 6; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTGGGCTGAACAATGGG 57  
DB 996 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTGGGCTGAACAATGGG 1052  
RESULT 9  
ADZ51325  
ID ADZ51325 standard; DNA; 1704 BP.  
XX  
XX ADZ51325;  
AC  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Nucleotide sequence of a PA63 gene fragment.  
XX  
KW protective antigen protein; PA63; PA83; antibacterial; vaccine;  
KW prophylactic immunization; anthrax infection; gene; ds.  
XX  
OS Bacillus anthracis.  
XX  
XX Key Location/Qualifiers  
FH 1..1704  
FT CDS  
FT /tag= a  
FT /partial  
FT /product= "PA63 fragment"  
FT /transl\_except= (pos:475..477, aa:Xaa)  
FT /note= "Xaa represents Asn, Phe, Ile, Gly"  
XX  
XX WO2005034841-A2.  
XX  
XX 21-APR-2005.  
XX  
XX 13-MAY-2004; 2004WO-US014971.  
XX  
XX 14-MAY-2003; 2003US-0470563P.  
XX  
XX (MERI ) MERCK & CO INC.



XX Hepler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L;  
XX WPI; 2005-306231/31.  
DR P-PSDB; ADZ51326.  
XX Producing recombinant Bacillus anthracis protective antigen protein  
PT encoded by an expression vector having a nucleotide sequence being codon-  
PT optimized for expression in yeast, useful for manufacturing anthrax  
PT vaccines.  
XX  
XX  
PS Example 1; SEQ ID NO 47; 91pp; English.  
CC The specification describes a method for producing recombinant Bacillus  
CC anthracis protective antigen protein. The method comprises providing an  
CC expression vector having a polynucleotide encoding a Bacillus anthracis  
CC protective antigen protein which is codon-optimized for expression in  
CC yeast, transforming a yeast with the vector, fermenting the transformed  
CC yeast for the expression of the protein, and isolating the protein. The  
CC protective antigen protein is PA63 or PA63. The method of the invention  
CC is useful for the produce of antigen protein, which is used for  
CC prophylactic immunization against anthrax infections. The present  
CC sequence encodes a PA63 fragment.  
SQ Sequence 1704 BP; 663 A; 248 C; 328 G; 465 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 14; Length 1704;  
Best Local Similarity 100.0%; Pred. No. 5,7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CGCAATTGATCATTCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57  
DB 495 CGCAATTGATCATTCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 551  
RESULT 10  
AEB63720  
ID AEB63720 standard; DNA; 1707 BP.  
XX  
AC AEB63720;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE DNA encoding anthrax protective antigen PA63.  
XX  
KW Antigen; bacillus anthracis infection; antibacterial; vaccine;  
KM protective antigen; PA; ds.  
XX  
XX  
OS Bacillus anthracis.  
XX  
PN WO2005068493-A1.  
XX  
PD 28-JUL-2005.  
XX  
PF 17-JAN-2005; 2005WO-GB000170.  
XX  
PR 17-JAN-2004; 2004GB-00001036.  
XX  
PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX  
PI Cutting SM;  
XX  
DR WPI; 2005-563956/57.  
XX  
PT New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
PS Disclosure; SEQ ID NO 8; 90pp; English.  
XX  
CC The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising

CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus badui; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA63 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen PA63.  
SQ Sequence 1707 BP; 665 A; 248 C; 327 G; 467 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 14; Length 1707;  
Best Local Similarity 100.0%; Pred. No. 5,7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 CGCAATTGATCATTCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57  
DB 495 CGCAATTGATCATTCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 551  
RESULT 11  
AAZ56877  
ID AAZ56877 standard; DNA; 1710 BP.  
XX  
AC AAZ56877;  
XX  
DT 25-APR-2000 (first entry)  
XX  
DE B. anthracis PA63 protein encoding DNA.  
XX  
KW Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
XX  
OS Bacillus anthracis.  
XX  
PN Key Location/Qualifiers  
FH 1. 1710  
FT CDS /tag= a  
FT /product= "MAT-PA protein"  
XX  
XX WO200002522-A2.  
XX  
PD 20-JAN-2000.  
XX  
PF 09-JUL-1999; 99WO-US015568.  
XX  
PR 10-JUL-1998; 98US-0092416P.  
XX  
PA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
PI Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX WPI; 2000-182165/16.  
DR P-PSDB; AAY56961.  
XX  
PT Recombinant DNA construct useful as vaccines for anthrax, in producing  
PT host cells for analyzing the drugs and agents inhibiting anthrax.  
XX  
PS Disclosure; Page 35; 35pp; English.



```
XX CC The invention provides a recombinant DNA construct that comprises a
CC vector and at least one nucleic acid (or its fragment) encoding a
CC combination of Bacillus anthracis proteins, selected from protective
CC antigen (PA), MA-PA (PA with its secretory signals removed), rPA-PA (PA
CC with its secretory signals replaced with those of tissue plasminogen
CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine
CC for anthrax and in producing infectious alpha virus particles. These
CC particles, expressing the B. anthracis proteins are useful also as
CC vaccines for anthrax. Host cells transformed with the construct are
CC useful for analyzing the effectiveness of drugs and agents that inhibit
CC anthrax or B. anthracis proteins. The present sequence represents a B.
CC anthracis PA63 protein encoding DNA
XX
SQ Sequence 1710 BP; 666 A; 248 C; 329 G; 467 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 3; Length 1710;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGCAATTGATCATCTACTATCTTACGAGGGGAAAGAACTTGCGCTGAACATGCG 57
Db 498 CGCAATTGATCATCTACTATCTTACGAGGGGAAAGAACTTGCGCTGAACATGCG 554
RESULT 12
ADL16356
ID ADL16356 standard; DNA; 1722 BP.
XX
AC ADL16356;
XX
DT 06-MAY-2004 (first entry)
XX
DS pBP111 vector DNA for expression of 64kDa PA deletion mutant (PA64).
XX
KW Immunogenic; vaccine; lethal infection; protective antigen; PA;
KW lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.
XX
OS Bacillus anthracis.
XX
FH Key Location/Qualifiers
FT 1..1722
FT CDS /tag= a
FT /product= "PA deletion mutant protein (PA64)"
FT /partial
FT /note= "No start codon"
XX
PN US2004028695-A1.
XX
PD 12-FEB-2004.
XX
PF 28-MAR-2003; 2003US-00402466.
XX
PR 12-APR-2002; 2002US-0372152P.
XX
PA (PARK/) PARK S.
PA (GIRI/) GIRI L.
PI Park S, Girl L;
XX
XX WPI: 2004-168865/16.
XX P-PSDB; ADL16357.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 21; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
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CC an animal. The compositions comprise an immunising amount of a
CC recombinant B. anthracis protective antigen (rPA) protein and a
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and
CC methods are useful in protecting against anthrax or lethal infections
CC caused by B. anthracis. The present sequence is pBP111 vector DNA for the
CC expression of Bacillus anthracis 64kDa N-terminal PA deletion mutant
CC (PA64). This sequence is used in the invention.
XX
SQ Sequence 1722 BP; 673 A; 251 C; 330 G; 468 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 12; Length 1722;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 CGCAATTGATCATCTACTATCTTACGAGGGGAAAGAACTTGCGCTGAACATGCG 57
Db 510 CGCAATTGATCATCTACTATCTTACGAGGGGAAAGAACTTGCGCTGAACATGCG 566
RESULT 13
AAD29120
ID AAD29120 standard; DNA; 1785 BP.
XX
AC AAD29120;
XX
DT 07-MAY-2002 (first entry)
XX
DS Bacillus subtilis protective antigen (PA) domain 1+2+3 DNA.
XX
KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT 1..1785
FT CDS /tag= a
FT /product= "Domain 1+2+3"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
PN WO200204646-A1.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-GB003065.
XX
PR 08-JUL-2000; 2000GB-00016702.
XX
PA (MINA ) UK SEC FOR DEFENCE.
XX
PA Williamson BD, Miller J, Walker ND, Baillie LMJ, Holden PT;
PI Flick-Smith HC, Bullifent HL, Tiddall RW, Topping AW;
XX
XX WPI: 2002-171720/22.
XX P-PSDB; AAE18288.
XX
XX New immunogenic reagent having a polypeptide of the full length
XX Protective Antigen of Bacillus anthracis, useful for treating B.
XX anthracis infection or in preparing a medicament for the prophylaxis or
XX treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
XX an immune response that is protective against Bacillus anthracis. The
XX reagent comprises one or more polypeptides which together represent up to
XX three domains of the full length Protective Antigen (PA) of Bacillus
XX anthracis or variants of these, and at least one of the domains comprises
XX domain 1 or domain 4 of PA or its variant. The invention is used as a
XX vaccine. The immunogenic reagent is useful in the preparation of a
XX medicament for the prophylaxis or treatment of B. anthracis infection.
XX The present sequence is Bacillus subtilis protective antigen domain 1+2+3
```



CC DNA  
 XX Sequence 1785 BP; 686 A; 285 C; 333 G; 481 T; 0 U; 0 Other;  
 SQ Query Match 100.0%; Score 57; DB 6; Length 1785;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 57  
 Db CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 1052

RESULT 14  
 AAQ70189 standard; DNA; 2160 BP.  
 ID AAQ70189  
 XX AAQ70189;  
 AC  
 XX 25-MAR-2003 (revised)  
 DT 04-APR-1995 (first entry)  
 XX  
 XX Sequence encoding modified protective antigen of *Bacillus anthracis*.  
 DE Anthrax; *Bacillus anthracis*; fusion protein; lethal factor;  
 XX protective antigen; cell killing; targeting; targeting; pathogen;  
 KM intracellular; HIV; human immunodeficiency virus; toxin; ss.  
 XX  
 OS *Bacillus anthracis*.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..2160  
 FT /\*tag= a  
 FT CDS /product= "Modified anthrax protective antigen."  
 XX  
 XX MO9418332-AZ.  
 XX  
 XX 18-AUG-1994.  
 PD  
 XX 14-FEB-1994; 94WO-US001624.  
 PF  
 XX 12-FEB-1993; 93US-00021601.  
 XX 25-JUN-1993; 93US-00082849.  
 PR  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 PI Lep1a SH, Klimpel K, Arora N, Singh Y, Nichols PJ;  
 XX MPI: 1994-279753/34.  
 DR P-PSDB; AAR60193.  
 XX  
 XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
 PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
 PT infected cells.  
 PT  
 XX Example 6; Page 111-113; 124pp; English.

The sequence encoding the protective antigen of *Bacillus anthracis* may be used in the construction of a nucleic acid which encodes a fusion protein comprising the anthrax protective antigen binding domain of the native anthrax lethal factor and a sequence encoding an actively inducing domain of a second protein. Such fusion proteins are useful for the specific killing of tumour cells or the killing of cells infected with intracellular pathogens, especially HIV, depending on the second component. The protective antigen and other toxins require proteolytic cleavage to acquire activity. Since some cells infected with an intracellular pathogen possess an active protease with quite a narrow substrate specificity e.g. HIV, the protease cleavage site found in the native toxin is replaced with an intracellular pathogen specific protease site (See AAR60184-88). The protease in cells that are infected with an intracellular pathogen cleaves the modified toxin which is then rendered active and kills the cell. This sequence encodes the *Bacillus anthracis* protective antigen but the nucleotides originally at positions 482-523

CC have been replaced with the cassette described in AAQ70186, resulting in  
 CC replacement in the corresponding protein of amino acids 162-171 with the  
 CC HIV protease cleavable sequence described in AAR60186. (Updated on 25-MAR  
 CC -2003 to correct FN field.)  
 XX  
 SQ Sequence 2160 BP; 828 A; 321 C; 408 G; 603 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 57; DB 2; Length 2160;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 57  
 Db CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 1064

RESULT 15  
 ADZ51331 standard; DNA; 2205 BP.  
 ID ADZ51331  
 XX ADZ51331;  
 AC  
 XX 30-JUN-2005 (first entry)  
 DT  
 XX  
 XX Nucleotide sequence of a PA83 gene fragment.  
 DE  
 XX protective antigen protein; PA63; PA83; antibacterial; vaccine;  
 KM prophylactic immunization; anthrax infection; ss.  
 XX  
 OS *Bacillus anthracis*.  
 XX  
 XX WO2005034841-AZ.  
 XX  
 XX 21-APR-2005.  
 PD  
 XX 13-MAY-2004; 2004WO-US014971.  
 PF  
 XX 14-MAY-2003; 2003US-0470563P.  
 PR  
 XX (MERI ) MERCK & CO INC.  
 PA  
 PI Hepler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L;  
 XX MPI: 2005-306231/31.  
 DR P-PSDB; ADZ51332.  
 XX  
 XX Producing recombinant *Bacillus anthracis* Protective Antigen protein  
 PT encoded by an expression vector having a nucleotide sequence being codon-  
 PT optimized for expression in yeast, useful for manufacturing anthrax  
 PT vaccines.  
 XX  
 XX Example 6; SEQ ID NO 53; 91pp; English.

The specification describes a method for producing recombinant *Bacillus anthracis* protective antigen protein. The method comprises providing an expression vector having a polynucleotide encoding a *Bacillus anthracis* protective antigen protein which is codon-optimized for expression in yeast, transforming a yeast with the vector, fermenting the transformed yeast for the expression of the protein, and isolating the protein. The protective antigen protein is PA63 or PA83. The method of the invention is useful for the production of antigen protein, which is used for prophylactic immunization against anthrax infections. The present sequence encodes a PA83 fragment.

CC  
 XX Sequence 2205 BP; 857 A; 322 C; 415 G; 611 T; 0 U; 0 Other;  
 SQ  
 Query Match 100.0%; Score 57; DB 14; Length 2205;  
 Best Local Similarity 100.0%; Pred. No. 5,7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 57  
 Db CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 1052



```

RESULT 16
AAD29121 ID AAD29121 standard; DNA; 2208 BP.
XX
AC AAD29121;
XX
DE 07-MAY-2002 (first entry)
XX
DE Bacillus subtilis protective antigen (PA) domain 1+2+3+4 DNA.
XX
KM Immunogenic reagent; immune response; protective antigen; PA; vaccine;
XX Bacillus anthracis infection; antibacterial; ds.
XX
OS Bacillus subtilis.
XX
FH Key Location/Qualifiers
FT CDS 1..2208
FT /tag= a
FT /product= "Domain 1+2+3+4"
FT /transl_except= (pos:853..855, aa:Gln)
FT /note= "CDS does not include start codon"
FT /partial
XX
PN WO200204646-A1.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-GB003065.
XX
PR 08-JUL-2000; 2000GB-00016702.
XX
PA (MINA ) UK SEC FOR DEFENCE.
XX
PI Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
PI Flick-Smith HC, Bullifent HL, Tibball RM, Topping AM;
XX
DR WPI; 2002-171720/22.
XX
DR P-PSDB; AAE18289.
XX
PT New immunogenic reagent having a polypeptide of the full length
PT Protective Antigen of Bacillus anthracis, useful for treating B
PT anthracis infection or in preparing a medicament for the prophylaxis or
PT treatment of the infection.
XX
PS Example 5; Fig 3; 40pp; English.
XX
CC The present invention relates to an immunogenic reagent, which produces
CC an immune response that is protective against Bacillus anthracis. The
CC reagent comprises one or more polypeptides which together represent up to
CC three domains of the full length Protective Antigen (PA) of Bacillus
CC anthracis or variants of these, and at least one of the domains comprises
CC domain 1 or domain 4 of PA or its variant. The invention is used as a
CC vaccine. The immunogenic reagent is useful in the preparation of a
CC medicament for the prophylaxis or treatment of B. anthracis infection.
CC The present sequence is Bacillus subtilis protective antigen domain
CC 1+2+3+4 DNA
XX
SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACATGGG 57
DB 996 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACATGGG 1052
XX
RESULT 17
AAI99904 ID AAI99904 standard; DNA; 2208 BP.

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```

XX
AC AAI99904;
XX
DT 01-FEB-2002 (first entry)
XX
DE Anthrax PA encoding polynucleotide.
XX
KM Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;
XX B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; ds.
XX
OS Bacillus anthracis.
XX
FH Key Location/Qualifiers
FT CDS 1..2211
FT /tag= a
FT /product= "PA"
XX
PN WO200182788-A2.
XX
PD 08-NOV-2001.
XX
PF 04-MAY-2001; 2001WO-US014372.
XX
PR 04-MAY-2000; 2000US-0201800P.
XX
PA (HARD ) HARVARD COLLEGE.
XX
PI Collier RJ, Sellman BR;
XX
DR WPI; 2002-017725/02.
XX
DR P-PSDB; AAM51483.
XX
PT Protecting humans against anthrax using mutant B groups (anthrax
PT protective antigens) of the pore-forming binary A-B toxin of Bacillus
PT anthracis.
XX
PS Disclosure; Fig 14; 77pp; English.
XX
CC The invention relates to antibacterial agents comprising mutant forms of
CC pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants
CC in the B moiety of the pore-forming binary A-B anthrax toxin, where the B
CC moiety is anthrax protective antigen (PA) and using these mutants or
CC compositions of them for protecting against Bacillus anthracis infections
CC in humans, especially as vaccines. The present sequence is that of the
CC anthrax PA encoding DNA
XX
SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACATGGG 57
DB 996 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACATGGG 1052
XX
RESULT 18
ADL16343 ID ADL16343 standard; DNA; 2208 BP.
XX
AC ADL16343;
XX
DT 06-MAY-2004 (first entry)
XX
DE Bacillus anthracis wild-type rPA DNA #1.
XX
KM Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
OS Bacillus anthracis.
XX
FH Key Location/Qualifiers

```



```

FT CDS 1..2208
FT /*tag= a
FT /product= "rPA protein"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16344.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 8; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis wild-
XX type rPA DNA used in the invention.
XX
XX Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 57; DB 12; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-21;
XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CGCAATTGATTCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
XX 996 CGCAATTGATTCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052
XX
XX RESULT 19
XX ADL16346
XX ID ADL16346 standard; DNA; 2208 BP.
XX
XX ADL16346;
XX
XX 06-MAY-2004 (first entry)
XX
XX Bacillus anthracis PA DNA from pBP105 vector.
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1..2208
XX /*tag= a
XX /product= "PA protein"
XX /partial
XX /note= "No start codon"
XX
XX US2004028695-A1.
XX

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PD 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16348.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 11; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis PA DNA
XX from pBP105 vector used in the invention.
XX
XX Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 57; DB 12; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 5.7e-21;
XX Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 CGCAATTGATTCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
XX 996 CGCAATTGATTCATCTACTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052
XX
XX RESULT 20
XX ADM05484
XX ID ADM05484 standard; DNA; 2208 BP.
XX
XX ADM05484;
XX
XX 07-APR-2005 (first entry)
XX
XX B. anthracis wild-type protective antigen, DNA.
XX
XX Protein engineering; Bacillus anthracis infection; protective antigen;
XX toxin; bacterial infection; vaccine; antibacterial; ds; gene.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1..2208
XX /*tag= a
XX /product= "Protective antigen"
XX /partial
XX /note= "No start codon shown"
XX
XX WO2005004791-A2.
XX
XX 20-JAN-2005.
XX
XX 10-NOV-2003; 2003WO-US035733.
XX
XX 08-NOV-2002; 2002US-0424987P.
XX
XX (HARD ) HARVARD COLLEGE.
XX (UYOK-) UNIV OKLAHOMA.
XX

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```
XX Collier RJ, Ballard JD, Tweten R, Mourez M;
PI WPI; 2005-091963/10.
XX P-PSDB; ADM05483.
DR
XX New B moiety of pore-forming binary A-B toxin or its fragment, where the
PT moiety has a mutation that inhibits its pore-forming ability, useful for
PT preventing or treating bacterial infection, e.g. anthrax.
XX
XX Disclosure; SEQ ID NO 22; 129pp; English.
XX
XX The invention relates to a B moiety of pore-forming binary A-B toxin or
CC its fragment, where the moiety has a mutation that inhibits its pore-
CC forming ability and is selected from S382, N399, and N422 of the Bacillus
CC anthracis protective antigen (PA) appearing as ADM05483. Also included
CC are a vaccine composition comprising the mutant B moiety or its fragment
CC (and a carrier), preventing or treating a bacterial infection in a mammal
CC by administering the vaccine to the mammal, a nucleic acid encoding the
CC mutant B moiety, a vector comprising the nucleic acid and a purified
CC antibody that specifically binds a B moiety, but fails to bind a
CC naturally occurring B moiety. The B moiety is selected from Clostridium
CC difficile, C. perfringens, C. spiriforme, C. botulinum, and Bacillus
CC cereus. The mutation inhibits the pore-forming ability of the toxin in
CC vivo. The B moiety and vaccine composition are useful for preventing or
CC treating a bacterial infection, e.g. anthrax. The present sequence
CC encodes the wild-type PA protein.
XX
SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 14; Length 2208;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57
Db 996 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1052
RESULT 21
AEB63729 100.0%; Score 57; DB 14; Length 2208;
ID AEB63729 standard; DNA; 2208 BP.
XX
AC AEB63729;
XX
DT 06-OCT-2005 (first entry)
XX
DE DNA encoding anthrax protective antigen, PA83.
XX
KM Antigen; bacillus anthracis infection; antibacterial; vaccine;
KM protective antigen; PA; ds; gene.
XX
XX Bacillus anthracis.
XX OS
XX WO2005068493-A1.
XX PN
XX 28-JUL-2005.
XX PD
XX 17-JAN-2005; 2005WO-GB000170.
XX PF
XX 17-JAN-2004; 2004GB-00001036.
XX PR
XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.
XX PA
XX Cutting SM;
XX P1
XX WPI; 2005-563956/57.
XX DR
XX New non-pathogenic spore comprising an antigenic fragment of anthrax
PT protective antigen, useful as an anthrax vaccine or for manufacturing an
PT anthrax vaccine.
XX
XX Disclosure; SEQ ID NO 17; 90pp; English.
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XX The present invention relates to a non-pathogenic spore comprising an
CC antigenic fragment of anthrax protective antigen. Also given is a
CC pharmaceutical composition comprising a non-pathogenic spore comprising
CC at least an antigenic fragment of anthrax protective antigen in
CC association with a pharmaceutical carrier and/or excipient, and methods
CC of inducing immunity to anthrax in a mammal susceptible to anthrax
CC infection. The Bacillus species spore is a spore from many species such
CC as Bacillus alvei; Bacillus badus; Bacillus brevis and preferably a
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment
CC of anthrax protective antigen in the form of a protein attached to the
CC proteinaceous coat of the spore. It comprises an antigenic fragment of
CC anthrax protective antigen encoded in the form of DNA which is adapted to
CC be expressed when the spore germinates. The antigenic fragment is one or
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23
CC which is a sequence of SEQ ID NO: 10. The composition further comprises
CC an adjuvant that potentiates an antigen-specific immune response. The
CC composition (including the spore) is useful as an anthrax vaccine or for
CC manufacturing an anthrax vaccine. The composition and method are used for
CC inducing an immune response against anthrax. The present sequence is DNA
CC encoding anthrax protective antigen, PA83.
XX
SQ Sequence 2208 BP; 859 A; 321 C; 414 G; 614 T; 0 U; 0 Other;
Query Match 100.0%; Score 57; DB 14; Length 2208;
Best Local Similarity 100.0%; Pred. No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 CGCAATTGATCATTCATCTTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 57
Db 996 CGCAATTGATCATTCATCTTAGCAGGGGAAAGAACTTGCGCTGAACAATGGG 1052
RESULT 22
AA256875 100.0%; Score 57; DB 14; Length 2208;
ID AA256875 standard; DNA; 2211 BP.
XX
AC AA256875;
XX
DT 25-APR-2000 (first entry)
XX
DE B. anthracis MAT-PA protein encoding DNA.
XX
KM Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;
KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.
XX
XX Bacillus anthracis.
XX OS
XX Key Location/Qualifiers
XX FT 1..2211
XX FT /*tag= a
XX FT /product= "MAT-PA protein"
XX CDS
XX WO200002522-A2.
XX PN
XX 20-JAN-2000.
XX PD
XX 09-JUL-1999; 99WO-US015568.
XX PF
XX 10-JUL-1998; 98US-0092416P.
XX PR
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PA
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;
XX WPI; 2000-182165/16.
XX DR
XX P-PSDB; AAY56959.
XX
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PT Recombinant DNA construct useful as vaccines for anthrax, in producing  
host cells for analyzing the drugs and agents inhibiting anthrax.

XX Diaclosure; Page 34; 35pp; English.

XX The invention provides a recombinant DNA construct that comprises a  
vector and at least one nucleic acid (or its fragment) encoding a  
combination of Bacillus anthracis proteins, selected from protective  
antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
with its secretory signals replaced with those of tissue plasminogen  
activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
for anthrax and in producing infectious alpha virus particles. These  
particles, expressing the B. anthracis proteins are useful also as  
vaccines for anthrax. Host cells transformed with the construct are  
useful for analyzing the effectiveness of drugs and agents that inhibit  
anthrax or B. anthracis proteins. The present sequence represents a B.  
anthracis MAT-PA protein encoding DNA

CC Sequence 2211 BP; 860 A; 322 C; 416 G; 613 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 57; DB 3; Length 2211;

CC Best Local Similarity 100.0%; Pred. No. 5.7e-21;

CC Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATTCATCTCTAGCAGGGAAGAACTTGAGCTGAACAATGGG 57

DB 999 CGCAATTGATCATTCATCTCTAGCAGGGAAGAACTTGAGCTGAACAATGGG 1055

RESULT 23

ID ADV84835 standard; DNA; 2211 BP.

AC ADV84835;

DT 02-JUN-2005 (first entry)

DE Bacillus anthracis protective antigen coding sequence.

KW Bacillus anthracis infection; vaccine; antibacterial; protective antigen;

KW gene; ds.

OS Bacillus anthracis.

PH Key Location/Qualifiers

FT CDS 1..2211

FT /tag= a

FT /product= "Protective antigen"

PN MO2005026203-A2.

PD 24-MAR-2005.

PF 20-SEP-2004; 2004MO-US030616.

PR 18-SEP-2003; 2003US-0504504P.

PR 18-SEP-2003; 2003US-0504505P.

XX (USNA ) US SEC OF NAVY.

PI Kopecko DJ, Osorio M, Bhattacharyya S, Giri CP, Blake M;

XX WPI; 2005-233481/24.

XX New attenuated bacterium capable of expressing a heterologous protein,

XX which is under the control of a promoter, useful as a vaccine against

XX Bacillus anthracis infection, or for treating Bacillus anthracis

XX infection.

XX Claim 10; SEQ ID NO 9; 83pp; English.

XX The invention provides an attenuated bacterium which is capable of

XX expressing a heterologous protein. The expression of the heterologous

CC protein is under the control of a promoter selected from 8 fully defined

CC sequences ADV84827-ADV84834. The attenuated bacterium is preferably

CC *Salmonella typhi* or *Salmonella typhimurium*. The heterologous protein

CC comprises an antigenic sequence derived from a virus, bacterium, fungus,

CC yeast or parasite, and is especially a protective antigen (PA) of

CC *Bacillus anthracis*. A claimed live attenuated vaccine for immunization

CC against anthrax comprises an attenuated galactose epimerase-less mutant

CC strain of *S. typhi* (e.g. strain Ty21a) carrying a *Bacillus anthracis* PA,

CC especially a wild-type PA or its immunogenic fragment. The PA is

CC preferably encoded by a low-copy plasmid such as pGB2. The plasmid

CC promotes expression of the PA by a *htrB* promoter or by a *Sec* signal

CC sequence. The vaccine is used in a claimed method of immunizing a

CC susceptible host against *B. anthracis* disease. The present sequence is

CC the *B. anthracis* PA coding sequence (wild-type).

CC Sequence 2211 BP; 860 A; 323 C; 415 G; 613 T; 0 U; 0 Other;

CC Query Match 100.0%; Score 57; DB 14; Length 2211;

CC Best Local Similarity 100.0%; Pred. No. 5.7e-21;

CC Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATTCATCTCTAGCAGGGAAGAACTTGAGCTGAACAATGGG 57

DB 999 CGCAATTGATCATTCATCTCTAGCAGGGAAGAACTTGAGCTGAACAATGGG 1055

RESULT 24

ID ADV96726 standard; DNA; 2220 BP.

AC ADV96726;

DT 24-FEB-2005 (first entry)

DE Gene of the invention SEQ ID NO:12.

KW antineoplastic; chemotherapy; toxin; tumor; cytostatic; ds; gene.

OS Unidentified.

PH Key Location/Qualifiers

FT CDS 1..2220

FT /tag= a

PN CN1513878-A.

PD 21-JUL-2004.

PF 13-JUN-2003; 2003CN-00143142.

PR 13-JUN-2003; 2003CN-00143142.

XX (MIUJ/) MI J.

XX M1 J;

XX WPI; 2004-710658/70.

XX P-PSDB; ADV96725.

XX Antitumor medicine containing recombination bacterial toxin protein

XX complex substance.

XX Claim 2; SEQ ID NO 12; 29pp; Chinese.

XX The invention relates to a novel antineoplastic medicine containing the

XX recombinant bacteriotoxin protein composition IPCB whose key components

XX are recombinant proteins IP33 and IP14. Under the action of a particular

XX enzyme generated by tumor cells, the non-toxic protein can be changed

XX into toxic protein to directly kill tumor cells specifically. The present

XX sequence encodes a protein of the invention.

XX Sequence 2220 BP; 860 A; 326 C; 419 G; 615 T; 0 U; 0 Other;



Query Match 100.0%; Score 57; DB 13; Length 2220;  
Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 1008 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 1064

RESULT 25  
ADRA40459  
ID ADRA40459 standard; DNA; 2235 BP.  
XX  
XX ADRA40459;  
AC  
XX 18-NOV-2004 (first entry)  
DT  
XX  
XX Bacillus anthracis protective antigen double mutant DNA seqid 3.  
DB  
XX  
XX antibacterial; vaccine; protective antigen; PA; proteolytic degradation;  
KW B.anthraxis toxin; B.anthraxis infection; passive immunisation;  
KW inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;  
KW gene; ds.  
XX  
XX Bacillus anthracis.  
OS Synthetic.  
XX  
XX  
XX Key Location/Qualifiers  
FH CDS 88..2235  
FT /\*tag= a  
FT /product= "Bacillus anthracis protective antigen double  
FT mutant"

XX US2004171121-A1.  
XX  
XX  
XX 02-SEP-2004.  
XX  
XX  
XX 08-AUG-2003; 2003US-00638006.  
XX  
XX  
XX 09-AUG-2002; 2002US-0402285P.  
XX  
XX  
XX (LEPP/) LEPP/PA S H.  
XX (ROSO/) ROSOVITZ M J.  
XX (HSUS/) HSU S D.  
XX  
XX Lepp/PA SH, Rosovitz MJ, Hsu SD;  
XX  
XX WPI; 2004-625107/60.  
XX P-PSDB; ADRA40457.  
XX  
XX Novel Bacillus anthracis protective antigen having mutations conferring  
PT enhanced resistance to proteolytic degradation compared to wild type  
PT antigen, useful for inducing antibodies having neutralizing activity  
PT anthrax toxin.  
XX  
XX Example 5; SEQ ID NO 3; 30pp; English.

XX The invention describes a recombinant Bacillus anthracis protective  
CC antigen (PA), modified to incorporate one or more mutations comprising an  
CC amino acid deletion or substitution in a flexible, exposed, or loop  
CC segment of the PA protein, where the one or more mutations confers  
CC enhanced resistance to proteolytic degradation compared to wild type PA.  
CC A pharmaceutical composition (I) comprising PA and physiologically  
CC acceptable carrier or a composition (II) comprising a synthetic construct  
CC encoding PA and a carrier is useful for inducing serum antibodies that  
CC have neutralising activity for a B.anthraxis toxin which involves  
CC administering (I) to a mammal (human), sufficient to elicit production of  
CC the antibodies. The antibodies protect the mammal against the infection.  
CC (I) is useful for vaccinating a human against B.anthraxis infection. An  
CC anti-PA-antibody containing composition is useful for passively  
CC immunising a mammal against the toxic effect of B.anthraxis. PA is useful  
CC as vaccines to induce serum antibodies which are useful to prevent, treat  
CC or reduced the severity of infections caused by B.anthraxis, such as

CC inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA  
CC exhibits enhanced stability to proteolytic degradation that is increased  
CC by at least 25% compared to proteolytic stability of wild-type PA under  
CC comparable conditions. This sequence encodes an exemplary double  
CC protective antigen (PA) mutant comprising deletion of residues 162-167  
CC and residues 304-317 and substitutions S168I and S319G.

SQ Sequence 2235 BP; 873 A; 325 C; 416 G; 621 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 13; Length 2235;  
Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 1023 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 1079

RESULT 26  
AAZ56876  
ID AAZ56876 standard; DNA; 2292 BP.  
XX  
XX  
XX AAZ56876;  
AC  
XX  
XX 25-APR-2000 (first entry)  
DT  
XX  
XX B. anthracis TPA-PA protein encoding DNA.  
DB  
XX  
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
XX Bacillus anthracis.  
OS  
XX  
XX Key Location/Qualifiers  
FH CDS 1..2292  
FT /\*tag= a  
FT /product= "TPA-PA protein"

XX WO200002522-A2.  
XX  
XX  
XX 20-JAN-2000.  
XX  
XX  
XX 09-JUL-1999; 99WO-US015568.  
XX  
XX  
XX 10-JUL-1998; 98US-0092416P.  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX  
XX WPI; 2000-182165/16.  
XX P-PSDB; AAY56960.  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
PT host cells for analyzing the drugs and agents inhibiting anthrax.  
PT  
XX  
XX Disclosure; Page 32; 35pp; English.

XX The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis TPA-PA protein encoding DNA

SQ Sequence 2292 BP; 874 A; 337 C; 446 G; 635 T; 0 U; 0 Other;



Query Match 100.0%; Score 57; DB 3; Length 2295;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 57  
 DB 1080 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 1136

# RESULT 27

AAZ56874  
 ID AAZ56874 standard; DNA; 2295 BP.

XX AAZ56874;

DT 25-APR-2000 (first entry)

DE B. anthracis protective antigen (PA) protein encoding DNA.

XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
 KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; de.  
 XX

OS Bacillus anthracis.

XX Key Location/Qualifiers

FT CDS 1..2295  
 /tag= a  
 /product= "PA protein"

FT WO200002522-A2.

XX 20-JAN-2000.

XX 09-JUL-1999; 99WO-US015568.

XX 10-JUL-1998; 98US-0092416P.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos LJ;  
 PI WPI; 2000-182165/16.  
 DR P-PSDB; AAY56958.

XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
 PT host cells for analyzing the drugs and agents inhibiting anthrax.

XX Disclosure; Page 33; 35pp; English.

XX The invention provides a recombinant DNA construct that comprises a  
 CC vector and at least one nucleic acid (or its fragment) encoding a  
 CC combination of Bacillus anthracis proteins, selected from protective  
 CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
 CC with its secretory signals replaced with those of tissue plasminogen  
 CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
 CC for anthrax and in producing infectious alpha virus particles. These  
 CC particles, expressing the B. anthracis proteins are useful also as  
 CC vaccines for anthrax. Host cells transformed with the construct are  
 CC useful for analyzing the effectiveness of drugs and agents that inhibit  
 CC anthrax or B. anthracis proteins. The present sequence represents a B.  
 CC anthracis PA protein encoding DNA

XX Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 57; DB 3; Length 2295;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 57  
 DB 1083 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 1139

RESULT 28  
 AAC66016  
 ID AAC66016 standard; CDNA; 2295 BP.

XX AAC66016;

DT 29-AUG-2001 (first entry)

DE Wild type B. anthracis protective antigen coding sequence.

XX Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine;  
 KW humoral; cell-mediated; immune memory response; ss.  
 XX

OS Bacillus anthracis.

XX Key Location/Qualifiers

FT sig\_peptide 1..87  
 /tag= a

FT mat\_peptide 88..2295  
 /tag= b

FT misc\_RNA 610..2295  
 /product= "PA"

FT /tag= c  
 /product= "Encodes PCPA peptide"

FT WO200145639-A2.

XX 28-JUN-2001.

XX 21-DEC-2000; 2000WO-US034912.

XX 22-DEC-1999; 99US-0171459P.

XX (OHIS ) UNITV OHIO STATE RES FOUND.  
 PA (GALL/) GALLOWAY D R.  
 PA (MATE/) MATECZUN A J.

XX Galloway DR, Mateczun AJ;  
 PI Galloway DR, Mateczun AJ;

XX WPI; 2001-408540/43.  
 DR P-PSDB; AAB47306.

XX Protecting animal against lethal infection with Bacillus anthracis, by  
 PT administering wildtype or mutated form of Bacillus anthracis lethal  
 PT factor protein or its fragment or a nucleic acid encoding the mutated  
 PT protein.

XX Claim 25; Fig 2; 33pp; English.

XX This sequence encodes the B. anthracis protective antigen (PA). An  
 CC immunogenic fragment of PA, PCPA, can be used to produce an immune  
 CC response which protects an animal against lethal infection with Bacillus  
 CC anthracis. DNA encoding the B. anthracis PA can be used in conjunction  
 CC with DNA encoding the lethal factor (LF) in a DNA vaccine. Using a DNA  
 CC vaccine which encodes the mutated LF protein or fragment alone or in  
 CC combination with a DNA encoding the PA protein or its fragment, both  
 CC components (humoral and cell-mediated) of the immune system are  
 CC stimulated, which results in longer term immune memory response. The  
 CC combined use of a mutated LF and PA gene or their fragments results in a  
 CC higher level of immune response, as judged by overall serum antibody in  
 CC titers for LF and PA antigens, than the use of either LF or PA genes in  
 CC separate immunizations

XX Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 57; DB 4; Length 2295;  
 Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
 Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 57  
 DB 1083 CGCAATTGATTCATCTCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGCG 1139



```
RESULT 29
ADM29247
ID ADM29247 standard; DNA; 2295 BP.
XX
XX AC ADM29247;
XX
XX DT 24-MAR-2005 (first entry)
XX
DE B. anthracis DNA encoding protective antigen, PA.
XX
XX KW Protective antigen; bacillus anthracis infection; vaccine; infection; ds;
XX KW antibacterial.
XX
XX OS Bacillus anthracis.
XX
XX FH Key Location/Qualifiers
XX CDS 1..2295
XX /*tag= a
XX /*product= "Protective antigen"
XX
XX MO200500884-A1.
XX
XX PD 06-JAN-2005.
XX
XX PF 04-JUN-2004; 2004MO-US017736.
XX
XX PR 05-JUN-2003; 2003US-0476598P.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Schneerson R, Leprie S, Robbins JB, Shiloach J, Kuhlner-Kielb J;
XX PI Liu D, Majadly F;
XX DR WPI; 2005-066555/07.
XX DR P-PSDB; ADM29248.
XX
XX PT Immunogenic conjugate, useful for inhibiting or treating infection and/or
XX PT disease caused by Bacillus anthracis or other bacilli, comprises Bacillus
XX PT capsular poly-gamma-glutamic acid polypeptide covalently linked to
XX PT carrier.
XX
XX PS Diaclosure; SEQ ID NO 2; 66pp; English.
XX
XX CC The invention relates to an immunogenic conjugate comprising a Bacillus
XX CC capsular poly-gamma-glutamic acid (gammaPGA) polypeptide covalently
XX CC linked to a carrier, where the conjugate elicits an immune response in a
XX CC subject. Also included are a composition comprising the conjugate and a
XX CC pharmaceutical acceptable carrier (for use in eliciting an immune
XX CC response against Bacillus antigenic epitope, preferably Bacillus
XX CC anthracis antigenic epitope in a subject) and an isolated antibody that
XX CC binds to the Bacillus capsular gammaPGA polypeptide (that recognizes
XX CC antigenic epitopes on both the Bacillus capsular gammaPGA polypeptide ,
XX CC or that binds Bacillus anthracis capsular gammaDPGA). The carrier may
XX CC comprise recombinant B. anthracis protective antigen. The composition and
XX CC conjugate are useful for eliciting an immune response against a Bacillus
XX CC antigenic epitope in a subject and for inhibiting or treating infection
XX CC and/or disease caused by B. anthracis or other bacilli. The immune
XX CC response comprises opsonophagocytic activity. The composition is useful
XX CC for active immunization for preventing B. anthracis infections and for
XX CC preparation of immune antibodies. The present sequence encodes Bacillus
XX CC anthracis protective antigen, PA.
XX
XX SQ Sequence 2295 BP; 892 A; 334 C; 432 G; 637 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 5,7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 30
AEB63728
ID AEB63728 standard; DNA; 2295 BP.
XX
XX AC AEB63728;
XX
XX DT 06-OCT-2005 (first entry)
XX
DE DNA encoding full length anthrax protective antigen, PA83.
XX
XX KW Antigen; bacillus anthracis infection; antibacterial; vaccine;
XX KW protective antigen; PA; ds; gene.
XX
XX OS Bacillus anthracis.
XX
XX PN MO2005068493-A1.
XX
XX PD 28-JUL-2005.
XX
XX PF 17-JAN-2005; 2005WO-GB000170.
XX
XX PR 17-JAN-2004; 2004GB-00001036.
XX
XX PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.
XX
XX PI Cutting SM;
XX PI WPI; 2005-563956/57.
XX
XX PT New non-pathogenic spore comprising an antigenic fragment of anthrax
XX PT protective antigen, useful as an anthrax vaccine or for manufacturing an
XX PT anthrax vaccine.
XX
XX PS Claim 5; SEQ ID NO 16; 90pp; English.
XX
XX CC The present invention relates to a non-pathogenic spore comprising an
XX CC antigenic fragment of anthrax protective antigen. Also given is a
XX CC pharmaceutical composition comprising a non-pathogenic spore comprising
XX CC at least an antigenic fragment of anthrax protective antigen in
XX CC association with a pharmaceutical carrier and/or excipient; and methods
XX CC of inducing immunity to anthrax in a mammal susceptible to anthrax
XX CC infection. The Bacillus species spore is a spore from many species such
XX CC as Bacillus alvei; Bacillus baduus; Bacillus brevis and preferably a
XX CC spore from Bacillus subtilis. The spore comprises an antigenic fragment
XX CC of anthrax protective antigen in the form of a protein attached to the
XX CC proteinaceous coat of the spore. It comprises an antigenic fragment of
XX CC anthrax protective antigen encoded in the form of DNA which is adapted to
XX CC be expressed when the spore germinates. The antigenic fragment is one or
XX CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which
XX CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen
XX CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen
XX CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen
XX CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the
XX CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23
XX CC which is a sequence of SEQ ID NO: 10. The composition further comprises
XX CC an adjuvant that potentiates an antigen-specific immune response. The
XX CC composition (including the spore) is useful as an anthrax vaccine or for
XX CC manufacturing an anthrax vaccine. The composition and method are used for
XX CC inducing an immune response against anthrax. The present sequence is DNA
XX CC encoding full length anthrax protective antigen, PA83.
XX
XX SQ Sequence 2295 BP; 892 A; 332 C; 432 G; 639 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 5,7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



```

RESULT 31
ADBE5871
ID ADBE5871 standard; DNA; 2605 BP.
XX
AC ADBE5871;
XX
DT 29-JAN-2004 (first entry)
XX
DE Bacillus anthracis PA antigen encoding sequence.
XX
KM Antibacterial; Vaccine; immune response; Bacillus anthracis; ds.
XX
OS Bacillus anthracis.
XX
FH Key Location/Qualifiers
FT CDS 3..2600
FT /tag= a
XX
PN WO2003087378-A1.
XX
PD 23-OCT-2003.
XX
PF 11-APR-2003; 2003WO-GB001553.
XX
PR 11-APR-2002; 2002US-0371416P.
XX
PA (POMD-) POWDERJECT RES LTD.
XX
PI Schmaljohn C, Fuller J;
XX
DR WPI; 2003-877105/81.
XX
DR P-PSDB; ADBE5872.
XX
PT New polynucleotide vaccine composition comprising a nucleic acid sequence
PT that encodes a Bacillus anthracis antigen, useful for eliciting a
PT protective immune response against Bacillus anthracis.
XX
PS Example 1; SEQ ID NO 3; 65pp; English.
XX
CC The present invention relates to a new polynucleotide vaccine composition
CC comprising a nucleic acid sequence that encodes a Bacillus anthracis
CC antigen and that is operatively linked to a promoter suitable for
CC expression of the antigen in a mammalian cell. The polynucleotide vaccine
CC composition is useful for eliciting a protective immune response against
CC Bacillus anthracis. The present sequence represents Bacillus anthracis PA
CC antigen encoding sequence.
XX
SQ Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 10; Length 2605;
Best Local Similarity 100.0%; Pred No. 5.7e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 CGCAATGATCACTTCTCTAGCAGGAGGAGAAAGAACTTGGCTGAAACAATGGG 57
DB 1256 CGCAATGATCACTTCTCTAGCAGGAGGAGAAAGAACTTGGCTGAAACAATGGG 1312
XX
RESULT 32
ABE20797
ID AEB20797 standard; DNA; 2605 BP.
XX
AC AEB20797;
XX
DT 08-SEP-2005 (first entry)
XX
DE Bacillus anthracis Protective Antigen (PA) gene, SEQ ID NO:3.
XX
KM Nucleic acid vaccine; Bacillus anthracis infection; Protective Antigen;
KM gene; ds.
XX
OS Bacillus anthracis.
XX

```

```

FH Key Location/Qualifiers
FT CDS 3..2603
FT /tag= a
FT /partial
FT /product= "Translated sequence shown in Fig 1A-O"
FT /note= "No start or stop codon given. Xaa corresponds to
FT in-frame stop codon"
FT /transl_except= (pos:15..17,aa:Xaa)
FT /transl_except= (pos:63..65,aa:Xaa)
FT /transl_except= (pos:81..83,aa:Xaa)
FT /transl_except= (pos:141..143,aa:Xaa)
FT /transl_except= (pos:147..149,aa:Xaa)
FT /transl_except= (pos:2466..2468,aa:Xaa)
FT /transl_except= (pos:2481..2483,aa:Xaa)
FT /transl_except= (pos:2556..2558,aa:Xaa)
FT /transl_except= (pos:2568..2570,aa:Xaa)
FT /transl_except= (pos:2586..2588,aa:Xaa)
FT /transl_except= (pos:2598..2600,aa:Xaa)
FT /transl_except= (pos:2604..2605,aa:Pro)
FT 174..2468
FT /tag= c
FT /product= "Bacillus anthracis Protective Antigen"
FT 174..245
FT /tag= b
FT mat_peptide 246..2465
FT /tag= d
FT /product= "Mature Protective Antigen"
XX
PN US2005148529-A1.
XX
PD 07-JUL-2005.
XX
PF 05-JAN-2004; 2004US-00751103.
XX
PR 05-JAN-2004; 2004US-00751103.
XX
PA (POMD-) POWDERJECT VACCINES INC.
XX
PI Schmaljohn CS, Fuller JT;
XX
DR WPI; 2005-478100/48.
XX
DR P-PSDB; AEB20798; AEB20803.
XX
PT New polynucleotide vaccine composition comprising a nucleic acid sequence
PT that encodes a Bacillus anthracis antigen, useful for eliciting an immune
PT response against B. anthracis in a subject.
XX
PS Example 1; SEQ ID NO 3; 40pp; English.
XX
CC The invention relates to a polynucleotide vaccine composition comprising
CC a Bacillus anthracis antigen-encoding nucleic acid which is operatively
CC linked to a promoter for expression of the antigen in a mammalian cell.
CC The invention also relates to use of the vaccine composition of the
CC invention for eliciting an immune response in an individual. Preferably,
CC the antigen encoded by the polynucleotide vaccine is obtained or derived
CC from the Bacillus anthracis Protective Antigen (PA), a non-toxic factor
CC responsible for binding to cell membranes which is known to confer active
CC protection against anthrax. The encoded Bacillus anthracis antigen may
CC also be linked to a leader signal peptide (such as the tissue plasminogen
CC activator (TPA) signal peptide) which permits its secretion. The vaccine
CC composition may additionally comprise an adjuvant component such as a CpG
CC sequence, a nucleic acid encoding a polypeptide adjuvant, a lipid, a non-
CC protein hormone or a vitamin. The polynucleotide vaccine composition of
CC the invention can be administered directly into skin or muscle tissue,
CC preferably in particulate form, and is useful for inducing a protective
CC immune response against Bacillus anthracis infection. The present
CC sequence represents the complete nucleotide sequence encoding the
CC Bacillus anthracis Protective Antigen, used in the construction of a
CC Bacillus anthracis polynucleotide vaccine in an example of the invention.
XX
SQ Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 57; DB 14; Length 2605;

```



Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 57  
DB 1256 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 1312

## RESULT 33

AAQ70184  
ID AAQ70184 standard; DNA; 2709 BP.

XX AAQ70184;

DT 25-MAR-2003 (revised)  
DT 04-APR-1995 (first entry)

DE PA(1-725)-----Human CD4 fusion protein coding sequence.

XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;  
KW protective antigen; cell killing; targeting; pathogen;  
KW intracellular; HIV; human immunodeficiency virus; toxin; Pseudomonas;  
KW exotoxin; ss.

OS Bacillus anthracis.  
XX Homo sapiens.

XX Key Location/Qualifiers  
FH 1. 2709  
FT CDS /\*tag= a  
FT /product= "Anthrax fusion protein."

XX W09418332-A2.

XX 18-AUG-1994.

XX 14-FEB-1994; 94MO-US001624.

XX 12-FEB-1993; 93US-00021601.  
XX 25-JUN-1993; 93US-00082849.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Leppla SH, Klimpel K, Arora N, Singh Y, Nichols PJ;

DR WPI; 1994-279753/34.

DR P-PSDB; AAR60183.

XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
XX infected cells.

PS Disclosure; Page 97-100; 124pp; English.

XX This sequence encodes a fusion protein comprising amino acid residues 1-  
CC 725 of the anthrax protective antigen protein and a sequence encoding  
CC residues 1-178 of human CD4, the portion which binds to gp120 on HIV  
CC infected cells. Such fusion proteins may be useful for the specific  
CC killing of tumour cells or the killing of cells infected with  
CC intracellular pathogens, especially HIV, depending on their components.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 2709 BP; 1006 A; 444 C; 551 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 2; Length 2709;

Best Local Similarity 100.0%; Pred. No. 5.7e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 57  
DB 996 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 1052

## RESULT 34

AAQ70180  
ID AAQ70180 standard; DNA; 4235 BP.

XX AAQ70180;

DT 25-MAR-2003 (revised)  
DT 03-APR-1995 (first entry)

DE Sequence encoding protective antigen of Bacillus anthracis.

XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;  
KW protective antigen; cell killing; targeting; pathogen;  
KW intracellular; HIV; human immunodeficiency virus; toxin; ss.

OS Bacillus anthracis.

XX Key Location/Qualifiers  
FH 1891. 4098  
FT CDS /\*tag= a  
FT /product= "Anthrax protective antigen."

XX W09418332-A2.

XX 18-AUG-1994.

XX 14-FEB-1994; 94MO-US001624.

XX 12-FEB-1993; 93US-00021601.  
XX 25-JUN-1993; 93US-00082849.

XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.

PI Leppla SH, Klimpel K, Arora N, Singh Y, Nichols PJ;

DR WPI; 1994-279753/34.

DR P-PSDB; AAR60179.

XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
XX infected cells.

PS Disclosure; Page 78-81; 124pp; English.

XX The sequence encoding the protective antigen of Bacillus anthracis may be  
CC used in the construction of a nucleic acid which encodes a fusion protein  
CC comprising the anthrax protective antigen binding domain of the native  
CC anthrax lethal factor and a sequence encoding an activity inducing domain  
CC of a second protein. The fusion proteins are useful for the specific  
CC killing of tumour cells or the killing of cells infected with  
CC intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to  
CC correct PN field.)

XX Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;

Query Match 100.0%; Score 57; DB 2; Length 4235;

Best Local Similarity 100.0%; Pred. No. 5.6e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 57  
DB 2886 CGCAATTGATCATCTATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGCG 2942

## RESULT 35

ACF58207  
ID ACF58207 standard; DNA; 4235 BP.

XX ACF58207;

DT 12-FEB-2004 (first entry)

XX B. anthracis protective antigen (PA) encoding DNA.



```
XX Molecular modeling; antibacterial; protozoacide; fungicide; vaccine;
KM protective antigen; PA; gene; ds.
XX Bacillus anthracis.
OS WO2003087129-A2.
XX
XX
XX 23-OCT-2003.
XX
XX 08-APR-2003; 2003WO-US010851.
XX
XX 08-APR-2002; 2002US-0371250P.
XX 08-APR-2002; 2002US-0371256P.
XX 17-APR-2002; 2002US-0373668P.
XX
XX (PLEX-) PLEXUS VACCINE INC.
XX
XX Katritch V, Borthner A, Deans RJ, Sumner M;
XX
XX MPI; 2003-853938/79.
XX P-PSDB; ABR39189.
XX
XX Identifying immunogenic peptides representative of a structural element
PT of a target protein comprising detecting an epitope corresponding to the
PT molecular model of the three dimensional structure of the epitope in the
PT target protein.
XX
XX Example 1; Page 106-108; Opp: English.
XX
XX The invention relates to identifying an immunogenic peptide
CC representative of a structural element of a target protein. The method
CC involves detecting in a molecular model of a chimeric polypeptide
CC comprising a selected epitope linked to a scaffold protein, an epitope
CC having a three dimensional conformation corresponding to the molecular
CC model of the three dimensional structure of the epitope in the target
CC protein. The methods of the invention are useful for identifying
CC immunogenic peptides of a target protein having a known three dimensional
CC structure, or of a target protein having a known amino acid sequence but
CC unknown three dimensional structure. The immunogenic peptides are useful
CC as vaccines for stimulating an immune response in a subject against
CC infectious microorganisms including protozoan (Entamoeba histolytica),
CC yeast (Candida albicans) or bacterium (Shigella flexneri, Yersinia
CC pestis, Serratia marcescens or Bacillus anthracis). The present sequence
CC represents a B. anthracis protective antigen (PA) DNA (Genbank Accession
CC No. 143380), where the antigen can be used as a target protein
XX
XX Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 57; DB 10; Length 4235;
Best Local Similarity 100.0%; Pred. No. 5.6e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCAATTGATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 57
DB 2886 CGCAATTGATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 2942
RESULT 36
ADL72868
ID ADL72868 standard; DNA; 4235 BP.
XX
XX ADL72868;
AC
XX
XX 17-JUN-2004 (first entry)
DT
XX
XX Anthrax vaccine polynucleotide SEQ ID NO: 3.
DE
XX
XX ds; gene; anthrax; vaccine; antibacterial; codon optimised.
KM
XX
XX Bacillus anthracis.
OS
XX
XX WO2004024067-A2.
PN
```

```
XX
XX 25-MAR-2004.
PD
XX
XX 10-SEP-2003; 2003WO-US028199.
XX
XX 10-SEP-2002; 2002US-0409307P.
XX 18-OCT-2002; 2002US-0419089P.
XX
XX (VICA-) VICAL INC.
XX
XX Hermanson GG;
XX
XX MPI; 2004-269870/25.
XX P-PSDB; ADL72869.
XX
XX Novel isolated codon-optimized polynucleotide encoding Bacillus anthracis
PT protective antigen, useful for creating anthrax infections in vertebrate.
XX
XX Example 1; Page 205-209; 288pp; English.
XX
XX The present invention relates to codon-optimised versions of the Bacillus
CC anthracis protective antigen coding sequence, and vectors containing such
CC sequences. These can be used in vaccines to protect vertebrates against
CC anthrax infection. The present sequence is a polynucleotide of the
CC invention.
XX
XX Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 57; DB 12; Length 4235;
Best Local Similarity 100.0%; Pred. No. 5.6e-21;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 CGCAATTGATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 57
DB 2886 CGCAATTGATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACAATGGG 2942
RESULT 37
ADL16342
ID ADL16342 standard; DNA; 8198 BP.
XX
XX ADL16342;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX pBp103 expression vector DNA for expression of rPA.
DE
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; ds.
XX
XX Unidentified.
OS
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 26-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
PI
XX
XX MPI; 2004-168865/16.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
PT infection of Bacillus anthracis in an animal, comprises an immunizing
PT amount of a recombinant B. anthracis protective antigen protein and/or
PT lethal factor protein.
XX
XX Disclosure; SEQ ID NO 7; 143pp; English.
XX
XX
```



XX The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is pBP103 expression vector  
CC DNA for the expression of rPA used in the invention.  
XX

SQ Sequence 8198 BP; 2786 A; 1349 C; 1776 G; 2287 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 12; Length 8198;  
Best Local Similarity 100.0%; Pred. No. 5.6e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGGCTGAACATGGG 57  
DB 4730 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGGCTGAACATGGG 4786

RESULT 38  
ADL16345  
XX ADL16345 standard; DNA; 9286 BP.  
XX  
XX ADL16345;  
XX  
XX 06-MAY-2004 (first entry)  
XX  
XX pBP105 expression vector DNA for expression of rPA and LF30.  
XX  
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;  
XX lethal factor; LF; anthrax; antibacterial; gene; ds.  
XX  
XX *Bacillus anthracis*.  
XX  
XX unidentified.  
XX  
XX  
XX Key Location/Qualifiers  
XX CDS 3735..5942  
XX /tag= a  
XX /product= "LF30 protein"  
XX /partial  
XX /note= "No start codon"  
XX 6391..7161  
XX /tag= b  
XX /product= "rPA protein"  
XX /partial  
XX /note= "No start codon"  
XX  
XX  
XX US2004028695-A1.  
XX  
XX 12-FEB-2004.  
XX  
XX 28-MAR-2003; 2003US-00402466.  
XX  
XX 12-APR-2002; 2002US-0372152P.  
XX  
XX (PARK/) PARK S.  
XX (GIRI/) GIRI L.  
XX  
XX Park S, Girl L;  
XX  
XX WPI; 2004-168865/16.  
XX P-PSDB; ADL16339; ADL16344.  
XX  
XX Immunogenic composition for preparing a vaccine against a lethal  
XX infection of *Bacillus anthracis* in an animal, comprises an immunizing  
XX amount of a recombinant B. anthracis protective antigen protein and/or  
XX lethal factor protein.  
XX  
XX Disclosure; SEQ ID NO 10; 143bp; English.  
XX  
XX The present invention relates to immunogenic compositions useful for

CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is pBP105 expression vector  
CC DNA for the expression of *Bacillus anthracis* rPA and LF30 used in the  
CC invention.  
XX

SQ Sequence 9286 BP; 3228 A; 1474 C; 1973 G; 2611 T; 0 U; 0 Other;  
Query Match 100.0%; Score 57; DB 12; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 5.6e-21;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGGCTGAACATGGG 57  
DB 4730 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACTTGGCTGAACATGGG 4786

RESULT 39  
ACC85231  
XX ACC85231 standard; DNA; 59 BP.  
XX  
XX ACC85231;  
XX  
XX 18-SEP-2003 (first entry)  
XX  
XX Anthrax toxin protective antigen PA mutagenic primer #17.  
XX  
XX Anthrax; anthrax toxin; vaccine; protective antigen; lethal factor;  
XX oedema factor; EF; LF; PA; PCR; mutagenic; primer; antibacterial; ss.  
XX  
XX *Bacillus anthracis*.  
XX  
XX Synthetic.  
XX  
XX WO2003048390-A1.  
XX  
XX 12-JUN-2003.  
XX  
XX 20-MAR-2002; 2002WO-IN000048.  
XX  
XX 05-DEC-2001; 2001IN-DE001222.  
XX  
XX (BHAT/) BHATNAGAR R.  
XX  
XX Bhattacharjee R, Gupta P, Batra S, Chauhan V, Singh A, Ahuja N;  
XX Kumar P;  
XX  
XX WPI; 2003-505303/47.  
XX  
XX  
XX New recombinant DNA construct comprising an expression vector and a DNA  
XX fragment including genes for wild or mutant type Protective Antigen,  
XX Lethal Factor or Edema Factor, useful for preventing or treating anthrax  
XX infection.  
XX  
XX Disclosure; Page 19; 42pp; English.  
XX  
XX  
XX The present invention relates to a recombinant DNA construct comprising  
XX an expression vector and a DNA fragment including genes for wild type or  
XX mutant type Protective Antigen (PA), Lethal Factor (LF) or Oedema Factor  
XX (EF) from *Bacillus anthracis* anthrax toxin. The recombinant DNA construct  
XX is useful for preparing a composition for preventing or treating anthrax  
XX infection, for example in a vaccine. The present sequence is a mutagenic  
XX primer used to create a mutant part of the anthrax toxin  
XX  
XX  
XX Sequence 59 BP; 18 A; 13 C; 15 G; 13 T; 0 U; 0 Other;  
XX

OY 1 CGCAATTGATCATTCATCTATCTTAGCAGGGGAAAGAACT 40  
Query Match 70.2%; Score 40; DB 10; Length 59;  
Best Local Similarity 100.0%; Pred. No. 9.8e-12;  
Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Db 5 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAGAACT 44

## RESULT 40

ACC85233 standard; DNA; 77 BP.

AC 85233;

DT 18-SEP-2003 (first entry)

DE Anthrax toxin protective antigen PA mutagenic primer #19.

KW Anthrax; anthrax toxin; vaccine; protective antigen; lethal factor;  
oedema factor; EF; LF; PA; PCR; mutagenic; primer; antibacterial; ss.

OS Bacillus anthracis.  
Synthetic.

PN WO2003048390-A1.

PD 12-JUN-2003.

PF 20-MAR-2002; 2002WO-IN000048.

PR 05-DEC-2001; 2001IN-DE001222.

PA (BHAT/) BHATTNAGAR R.

PI Bhatnagar R, Gupta P, Batra S, Chauhan V, Singh A, Ahuja N;  
Kumar P;

DR WPI; 2003-505303/47.

PT New recombinant DNA construct comprising an expression vector and a DNA  
fragment including genes for wild or mutant type Protective Antigen,  
lethal factor or Edema Factor, useful for preventing or treating anthrax  
infection.

PS Disclosure; Page 20; 42pp; English.

CC The present invention relates to a recombinant DNA construct comprising  
an expression vector and a DNA fragment including genes for wild type or  
mutant type Protective Antigen (PA), lethal factor (LF) or Oedema Factor  
(EF) from Bacillus anthracis anthrax toxin. The recombinant DNA construct  
is useful for preparing a composition for preventing or treating anthrax  
infection, for example in a vaccine. The present sequence is a mutagenic  
primer used to create a mutant part of the anthrax toxin

Sequence 77 BP; 22 A; 18 C; 21 G; 16 T; 0 U; 0 Other;

Query Match 70.2%; Score 40; DB 10; Length 77;

Best Local Similarity 100.0%; Pred. No. 9.7e-12;

Matches 40; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAGAACT 40  
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DB 5 CGCAATTGATCATCTACTCTCTAGCAGGGGAAAGAACT 44

Search completed: April 11, 2006, 16:26:55  
Job time : 96.4164 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 04:34:31 ; Search time 154.397 Seconds

(without alignments)  
3052.864 Million cell updates/sec

Title: US-10-712-654-22

Perfect score: 57

Sequence: 1 cgcacatgacatcaccatc.....actggctgaacaatg99 57

Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

Word size : 1

Total number of hits satisfying chosen parameters: 19584538

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA Main:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	57	100.0	693	6 US-10-442-502-13	Sequence 13, Appl
2	57	100.0	954	7 US-10-332-282-8	Sequence 8, Appl
3	57	100.0	1272	7 US-10-402-466A-23	Sequence 20, Appl
4	57	100.0	1278	6 US-10-332-282-10	Sequence 10, Appl
5	57	100.0	1461	6 US-10-332-282-6	Sequence 6, Appl
6	57	100.0	1710	6 US-10-442-502-4	Sequence 4, Appl
7	57	100.0	1722	7 US-10-402-466A-21	Sequence 21, Appl
8	57	100.0	1785	6 US-10-332-282-12	Sequence 12, Appl
9	57	100.0	2208	6 US-09-848-909-22	Sequence 22, Appl
10	57	100.0	2208	6 US-10-332-282-14	Sequence 14, Appl
11	57	100.0	2208	7 US-10-402-466A-8	Sequence 8, Appl
12	57	100.0	2208	7 US-10-402-466A-11	Sequence 11, Appl
13	57	100.0	2211	6 US-10-442-502-2	Sequence 2, Appl
14	57	100.0	2235	7 US-10-638-006-3	Sequence 3, Appl
15	57	100.0	2292	6 US-10-442-502-3	Sequence 3, Appl
16	57	100.0	2295	6 US-09-747-521-3	Sequence 3, Appl
17	57	100.0	2295	5 US-10-106-014-3	Sequence 3, Appl
18	57	100.0	2295	5 US-10-105-695-3	Sequence 3, Appl
19	57	100.0	2295	5 US-10-105-694-3	Sequence 3, Appl
20	57	100.0	2295	6 US-10-442-502-1	Sequence 1, Appl
21	57	100.0	2605	6 US-10-751-103-3	Sequence 3, Appl
22	57	100.0	4235	6 US-10-410-647-29	Sequence 29, Appl
23	57	100.0	8198	7 US-10-402-466A-7	Sequence 7, Appl

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38	18	31.6	1305	9 US-10-450-763-6904	Sequence 6904, Ap
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41	17	29.8	510	9 US-10-779-543-20120	Sequence 20120, A
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44	17	29.8	2676	9 US-10-450-763-3425	Sequence 3425, Ap
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66	16	28.1	484	3 US-09-918-995-13497	Sequence 13497, A
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C 100	16	28.1	1199	7	US-10-425-114-580	Sequence 580, App	C 173	15	26.3	417	9	US-10-972-079-65016	Sequence 65016, A
C 101	16	28.1	1130	8	US-10-425-115-4456	Sequence 44456, A	C 174	15	26.3	418	9	US-10-972-079-65015	Sequence 65015, A
C 102	16	28.1	1136	7	US-10-425-114-2736	Sequence 2736, Ap	C 175	15	26.3	419	7	US-10-424-599-66155	Sequence 68155, A
C 103	16	28.1	1184	8	US-10-425-115-44464	Sequence 44464, A	C 176	15	26.3	423	8	US-10-357-930-39083	Sequence 39083, A
C 104	16	28.1	1198	7	US-10-425-114-5749	Sequence 5749, Ap	C 177	15	26.3	419	8	US-10-357-930-39016	Sequence 39016, A
C 105	16	28.1	1458	4	US-09-925-065A-684568	Sequence 684568,	C 178	15	26.3	427	4	US-09-925-065A-174778	Sequence 474778, A
C 106	16	28.1	1458	4	US-09-925-065A-684569	Sequence 684569,	C 179	15	26.3	432	7	US-10-424-599-101497	Sequence 101497, A
C 107	16	28.1	1521	7	US-10-425-114-5184	Sequence 5184, Ap	C 180	15	26.3	436	8	US-10-357-930-38942	Sequence 38942, A
C 108	16	28.1	1545	7	US-10-767-701-31353	Sequence 13352, A	C 181	15	26.3	443	8	US-10-357-930-33304	Sequence 32304, A
C 109	16	28.1	1706	7	US-10-425-114-31783	Sequence 13783, A	C 182	15	26.3	443	8	US-10-357-930-44803	Sequence 44803, A
C 110	16	28.1	1762	4	US-09-925-065A-684593	Sequence 684593,	C 183	15	26.3	444	5	US-10-027-632-181778	Sequence 181778, A
C 111	16	28.1	1907	8	US-10-425-115-44460	Sequence 44460, A	C 184	15	26.3	444	5	US-10-027-632-308260	Sequence 308260, A
C 112	16	28.1	1959	7	US-10-425-114-9056	Sequence 9056, Ap	C 185	15	26.3	444	6	US-10-027-632-181778	Sequence 181778, A
C 113	16	28.1	1983	3	US-09-745-763-45	Sequence 45, Appl	C 186	15	26.3	444	6	US-10-027-632-308260	Sequence 308260, A
C 114	16	28.1	2114	7	US-10-425-114-24390	Sequence 24390, A	C 187	15	26.3	446	7	US-10-437-963-56702	Sequence 56702, A
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C 130	16	28.1	2907	9	US-10-122-851-511	Sequence 511, Appl	C 203	15	26.3	510	8	US-10-357-930-32310	Sequence 32310, A
C 131	16	28.1	8429	3	US-09-738-885-3	Sequence 3, Appl	C 204	15	26.3	510	8	US-10-357-930-41156	Sequence 41156, A
C 132	16	28.1	8688	3	US-09-938-842A-1748	Sequence 1748, Ap	C 205	15	26.3	510	8	US-10-357-930-41286	Sequence 41286, A
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C 135	16	28.1	96276	8	US-10-723-860-451	Sequence 451, App	C 208	15	26.3	520	4	US-09-925-065A-501053	Sequence 501053, A
C 136	16	28.1	100364	8	US-10-719-993-6776	Sequence 6776, Ap	C 209	15	26.3	520	4	US-09-925-065A-501054	Sequence 501054, A
C 137	16	28.1	113819	8	US-10-719-993-6852	Sequence 6852, Ap	C 210	15	26.3	520	4	US-09-925-065A-501055	Sequence 501055, A
C 138	16	28.1	352938	7	US-10-322-696-79	Sequence 79, Appl	C 211	15	26.3	520	4	US-09-925-065A-501056	Sequence 501056, A
C 139	16	28.1	357652	7	US-10-322-696-34	Sequence 34, Appl	C 212	15	26.3	522	4	US-09-925-065A-169329	Sequence 169329, A
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C 143	16	28.1	1503841	9	US-09-946-807-1	Sequence 1, Appl	C 216	15	26.3	550	4	US-09-925-065A-33419	Sequence 33419, A
C 144	15	26.3	25	8	US-10-995-011-1	Sequence 721052,	C 217	15	26.3	552	4	US-09-925-065A-615168	Sequence 615168, A
C 145	15	26.3	40	8	US-09-132-231-17	Sequence 17, Appl	C 218	15	26.3	554	3	US-09-864-761-15742	Sequence 15742, A
C 146	15	26.3	384	8	US-10-425-115-68607	Sequence 68607, A	C 219	15	26.3	554	3	US-09-864-761-15394	Sequence 15394, A
C 147	15	26.3	304	3	US-09-922-293-1634	Sequence 1634, Ap	C 220	15	26.3	554	3	US-09-864-761-15394	Sequence 15394, A
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C 149	15	26.3	323	7	US-10-424-599-40767	Sequence 40767, A	C 222	15	26.3	560	7	US-10-424-599-92386	Sequence 92386, A
C 150	15	26.3	333	7	US-10-424-599-142025	Sequence 142025,	C 223	15	26.3	565	4	US-09-925-065A-628412	Sequence 628412, A
C 151	15	26.3	336	7	US-10-424-599-42094	Sequence 42094, A	C 224	15	26.3	565	4	US-09-925-065A-628413	Sequence 628413, A
C 152	15	26.3	337	8	US-10-357-930-14890	Sequence 14890, A	C 225	15	26.3	565	8	US-10-357-930-41242	Sequence 41242, A
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C 154	15	26.3	338	8	US-10-357-930-11131	Sequence 11131, A	C 227	15	26.3	581	4	US-09-925-065A-526271	Sequence 526271, A
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C 157	15	26.3	339	8	US-10-357-930-11118	Sequence 11118, A	C 230	15	26.3	582	8	US-10-357-930-34291	Sequence 34291, A
C 158	15	26.3	339	8	US-10-357-930-14902	Sequence 14902, A	C 231	15	26.3	583	5	US-10-027-632-299312	Sequence 299312, A
C 159	15	26.3	339	8	US-10-357-930-14972	Sequence 14972, A	C 232	15	26.3	583	5	US-10-027-632-299312	Sequence 299312, A
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C 161	15	26.3	340	8	US-10-357-930-11137	Sequence 11137, A	C 234	15	26.3	583	6	US-10-027-632-299312	Sequence 299312, A
C 162	15	26.3	341	8	US-10-357-930-11051	Sequence 11051, A	C 235	15	26.3	584	4	US-09-925-065A-446182	Sequence 446182, A
C 163	15	26.3	341	8	US-10-357-930-14826	Sequence 14826, A	C 236	15	26.3	585	5	US-10-027-632-224840	Sequence 224840, A
C 164	15	26.3	348	3	US-09-918-995-18574	Sequence 18574, A	C 237	15	26.3	585	6	US-10-027-632-224840	Sequence 224840, A
C 165	15	26.3	350	7	US-10-437-963-82134	Sequence 82134, A	C 238	15	26.3	587	4	US-09-925-065A-571772	Sequence 571772, A
C 166	15	26.3	357	8	US-10-357-930-1882	Sequence 1882, Ap	C 239	15	26.3	593	4	US-09-925-065A-572577	Sequence 572577, A
C 167	15	26.3	380	4	US-09-925-065A-476117	Sequence 476117, A	C 240	15	26.3	594	4	US-09-925-065A-786177	Sequence 786177, A
C 168	15	26.3	395	8	US-10-357-930-5657	Sequence 5657, Ap	C 241	15	26.3	600	9	US-10-972-079-17187	Sequence 17187, A
C 169	15	26.3	405	4	US-09-925-065A-141559	Sequence 141559,	C 242	15	26.3	600	9	US-10-972-079-17188	Sequence 17188, A



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C 253	15	26.3	622	4	US-09-925-065A-505916	Sequence 505916,
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C 255	15	26.3	624	5	US-10-027-632-233242	Sequence 233242,
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C 260	15	26.3	645	3	US-09-860-670-44	Sequence 44, Appl
C 261	15	26.3	645	3	US-09-764-886-35	Sequence 35, Appl
C 262	15	26.3	645	3	US-10-027-632-15626	Sequence 15626, A
C 263	15	26.3	655	6	US-10-027-632-15626	Sequence 15626, A
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C 267	15	26.3	693	6	US-10-027-632-126342	Sequence 126342,
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C 271	15	26.3	761	6	US-10-027-632-126343	Sequence 126343,
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C 274	15	26.3	768	4	US-09-925-065A-5508	Sequence 5508, Ap
C 275	15	26.3	768	4	US-09-925-065A-5509	Sequence 5509, Ap
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C 302	15	26.3	1172	4	US-09-925-065A-74836	Sequence 74836, A
C 303	15	26.3	1211	7	US-10-303-172-270	Sequence 270, App
C 304	15	26.3	1224	3	US-09-974-300-8308	Sequence 8308, Ap
C 305	15	26.3	1273	4	US-10-424-559-96634	Sequence 96634, A
C 306	15	26.3	1367	7	US-09-925-065A-676432	Sequence 676432,
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C 308	15	26.3	1482	7	US-10-437-963-20760	Sequence 20760, A
C 309	15	26.3	1563	8	US-10-425-115-169192	Sequence 169192,
C 310	15	26.3	1686	3	US-09-938-842A-2040	Sequence 2040, Ap
C 311	15	26.3	1686	3	US-09-938-842A-2040	Sequence 2040, Ap
C 312	15	26.3	1770	7	US-10-282-122A-24588	Sequence 24588, A
C 313	15	26.3	1770	7	US-10-425-114-20663	Sequence 20663, A
C 314	15	26.3	1908	7	US-10-282-1322A-41281	Sequence 41281, A
C 315	15	26.3	1953	7	US-10-424-559-91563	Sequence 91563, A
C 316	15	26.3	2038	7	US-10-424-559-116095	Sequence 116095,
C 317	15	26.3	2228	4	US-09-925-065A-549653	Sequence 549653,
C 318	15	26.3	2302	4	US-09-925-065A-81948	Sequence 81948, A
C 319	15	26.3	2302	4	US-09-925-065A-81949	Sequence 81949, A
C 320	15	26.3	2302	4	US-09-925-065A-81950	Sequence 81950, A
C 321	15	26.3	2415	4	US-09-925-065A-81950	Sequence 81950, A
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C 324	15	26.3	3193	4	US-09-925-065A-671765	Sequence 671765,
C 325	15	26.3	3375	8	US-10-473-974-178	Sequence 178, App
C 326	15	26.3	3580	8	US-10-473-974-207	Sequence 207, App
C 327	15	26.3	3774	8	US-09-925-065A-688739	Sequence 688739,
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C 329	15	26.3	3977	5	US-10-285-976-84	Sequence 4, Appl
C 330	15	26.3	3981	7	US-10-198-846-10510	Sequence 10510, A
C 331	15	26.3	4090	7	US-10-231-956A-308	Sequence 308, App
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C 333	15	26.3	4590	7	US-10-437-963-63194	Sequence 63194, A
C 334	15	26.3	7887	7	US-10-398-221-3883	Sequence 3883, Ap
C 335	15	26.3	8297	8	US-10-723-860-8101	Sequence 4101, Ap
C 336	15	26.3	11029	10	US-11-097-143-27907	Sequence 27907, A
C 337	15	26.3	12880	6	US-10-295-027-927	Sequence 927, App
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C 339	15	26.3	14943	8	US-10-741-600-17979	Sequence 17979, A
C 340	15	26.3	19399	10	US-11-097-143-6253	Sequence 6253, Ap
C 341	15	26.3	24741	5	US-10-087-192-1042	Sequence 1042, Ap
C 342	15	26.3	26555	5	US-09-860-670-161	Sequence 161, App
C 343	15	26.3	26555	6	US-10-227-646-161	Sequence 161, App
C 344	15	26.3	32152	5	US-10-205-428-927	Sequence 927, App
C 345	15	26.3	34895	8	US-10-741-600-17927	Sequence 17927, App
C 346	15	26.3	35403	6	US-10-085-117-85	Sequence 85, Appl
C 347	15	26.3	42348	7	US-10-715-066-2	Sequence 2, Appl1
C 348	15	26.3	57665	7	US-10-741-601-1662	Sequence 5662, Ap
C 349	15	26.3	60500	5	US-10-087-192-832	Sequence 1024, Ap
C 350	15	26.3	65621	5	US-10-087-192-832	Sequence 832, App
C 351	15	26.3	78785	3	US-09-978-167-3	Sequence 3, Appl1
C 352	15	26.3	85859	5	US-10-087-192-562	Sequence 562, App
C 353	15	26.3	96588	6	US-10-085-117-76	Sequence 76, Appl
C 354	15	26.3	96599	7	US-10-105-948-4	Sequence 4, Appl1
C 355	15	26.3	96599	7	US-10-052-482-178	Sequence 178, App
C 356	15	26.3	115434	8	US-10-719-993-7058	Sequence 7058, Ap
C 357	15	26.3	124289	5	US-10-087-192-817	Sequence 817, App
C 358	15	26.3	124933	9	US-10-737-082-97	Sequence 97, Appl
C 359	15	26.3	124933	9	US-10-765-790-97	Sequence 97, Appl
C 360	15	26.3	124933	9	US-10-737-082-955	Sequence 65, Appl
C 361	15	26.3	127602	9	US-10-765-790-65	Sequence 65, Appl
C 362	15	26.3	127602	9	US-10-765-790-65	Sequence 127, App
C 363	15	26.3	143899	8	US-10-972-546-15	Sequence 15, Appl
C 364	15	26.3	143899	8	US-10-735-256-15	Sequence 15, Appl
C 365	15	26.3	148999	5	US-10-087-192-1672	Sequence 1672, App
C 366	15	26.3	160921	8	US-10-484-577-660	Sequence 660, App
C 367	15	26.3	177531	8	US-10-087-192-1755	Sequence 355, App
C 368	15	26.3	194945	5	US-10-085-117-355	Sequence 1126, Ap
C 369	15	26.3	212231	6	US-10-087-192-1126	Sequence 16, Appl
C 370	15	26.3	215980	3	US-09-972-546-16	Sequence 16, Appl
C 371	15	26.3	215980	3	US-10-735-256-16	Sequence 16, Appl
C 372	15	26.3	218802	9	US-10-897-508-1	Sequence 1, Appl1
C 373	15	26.3	220224	5	US-10-087-192-1282	Sequence 1282, Ap
C 374	15	26.3	247682	7	US-10-235-192A-28	Sequence 28, Appl
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C 376	15	26.3	713059	6	US-10-027-632-174581	Sequence 174581,
C 377	15	26.3	713059	6	US-10-027-632-174581	Sequence 174581,
C 378	15	26.3	713059	6	US-10-027-632-174581	Sequence 6817, App
C 379	15	26.3	717651	6	US-10-719-993-6817	Sequence 19, Appl
C 380	14	24.6	20	7	US-10-381-906-19	Sequence 20, Appl
C 381	14	24.6	20	7	US-10-381-906-19	Sequence 168445,
C 382	14	24.6	25	7	US-10-719-956-218845	Sequence 218845,
C 383	14	24.6	25	7	US-10-719-956-218845	Sequence 390224,
C 384	14	24.6	25	7	US-10-719-956-218845	Sequence 69469,
C 385	14	24.6	25	8	US-10-719-956-69469	Sequence 953786,
C 386	14	24.6	25	8	US-10-719-956-69469	Sequence 487555,
C 387	14	24.6	25	10	US-11-036-317-487585	Sequence 789546,
C 388	14	24.6	25	10	US-11-036-317-789546	Sequence 789546,



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391	14	24.6	49	6	US-10-026-925-37	Sequence 37, Appl	C 464	14	24.6	303	7	US-10-437-963-101256	Sequence 101256,
392	14	24.6	49	6	US-10-026-925-39	Sequence 39, Appl	C 465	14	24.6	306	8	US-10-425-115-134898	Sequence 134898,
393	14	24.6	51	3	US-09-837-306-11	Sequence 11, Appl	C 466	14	24.6	311	3	US-09-535-459-1583	Sequence 1583, Ap
C 394	14	24.6	51	6	US-10-045-674-530	Sequence 530, App	C 467	14	24.6	320	3	US-09-535-459-1529	Sequence 1529, Ap
C 395	14	24.6	65	8	US-10-741-849-2235	Sequence 2235, App	C 468	14	24.6	323	6	US-10-026-925-81	Sequence 23, Appl
C 396	14	24.6	94	3	US-09-837-306-189	Sequence 189, App	C 469	14	24.6	332	9	US-10-916-758-83	Sequence 83, Appl
C 397	14	24.6	94	6	US-10-045-674-492	Sequence 492, App	C 470	14	24.6	335	7	US-10-637-885-406	Sequence 406, App
C 398	14	24.6	133	3	US-10-702-075-886	Sequence 886, App	C 471	14	24.6	339	3	US-09-814-353-14575	Sequence 14575, A
C 399	14	24.6	147	3	US-09-535-459-1526	Sequence 1526, App	C 472	14	24.6	339	3	US-09-814-353-20122	Sequence 20122, A
C 400	14	24.6	172	7	US-10-424-599-7586	Sequence 7586, App	C 473	14	24.6	339	9	US-10-916-840-105	Sequence 105, App
C 401	14	24.6	173	3	US-09-864-761-30409	Sequence 30409, A	C 474	14	24.6	341	9	US-10-916-840-71	Sequence 71, App
C 402	14	24.6	187	8	US-10-425-115-111246	Sequence 111246,	C 475	14	24.6	341	9	US-10-916-758-75	Sequence 75, Appl
C 403	14	24.6	189	3	US-09-535-459-1534	Sequence 1534, Ap	C 476	14	24.6	341	9	US-10-916-758-79	Sequence 79, Appl
C 404	14	24.6	192	8	US-10-357-930-35288	Sequence 35288, A	C 477	14	24.6	341	9	US-10-916-758-87	Sequence 87, Appl
C 405	14	24.6	192	8	US-10-357-930-44126	Sequence 44126, A	C 478	14	24.6	341	9	US-10-916-758-91	Sequence 91, Appl
C 406	14	24.6	195	3	US-09-535-459-1581	Sequence 1581, Ap	C 479	14	24.6	342	7	US-10-663-244-72	Sequence 72, Appl
C 407	14	24.6	199	3	US-09-535-459-1582	Sequence 1582, Ap	C 480	14	24.6	342	9	US-10-916-758-31	Sequence 31, Appl
C 408	14	24.6	200	3	US-09-535-459-1543	Sequence 1543, Ap	C 481	14	24.6	342	9	US-10-916-758-39	Sequence 39, Appl
C 409	14	24.6	201	7	US-10-741-601-17027	Sequence 17027, A	C 482	14	24.6	342	9	US-10-916-758-43	Sequence 43, Appl
C 410	14	24.6	201	8	US-10-719-993-12415	Sequence 12415, A	C 483	14	24.6	344	9	US-10-916-758-27	Sequence 27, Appl
C 411	14	24.6	201	8	US-10-719-993-38495	Sequence 38495, A	C 484	14	24.6	344	9	US-10-916-758-35	Sequence 35, Appl
C 412	14	24.6	201	8	US-10-719-993-38691	Sequence 38691, A	C 485	14	24.6	344	9	US-10-916-758-47	Sequence 47, Appl
C 413	14	24.6	201	8	US-10-719-993-49582	Sequence 49582, A	C 486	14	24.6	348	7	US-10-663-244-60	Sequence 60, Appl
C 414	14	24.6	201	8	US-10-719-993-53148	Sequence 53148, A	C 487	14	24.6	348	7	US-10-663-244-88	Sequence 88, Appl
C 415	14	24.6	201	8	US-10-741-600-34938	Sequence 34938, A	C 488	14	24.6	348	7	US-10-663-244-92	Sequence 92, Appl
C 416	14	24.6	201	8	US-10-741-600-46432	Sequence 46432, A	C 489	14	24.6	351	7	US-10-663-244-76	Sequence 76, Appl
C 417	14	24.6	215	3	US-09-535-459-1554	Sequence 1554, Ap	C 490	14	24.6	351	8	US-10-783-311-59	Sequence 59, Appl
C 418	14	24.6	219	3	US-09-814-353-1844	Sequence 1844, Ap	C 491	14	24.6	351	8	US-10-783-311-62	Sequence 62, Appl
C 419	14	24.6	219	3	US-09-814-353-8191	Sequence 8191, Ap	C 492	14	24.6	351	8	US-10-783-311-77	Sequence 77, Appl
C 420	14	24.6	221	3	US-09-535-459-1565	Sequence 1565, Ap	C 493	14	24.6	354	7	US-10-663-244-64	Sequence 64, Appl
C 421	14	24.6	223	7	US-10-424-599-105702	Sequence 105702,	C 494	14	24.6	354	7	US-10-663-244-68	Sequence 68, Appl
C 422	14	24.6	224	3	US-09-535-459-1568	Sequence 1568, Ap	C 495	14	24.6	354	8	US-10-357-990-56216	Sequence 56216, A
C 423	14	24.6	227	7	US-10-424-599-7185	Sequence 7185, Ap	C 496	14	24.6	355	8	US-10-425-115-144201	Sequence 144201, A
C 424	14	24.6	231	3	US-09-535-459-1649	Sequence 1649, Ap	C 497	14	24.6	355	8	US-10-357-990-41167	Sequence 41767, A
C 425	14	24.6	234	3	US-09-535-459-1550	Sequence 1550, Ap	C 498	14	24.6	357	7	US-10-663-244-6	Sequence 6, Appl
C 426	14	24.6	235	3	US-09-535-459-1555	Sequence 1555, Ap	C 499	14	24.6	360	7	US-10-663-244-10	Sequence 10, Appl
C 427	14	24.6	236	3	US-09-535-459-1617	Sequence 1617, Ap	C 500	14	24.6	360	7	US-10-663-244-84	Sequence 84, Appl
C 428	14	24.6	238	7	US-10-424-599-110289	Sequence 110289,	C 501	14	24.6	363	9	US-10-916-840-09	Sequence 97, Appl
C 429	14	24.6	242	3	US-09-813-358-152	Sequence 152, App	C 502	14	24.6	364	3	US-09-916-995-33624	Sequence 33624, A
C 430	14	24.6	242	3	US-09-997-279-152	Sequence 152, App	C 503	14	24.6	364	7	US-10-437-963-53948	Sequence 53948, A
C 431	14	24.6	242	3	US-09-987-899-6369	Sequence 6369, Ap	C 504	14	24.6	366	7	US-10-663-244-14	Sequence 14, Appl
C 432	14	24.6	244	8	US-10-425-115-87157	Sequence 87157, A	C 505	14	24.6	369	7	US-10-663-244-14	Sequence 96, Appl
C 433	14	24.6	248	3	US-09-535-459-1593	Sequence 1593, Ap	C 506	14	24.6	369	7	US-10-663-244-96	Sequence 41, Appl
C 434	14	24.6	249	3	US-09-535-459-1599	Sequence 1599, Ap	C 507	14	24.6	369	8	US-10-783-311-41	Sequence 42, Appl
C 435	14	24.6	253	3	US-09-535-459-1570	Sequence 1570, Ap	C 508	14	24.6	369	8	US-10-783-311-42	Sequence 43, Appl
C 436	14	24.6	254	3	US-09-535-459-1551	Sequence 1551, Ap	C 509	14	24.6	369	8	US-10-783-311-43	Sequence 44, Appl
C 437	14	24.6	254	3	US-09-535-459-1645	Sequence 1645, Ap	C 510	14	24.6	369	8	US-10-783-311-44	Sequence 45, Appl
C 438	14	24.6	255	3	US-09-535-459-1525	Sequence 1525, Ap	C 511	14	24.6	369	8	US-10-783-311-45	Sequence 50, Appl
C 439	14	24.6	256	3	US-09-535-459-1516	Sequence 1516, Ap	C 512	14	24.6	369	8	US-10-783-311-50	Sequence 59, Appl
C 440	14	24.6	267	3	US-09-535-459-1451	Sequence 1451, Ap	C 513	14	24.6	369	8	US-10-783-311-59	Sequence 59, Appl
C 441	14	24.6	272	3	US-09-535-459-1523	Sequence 1523, Ap	C 514	14	24.6	369	9	US-10-916-840-59	Sequence 43, Appl
C 442	14	24.6	272	3	US-09-535-459-1596	Sequence 1596, Ap	C 515	14	24.6	375	9	US-10-916-840-43	Sequence 8067, Ap
C 443	14	24.6	274	3	US-09-535-459-1590	Sequence 1590, Ap	C 516	14	24.6	382	3	US-09-960-352-8067	Sequence 51, Appl
C 444	14	24.6	276	3	US-09-535-459-1427	Sequence 1427, Ap	C 517	14	24.6	382	9	US-10-916-758-55	Sequence 55, Appl
C 445	14	24.6	278	8	US-10-357-930-60100	Sequence 60100, A	C 518	14	24.6	382	9	US-10-916-758-59	Sequence 59, Appl
C 446	14	24.6	282	7	US-10-242-535A-49196	Sequence 49196, A	C 519	14	24.6	382	9	US-10-916-758-63	Sequence 63, Appl
C 447	14	24.6	282	7	US-10-085-783A-49196	Sequence 49196, A	C 520	14	24.6	382	9	US-10-916-758-63	Sequence 67, Appl
C 448	14	24.6	283	3	US-09-535-459-1459	Sequence 1459, Ap	C 521	14	24.6	382	9	US-10-916-758-67	Sequence 63, Appl
C 449	14	24.6	287	3	US-09-535-459-1613	Sequence 1613, Ap	C 522	14	24.6	384	3	US-09-954-456-2227	Sequence 2227, Ap
C 450	14	24.6	289	7	US-10-424-599-68256	Sequence 68256, A	C 523	14	24.6	384	3	US-09-873-367C-798	Sequence 798, App
C 451	14	24.6	292	3	US-09-962-436-63	Sequence 63, Appl	C 524	14	24.6	384	3	US-10-242-535A-52020	Sequence 52020, A
C 452	14	24.6	292	9	US-10-843-641A-15522	Sequence 2522, Ap	C 525	14	24.6	384	7	US-10-086-753A-52020	Sequence 52020, A
C 453	14	24.6	293	4	US-09-925-065A-16156	Sequence 16156,	C 526	14	24.6	384	8	US-10-086-753A-52020	Sequence 52020, A
C 454	14	24.6	295	3	US-09-864-761-30793	Sequence 30793, A	C 527	14	24.6	384	8	US-10-783-311-65	Sequence 65, Appl
C 455	14	24.6	295	3	US-09-764-869-143	Sequence 143, App	C 528	14	24.6	384	9	US-10-843-661A-798	Sequence 798, App
C 456	14	24.6	295	3	US-09-764-869-1490	Sequence 1490, Ap	C 529	14	24.6	384	9	US-10-843-661A-5254	Sequence 5254, Ap
C 457	14	24.6	295	5	US-10-091-504-143	Sequence 143, App	C 530	14	24.6	386	9	US-10-916-840-75	Sequence 75, Appl
C 458	14	24.6	295	5	US-10-091-504-1490	Sequence 1490, Ap	C 531	14	24.6	386	9	US-10-916-840-101	Sequence 101, App
C 459	14	24.6	295	6	US-10-227-577-143	Sequence 143, App	C 532	14	24.6	387	8	US-10-783-311-40	Sequence 40, Appl
C 460	14	24.6	295	6	US-10-227-577-1490	Sequence 1490, Ap	C 533	14	24.6	387	8	US-10-783-311-48	Sequence 48, Appl
C 461	14	24.6	297	8	US-10-425-115-69710	Sequence 69710, A	C 534	14	24.6	389	9	US-10-916-758-23	Sequence 23, Appl



C 535	14	24.6	390	7	US-10-242-535A-53867	Sequence 53867, A	608	14	24.6	455	3	US-09-918-995-12691	Sequence 12691, A
C 536	14	24.6	390	7	US-10-085-783A-53867	Sequence 53867, A	609	14	24.6	455	9	US-10-972-079-65805	Sequence 65805, A
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539	14	24.6	393	8	US-10-783-311-46	Sequence 46, Appl	C 612	14	24.6	459	7	US-10-242-535A-43003	Sequence 43003, A
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545	14	24.6	393	8	US-10-783-311-73	Sequence 73, Appl	C 618	14	24.6	466	6	US-10-027-632-88088	Sequence 88088, A
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549	14	24.6	396	3	US-09-864-761-1242	Sequence 14242, A	C 622	14	24.6	467	5	US-10-027-632-282940	Sequence 282940, A
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552	14	24.6	396	8	US-10-783-311-56	Sequence 56, Appl	C 625	14	24.6	470	5	US-10-027-632-116854	Sequence 316854, A
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559	14	24.6	396	9	US-10-916-840-31	Sequence 31, Appl	632	14	24.6	472	3	US-09-770-444A-148	Sequence 148, App
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565	14	24.6	408	8	US-10-783-311-71	Sequence 71, Appl	C 638	14	24.6	475	8	US-10-566-639-220	Sequence 220, App
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C 582	14	24.6	419	7	US-10-424-599A-116202	Sequence 116202, A	655	14	24.6	510	5	US-10-027-632-84728	Sequence 84728, A
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C 585	14	24.6	421	3	US-09-535-459-1457	Sequence 1457, Ap	658	14	24.6	510	5	US-10-027-632-293484	Sequence 293484, A
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587	14	24.6	425	3	US-10-916-840-113	Sequence 113, App	660	14	24.6	510	5	US-10-027-632-293486	Sequence 293486, A
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589	14	24.6	427	7	US-10-437-963-8004	Sequence 8004, Ap	662	14	24.6	510	6	US-10-027-632-84728	Sequence 84728, A
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C 592	14	24.6	435	7	US-10-242-535A-33428	Sequence 43428, A	665	14	24.6	510	6	US-10-027-632-293484	Sequence 293484, A
C 593	14	24.6	435	7	US-10-085-783A-43428	Sequence 43428, A	666	14	24.6	510	6	US-10-027-632-293485	Sequence 293485, A
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598	14	24.6	441	3	US-10-916-840-51	Sequence 51, Appl	671	14	24.6	514	5	US-10-027-632-776939	Sequence 776939, A
599	14	24.6	441	3	US-10-970-713-45	Sequence 45, Appl	672	14	24.6	514	6	US-10-027-632-776938	Sequence 776938, A
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C 603	14	24.6	448	5	US-10-016-349A-104	Sequence 104, App	C 676	14	24.6	523	9	US-10-972-079-65183	Sequence 65183, A
C 604	14	24.6	448	5	US-10-060-036-4002	Sequence 4002, Ap	C 677	14	24.6	525	6	US-10-264-049-1873	Sequence 1873, Ap
C 605	14	24.6	454	5	US-10-027-632-304931	Sequence 304931, A	678	14	24.6	526	6	US-09-925-065A-361506	Sequence 361506, A
C 606	14	24.6	454	6	US-10-027-632-304931	Sequence 304931, A	679	14	24.6	530	9	US-10-779-543-81593	Sequence 21595, A
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C 682	14	24.6	535	7	US-10-437-963A-1593	Sequence 1593, Ap	C 755	14	24.6	571	4	US-09-925-065A-332161	Sequence 332161,
C 683	14	24.6	536	4	US-09-925-065A-184711	Sequence 184711, A	C 756	14	24.6	571	4	US-09-925-065A-332162	Sequence 332162,
C 684	14	24.6	538	4	US-09-925-065A-605172	Sequence 605172, A	C 757	14	24.6	571	4	US-09-925-065A-332163	Sequence 332163,
C 685	14	24.6	539	4	US-09-925-065A-12903	Sequence 12903, A	C 758	14	24.6	571	4	US-09-925-065A-512291	Sequence 512291,
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C 689	14	24.6	543	4	US-09-925-065A-139777	Sequence 139777, A	762	14	24.6	573	4	US-09-925-065A-395022	Sequence 395022,
C 690	14	24.6	543	4	US-09-925-065A-9572	Sequence 9572, Ap	763	14	24.6	573	4	US-09-925-065A-395023	Sequence 395023,
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C 692	14	24.6	544	4	US-09-925-065A-9574	Sequence 9574, Ap	765	14	24.6	576	6	US-10-027-632-228050	Sequence 228050,
C 693	14	24.6	544	5	US-10-027-632-75690	Sequence 75690, A	766	14	24.6	576	6	US-10-654-102-104	Sequence 104, App
C 694	14	24.6	544	5	US-10-027-632-756319	Sequence 756319, A	767	14	24.6	576	7	US-10-654-102-1178	Sequence 1178, App
C 695	14	24.6	544	6	US-10-027-632-75690	Sequence 75690, A	C 768	14	24.6	577	9	US-10-972-079-65745	Sequence 65745, A
C 696	14	24.6	544	6	US-10-027-632-756319	Sequence 756319, A	C 769	14	24.6	578	4	US-09-925-065A-190058	Sequence 190058,
C 697	14	24.6	545	4	US-09-925-065A-250171	Sequence 250171, A	C 770	14	24.6	578	4	US-10-027-632-886626	Sequence 886626, A
C 698	14	24.6	545	4	US-09-925-065A-250172	Sequence 250172, A	C 771	14	24.6	578	6	US-10-027-632-886626	Sequence 886626, A
C 699	14	24.6	545	4	US-09-925-065A-549529	Sequence 549529, A	C 772	14	24.6	579	4	US-09-925-065A-333452	Sequence 333452,
700	14	24.6	547	4	US-09-925-065A-104840	Sequence 104840, A	C 773	14	24.6	579	4	US-09-925-065A-333452	Sequence 333452,
C 701	14	24.6	548	4	US-09-925-065A-165837	Sequence 165837, A	C 774	14	24.6	579	4	US-09-925-065A-848561	Sequence 848561,
C 702	14	24.6	549	4	US-09-925-065A-516685	Sequence 516685, A	C 775	14	24.6	580	4	US-09-925-065A-784934	Sequence 784934,
C 703	14	24.6	550	4	US-09-925-065A-869188	Sequence 869188, A	C 776	14	24.6	580	5	US-10-027-632-268351	Sequence 268351,
C 704	14	24.6	551	4	US-09-925-065A-246704	Sequence 246704, A	C 777	14	24.6	580	6	US-10-027-632-268351	Sequence 268351,
C 705	14	24.6	554	7	US-10-242-535A-51826	Sequence 51826, A	C 778	14	24.6	581	4	US-09-925-065A-523022	Sequence 523022,
C 706	14	24.6	554	7	US-10-085-783A-51826	Sequence 51826, A	C 779	14	24.6	582	4	US-09-925-065A-141980	Sequence 141980,
C 707	14	24.6	555	4	US-09-925-065A-655757	Sequence 655757, A	C 780	14	24.6	582	4	US-09-925-065A-141981	Sequence 141981,
C 708	14	24.6	555	5	US-10-027-632-35161	Sequence 35161, A	C 781	14	24.6	582	4	US-09-925-065A-141982	Sequence 141982,
C 709	14	24.6	555	6	US-10-027-632-35161	Sequence 35161, A	C 782	14	24.6	582	4	US-09-925-065A-713921	Sequence 713921,
C 710	14	24.6	556	4	US-09-925-065A-150515	Sequence 150515, A	C 783	14	24.6	582	5	US-10-027-632-280717	Sequence 280717,
C 711	14	24.6	558	4	US-09-925-065A-181094	Sequence 181094, A	C 784	14	24.6	582	6	US-10-029-386-203719	Sequence 203719, A
C 712	14	24.6	558	4	US-09-925-065A-626234	Sequence 626234, A	C 785	14	24.6	582	6	US-10-027-632-290717	Sequence 290717,
C 713	14	24.6	558	4	US-09-925-065A-626235	Sequence 626235, A	C 786	14	24.6	583	4	US-09-925-065A-875025	Sequence 875025,
C 714	14	24.6	558	4	US-09-925-065A-626236	Sequence 626236, A	C 787	14	24.6	584	5	US-10-027-632-89171	Sequence 89171, A
C 715	14	24.6	559	5	US-10-027-632-319793	Sequence 319793, A	C 788	14	24.6	584	6	US-10-027-632-89171	Sequence 89171, A
C 716	14	24.6	559	6	US-10-027-632-319793	Sequence 319793, A	C 789	14	24.6	585	4	US-09-925-065A-333031	Sequence 333031,
C 717	14	24.6	560	4	US-09-925-065A-206341	Sequence 206341, A	C 790	14	24.6	589	8	US-10-425-115-103989	Sequence 103989,
C 718	14	24.6	560	5	US-10-027-632-64763	Sequence 64763, A	C 791	14	24.6	590	4	US-09-925-065A-421055	Sequence 421055,
C 719	14	24.6	560	5	US-10-027-632-64763	Sequence 64763, A	C 792	14	24.6	592	4	US-09-925-065A-821055	Sequence 821055,
C 720	14	24.6	560	5	US-10-027-632-107848	Sequence 107848, A	C 793	14	24.6	592	4	US-09-925-065A-821055	Sequence 821055,
C 721	14	24.6	560	5	US-10-027-632-284828	Sequence 284828, A	C 794	14	24.6	592	4	US-09-925-065A-821055	Sequence 821055,
C 722	14	24.6	560	5	US-10-027-632-310465	Sequence 310465, A	C 795	14	24.6	594	4	US-09-925-065A-860591	Sequence 860591,
C 723	14	24.6	560	6	US-10-027-632-63871	Sequence 63871, A	C 796	14	24.6	595	4	US-09-925-065A-399004	Sequence 399004,
C 724	14	24.6	560	6	US-10-027-632-64763	Sequence 64763, A	C 797	14	24.6	595	4	US-09-925-065A-928184	Sequence 928184,
C 725	14	24.6	560	6	US-10-027-632-107848	Sequence 107848, A	C 798	14	24.6	595	7	US-10-021-323-5790	Sequence 5790, Ap
C 726	14	24.6	560	6	US-10-027-632-284828	Sequence 284828, A	C 799	14	24.6	596	8	US-10-357-930-55282	Sequence 55282, A
C 727	14	24.6	560	6	US-10-027-632-310465	Sequence 310465, A	C 800	14	24.6	596	8	US-10-027-632-202288	Sequence 202288,
C 728	14	24.6	563	4	US-09-925-065A-209237	Sequence 209237, A	C 801	14	24.6	598	5	US-10-027-632-202288	Sequence 202288,
C 729	14	24.6	563	4	US-09-925-065A-209238	Sequence 209238, A	C 802	14	24.6	598	6	US-10-027-632-202288	Sequence 202288,
C 730	14	24.6	565	4	US-09-925-065A-192231	Sequence 192231, A	C 803	14	24.6	599	4	US-09-925-065A-760118	Sequence 760118,
C 731	14	24.6	565	4	US-09-925-065A-800707	Sequence 800707, A	C 804	14	24.6	599	4	US-09-925-065A-760119	Sequence 760119,
C 732	14	24.6	565	5	US-10-027-632-51437	Sequence 51437, A	C 805	14	24.6	599	4	US-09-925-065A-760120	Sequence 760120,
C 733	14	24.6	565	5	US-10-027-632-83069	Sequence 83069, A	C 806	14	24.6	599	4	US-09-925-065A-760121	Sequence 760121,
C 734	14	24.6	565	5	US-10-027-632-315967	Sequence 315967, A	C 807	14	24.6	599	4	US-09-925-065A-770315	Sequence 770315,
C 735	14	24.6	565	6	US-10-027-632-51437	Sequence 51437, A	C 808	14	24.6	599	4	US-09-925-065A-770316	Sequence 770316,
C 736	14	24.6	565	6	US-10-027-632-83069	Sequence 83069, A	C 809	14	24.6	599	9	US-10-972-079-90142	Sequence 90142, A
C 737	14	24.6	565	6	US-10-027-632-315967	Sequence 315967, A	C 810	14	24.6	599	9	US-10-972-079-90143	Sequence 90143, A
C 738	14	24.6	566	3	US-09-770-152-343	Sequence 343, App	C 811	14	24.6	599	9	US-10-972-079-90144	Sequence 90144, A
C 739	14	24.6	566	4	US-09-925-065A-106334	Sequence 106334, A	C 812	14	24.6	599	9	US-10-972-079-90144	Sequence 90144, A
C 740	14	24.6	566	4	US-09-925-065A-719088	Sequence 719088, A	C 813	14	24.6	600	4	US-09-925-065A-111928	Sequence 111928,
C 741	14	24.6	566	4	US-09-925-065A-719089	Sequence 719089, A	C 814	14	24.6	600	7	US-10-885-783A-44491	Sequence 44491, A
C 742	14	24.6	566	5	US-10-027-632-93683	Sequence 93683, A	C 815	14	24.6	600	7	US-10-085-783A-44491	Sequence 44491, A
C 743	14	24.6	566	6	US-10-027-632-93683	Sequence 93683, A	C 816	14	24.6	600	9	US-10-972-079-18087	Sequence 18087, A
C 744	14	24.6	567	7	US-10-425-114-18361	Sequence 18361, A	C 817	14	24.6	600	9	US-10-972-079-18088	Sequence 18088, A
C 745	14	24.6	568	4	US-09-925-065A-215203	Sequence 215203, A	C 818	14	24.6	600	9	US-10-972-079-31683	Sequence 31683, A
C 746	14	24.6	568	4	US-09-925-065A-364977	Sequence 364977, A	C 819	14	24.6	600	9	US-10-972-079-31683	Sequence 31683, A
C 747	14	24.6	569	5	US-10-027-632-59437	Sequence 59437, A	C 820	14	24.6	600	9	US-10-972-079-44897	Sequence 44897, A
C 748	14	24.6	569	5	US-10-027-632-63540	Sequence 63540, A	C 821	14	24.6	600	9	US-10-972-079-44899	Sequence 44899, A
C 749	14	24.6	569	6	US-10-027-632-59437	Sequence 59437, A	C 822	14	24.6	600	9	US-10-972-079-44751	Sequence 44751, A
C 750	14	24.6	569	6	US-10-027-632-63540	Sequence 63540, A	C 823	14	24.6	600	9	US-10-972-079-44812	Sequence 44812, A
C 751	14	24.6	570	4	US-09-925-065A-482176	Sequence 482176, A	C 824	14	24.6	600	9	US-10-972-079-65182	Sequence 65182, A
C 752	14	24.6	570	4	US-09-925-065A-662226	Sequence 662226, A	C 825	14	24.6	600	9	US-10-972-079-65184	Sequence 65184, A
C 753	14	24.6	570	4	US-09-925-065A-895883	Sequence 895883, A	C 826	14	24.6	600	9	US-10-972-079-65804	Sequence 65804, A



C 827	14	24.6	600	9	US-10-972-079-82486	Sequence 82486, A	900	14	24.6	632	4	US-09-925-065A-805081	Sequence 805081,
C 828	14	24.6	600	9	US-10-972-079-90145	Sequence 90145, A	C 901	14	24.6	633	4	US-09-925-065A-522719	Sequence 522719,
C 829	14	24.6	600	9	US-10-972-079-95510	Sequence 95510, A	C 902	14	24.6	633	4	US-09-925-065A-522720	Sequence 522720,
C 830	14	24.6	601	4	US-09-925-065A-291604	Sequence 291604, A	C 903	14	24.6	633	4	US-09-925-065A-749638	Sequence 749638,
C 831	14	24.6	601	4	US-09-925-065A-879061	Sequence 879061, A	C 904	14	24.6	633	4	US-09-925-065A-756429	Sequence 756429,
C 832	14	24.6	601	9	US-10-893-315-689	Sequence 689, App	C 905	14	24.6	633	4	US-09-925-065A-793578	Sequence 793578,
C 833	14	24.6	601	9	US-10-893-315-690	Sequence 690, App	C 906	14	24.6	633	4	US-09-925-065A-826491	Sequence 826491,
C 834	14	24.6	601	9	US-10-893-315-691	Sequence 691, App	C 907	14	24.6	634	4	US-09-925-065A-762880	Sequence 762880,
C 835	14	24.6	601	9	US-10-893-315-1154	Sequence 1154, App	C 908	14	24.6	634	4	US-09-925-065A-830876	Sequence 830876,
C 836	14	24.6	601	9	US-10-893-315-1155	Sequence 1155, App	C 909	14	24.6	635	4	US-09-925-065A-800526	Sequence 800526,
C 837	14	24.6	601	9	US-10-893-315-1156	Sequence 1156, App	C 910	14	24.6	638	4	US-09-925-065A-833900	Sequence 833900,
C 838	14	24.6	602	4	US-09-925-065A-241161	Sequence 241161, A	C 911	14	24.6	638	4	US-09-925-065A-833901	Sequence 833901,
C 839	14	24.6	602	4	US-09-925-065A-679473	Sequence 679473, A	C 912	14	24.6	639	4	US-09-925-065A-713388	Sequence 713388,
C 840	14	24.6	604	4	US-09-925-065A-399858	Sequence 399858, A	C 913	14	24.6	639	4	US-09-925-065A-617389	Sequence 617389,
C 841	14	24.6	605	4	US-09-925-065A-357787	Sequence 357787, A	C 914	14	24.6	641	5	US-10-027-632-112577	Sequence 112577,
C 842	14	24.6	605	4	US-09-925-065A-326976	Sequence 326976, A	C 915	14	24.6	641	6	US-10-027-632-112577	Sequence 112577,
C 843	14	24.6	606	4	US-09-925-065A-693744	Sequence 693744, A	C 916	14	24.6	642	4	US-09-925-065A-719595	Sequence 719595,
C 844	14	24.6	608	4	US-09-925-065A-432418	Sequence 432418, A	C 917	14	24.6	642	4	US-09-925-065A-719596	Sequence 719596,
C 845	14	24.6	609	4	US-09-925-065A-752874	Sequence 752874, A	C 918	14	24.6	642	4	US-09-925-065A-719597	Sequence 719597,
C 846	14	24.6	609	4	US-09-925-065A-752875	Sequence 752875, A	C 919	14	24.6	642	4	US-09-925-065A-719598	Sequence 719598,
C 847	14	24.6	609	9	US-10-450-763-27448	Sequence 27448, A	C 920	14	24.6	642	4	US-09-925-065A-719599	Sequence 719599,
C 848	14	24.6	610	4	US-09-925-065A-720581	Sequence 720581, A	C 921	14	24.6	644	4	US-09-925-065A-887736	Sequence 887736,
C 849	14	24.6	610	4	US-09-925-065A-720582	Sequence 720582, A	C 922	14	24.6	644	4	US-09-925-065A-887748	Sequence 887748,
C 850	14	24.6	610	4	US-09-925-065A-816282	Sequence 816282, A	C 923	14	24.6	644	4	US-09-925-065A-872749	Sequence 872749,
C 851	14	24.6	611	5	US-10-027-632-313686	Sequence 313686, A	C 924	14	24.6	644	4	US-09-925-065A-872750	Sequence 872750,
C 852	14	24.6	611	6	US-10-027-632-313686	Sequence 313686, A	C 925	14	24.6	644	4	US-09-925-065A-903160	Sequence 903160,
C 853	14	24.6	612	4	US-09-925-065A-767226	Sequence 767226, A	C 926	14	24.6	646	4	US-09-925-065A-226254	Sequence 226254,
C 854	14	24.6	612	4	US-09-925-065A-851805	Sequence 851805, A	C 927	14	24.6	646	4	US-09-925-065A-626766	Sequence 626766,
C 855	14	24.6	613	9	US-10-779-5443-16413	Sequence 16413, A	C 928	14	24.6	649	4	US-09-925-065A-829592	Sequence 829592, A
C 856	14	24.6	613	4	US-09-925-065A-51343	Sequence 51343, A	C 929	14	24.6	649	4	US-09-925-065A-683456	Sequence 683456,
C 857	14	24.6	613	4	US-09-925-065A-442105	Sequence 442105, A	C 930	14	24.6	649	4	US-09-925-065A-683457	Sequence 683457,
C 858	14	24.6	613	4	US-09-925-065A-442106	Sequence 442106, A	C 931	14	24.6	650	5	US-10-027-632-284881	Sequence 284881,
C 859	14	24.6	613	4	US-09-925-065A-629510	Sequence 629510, A	C 932	14	24.6	650	6	US-10-027-632-284881	Sequence 284881,
C 860	14	24.6	614	4	US-09-925-065A-118556	Sequence 118556, A	C 933	14	24.6	651	4	US-09-925-065A-256711	Sequence 256711,
C 861	14	24.6	614	4	US-09-925-065A-121235	Sequence 121235, A	C 934	14	24.6	651	4	US-09-925-065A-256712	Sequence 256712,
C 862	14	24.6	614	4	US-09-925-065A-441214	Sequence 441214, A	C 935	14	24.6	651	4	US-09-925-065A-256713	Sequence 256713,
C 863	14	24.6	614	8	US-10-425-115-48375	Sequence 48375, A	C 936	14	24.6	651	4	US-09-925-065A-256714	Sequence 256714,
C 864	14	24.6	615	4	US-09-925-065A-718501	Sequence 718501, A	C 937	14	24.6	651	4	US-09-925-065A-691445	Sequence 691445,
C 865	14	24.6	616	4	US-09-925-065A-556578	Sequence 556578, A	C 938	14	24.6	651	4	US-09-925-065A-691446	Sequence 691446,
C 866	14	24.6	616	4	US-09-925-065A-831958	Sequence 831958, A	C 939	14	24.6	651	4	US-09-925-065A-691447	Sequence 691447,
C 867	14	24.6	617	4	US-09-925-065A-456183	Sequence 456183, A	C 940	14	24.6	655	4	US-09-925-065A-204592	Sequence 204592,
C 868	14	24.6	619	4	US-09-925-065A-496993	Sequence 496993, A	C 941	14	24.6	660	4	US-09-925-065A-872318	Sequence 872318,
C 869	14	24.6	619	4	US-09-925-065A-496994	Sequence 496994, A	C 942	14	24.6	660	4	US-09-925-065A-872319	Sequence 872319,
C 870	14	24.6	619	4	US-09-925-065A-496995	Sequence 496995, A	C 943	14	24.6	660	4	US-09-925-065A-872320	Sequence 872320,
C 871	14	24.6	619	5	US-10-027-632-248470	Sequence 248470, A	C 944	14	24.6	660	4	US-09-925-065A-902929	Sequence 902929,
C 872	14	24.6	619	5	US-10-027-632-248471	Sequence 248471, A	C 945	14	24.6	660	4	US-09-925-065A-904644	Sequence 904644,
C 873	14	24.6	619	6	US-10-027-632-248470	Sequence 248470, A	C 946	14	24.6	663	5	US-10-027-632-181341	Sequence 181341,
C 874	14	24.6	619	6	US-10-027-632-248471	Sequence 248471, A	C 947	14	24.6	663	5	US-10-027-632-181343	Sequence 181343,
C 875	14	24.6	620	4	US-09-925-065A-760427	Sequence 760427, A	C 948	14	24.6	663	5	US-10-027-632-181343	Sequence 181343,
C 876	14	24.6	620	4	US-09-925-065A-760428	Sequence 760428, A	C 949	14	24.6	663	6	US-10-027-632-181341	Sequence 181341,
C 877	14	24.6	621	4	US-09-925-065A-430160	Sequence 430160, A	C 950	14	24.6	663	6	US-10-027-632-181342	Sequence 181342,
C 878	14	24.6	621	4	US-09-925-065A-760550	Sequence 760550, A	C 951	14	24.6	663	6	US-10-027-632-181343	Sequence 181343,
C 879	14	24.6	621	4	US-09-925-065A-760551	Sequence 760551, A	C 952	14	24.6	665	4	US-09-925-065A-699104	Sequence 699104,
C 880	14	24.6	621	4	US-09-925-065A-760552	Sequence 760552, A	C 953	14	24.6	665	4	US-09-925-065A-699105	Sequence 699105,
C 881	14	24.6	621	4	US-09-925-065A-767662	Sequence 767662, A	C 954	14	24.6	665	4	US-09-925-065A-807031	Sequence 807031,
C 882	14	24.6	623	5	US-10-027-632-43049	Sequence 43049, A	C 955	14	24.6	666	5	US-10-027-632-154788	Sequence 154788,
C 883	14	24.6	623	6	US-10-027-632-43049	Sequence 43049, A	C 956	14	24.6	666	5	US-10-027-632-154789	Sequence 154789,
C 884	14	24.6	624	4	US-09-925-065A-232357	Sequence 232357, A	C 957	14	24.6	666	6	US-10-027-632-154788	Sequence 154788,
C 885	14	24.6	624	4	US-09-925-065A-806461	Sequence 806461, A	C 958	14	24.6	666	6	US-10-027-632-154789	Sequence 154789,
C 886	14	24.6	625	4	US-09-925-065A-295290	Sequence 295290, A	C 959	14	24.6	668	4	US-09-925-065A-831444	Sequence 831444,
C 887	14	24.6	625	4	US-09-925-065A-800096	Sequence 800096, A	C 960	14	24.6	668	4	US-09-925-065A-295289	Sequence 295289,
C 888	14	24.6	626	4	US-09-925-065A-802959	Sequence 802959, A	C 961	14	24.6	671	4	US-09-925-065A-295289	Sequence 295289,
C 889	14	24.6	626	4	US-09-925-065A-856433	Sequence 856433, A	C 962	14	24.6	671	4	US-09-925-065A-723721	Sequence 723721,
C 890	14	24.6	628	4	US-09-925-065A-62051	Sequence 62051, A	C 963	14	24.6	679	8	US-10-653-047-4518	Sequence 4518, App
C 891	14	24.6	629	4	US-09-925-065A-62051	Sequence 62051, A	C 964	14	24.6	683	4	US-09-925-065A-80956	Sequence 80956, A
C 892	14	24.6	629	4	US-09-925-065A-893382	Sequence 893382, A	C 965	14	24.6	684	4	US-09-925-065A-912888	Sequence 912888,
C 893	14	24.6	630	4	US-09-925-065A-367970	Sequence 367970, A	C 966	14	24.6	684	4	US-09-925-065A-896045	Sequence 896045,
C 894	14	24.6	630	4	US-09-925-065A-791687	Sequence 791687, A	C 967	14	24.6	684	5	US-10-008-063-12	Sequence 890646,
C 895	14	24.6	631	4	US-09-925-065A-489602	Sequence 489602, A	C 968	14	24.6	689	7	US-10-404-599-33299	Sequence 33299, App
C 896	14	24.6	631	4	US-09-925-065A-650061	Sequence 650061, A	C 969	14	24.6	690	4	US-09-925-065A-915337	Sequence 915337,
C 897	14	24.6	631	4	US-09-925-065A-744331	Sequence 744331, A	C 970	14	24.6	691	5	US-10-027-632-135114	Sequence 135114,
C 898	14	24.6	631	4	US-09-925-065A-818941	Sequence 818941, A	C 971	14	24.6	691	6	US-10-027-632-135114	Sequence 135114,
C 899	14	24.6	632	4	US-09-925-065A-798352	Sequence 798352, A	C 972	14	24.6	695	3	US-09-828-634-52	Sequence 52, App1



```
C 973 14 24.6 696 3 US-09-974-300-7654 Sequence 7654, Ap
C 974 14 24.6 697 4 US-09-925-065A-58451 Sequence 58451, A
C 975 14 24.6 704 5 US-10-027-632-131208 Sequence 131208,
C 976 14 24.6 704 6 US-10-027-632-131208 Sequence 131208,
C 977 14 24.6 705 7 US-10-398-221-1581 Sequence 1581, Ap
C 978 14 24.6 710 3 US-09-925-300-17 Sequence 17, Appl
C 979 14 24.6 711 8 US-10-425-115-143954 Sequence 143954,
C 980 14 24.6 713 4 US-09-925-065A-719143 Sequence 719143,
C 981 14 24.6 725 7 US-10-260-238-3050 Sequence 3050, Ap
C 982 14 24.6 728 7 US-10-437-963-99734 Sequence 99734, A
C 983 14 24.6 742 4 US-09-925-065A-93710 Sequence 93710, A
C 984 14 24.6 743 4 US-09-925-065A-7056 Sequence 7056, Ap
C 985 14 24.6 743 4 US-09-925-065A-7057 Sequence 7057, Ap
C 986 14 24.6 743 9 US-10-487-901-4179 Sequence 4179, Ap
C 987 14 24.6 750 4 US-09-925-065A-29633 Sequence 29633, A
C 988 14 24.6 750 4 US-09-925-065A-29634 Sequence 29634, A
C 989 14 24.6 763 9 US-10-779-543-4518 Sequence 4518, Ap
C 990 14 24.6 770 4 US-09-925-065A-85478 Sequence 85478, A
C 991 14 24.6 770 4 US-09-925-065A-85479 Sequence 85479, A
C 992 14 24.6 776 5 US-10-027-632-123324 Sequence 123324,
C 993 14 24.6 776 6 US-10-027-632-123324 Sequence 123324,
C 994 14 24.6 782 5 US-10-027-632-132198 Sequence 132198,
C 995 14 24.6 782 6 US-10-027-632-132198 Sequence 132198,
C 996 14 24.6 797 5 US-10-027-632-151241 Sequence 151241,
C 997 14 24.6 797 6 US-10-027-632-151241 Sequence 151241,
C 998 14 24.6 799 3 US-09-809-391-288 Sequence 288, App
C 999 14 24.6 799 3 US-09-882-171-288 Sequence 288, App
C1000 14 24.6 799 6 US-10-164-861-288 Sequence 288, App
```

## ALIGNMENTS

```
RESULT 1
US-10-442-502-13
; Sequence 13, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSKHO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; US-10-442-502-13

Query Match 100.0%; Score 57; DB 6; Length 693;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 57
DB 228 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 284

RESULT 2
US-10-332-282-8
; Sequence 8, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
```

```
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
US-10-332-282-8

Query Match 100.0%; Score 57; DB 6; Length 954;
Best Local Similarity 100.0%; Pred. No. 1.4e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 57
DB 489 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 545
```

```
RESULT 3
US-10-402-466A-23
; Sequence 23, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gil, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 23
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP13 for a PA deletion mutant PA47.
US-10-402-466A-23

Query Match 100.0%; Score 57; DB 7; Length 1272;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 57
DB 60 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACAATGGG 116

RESULT 4
US-10-332-282-10
; Sequence 10, Application US/10332282
; Publication No. US20030170263A1
```



GENERAL INFORMATION:  
APPLICANT: The Secretary of State for Defence  
APPLICANT: Williamson, Ethel D  
APPLICANT: Walker, Julie  
APPLICANT: Walker, Nicola J  
APPLICANT: Baillie, Leslie WJ  
APPLICANT: Holden, Paula T  
APPLICANT: Flick-Smith, Helen C  
APPLICANT: Bullifent, Helen L  
APPLICANT: Tibball, Richard W  
TITLE OF INVENTION: Expression System  
FILE REFERENCE: CG/P/110/00D  
CURRENT APPLICATION NUMBER: US/10/332,282  
CURRENT FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: GB 0016702.3  
PRIOR FILING DATE: 2000-07-08  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 10  
LENGTH: 1278  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
US-10-332-282-10

Query Match 100.0%; Score 57; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
489 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 545

RESULT 5  
US-10-332-282-6  
Sequence 6, Application US/10332282  
Publication No. US20030170263A1  
GENERAL INFORMATION:  
APPLICANT: The Secretary of State for Defence  
APPLICANT: Williamson, Ethel D  
APPLICANT: Walker, Julie  
APPLICANT: Walker, Nicola J  
APPLICANT: Baillie, Leslie WJ  
APPLICANT: Holden, Paula T  
APPLICANT: Flick-Smith, Helen C  
APPLICANT: Bullifent, Helen L  
APPLICANT: Tibball, Richard W  
TITLE OF INVENTION: Expression System  
FILE REFERENCE: CG/P/110/00D  
CURRENT APPLICATION NUMBER: US/10/332,282  
CURRENT FILING DATE: 2003-01-07  
PRIOR APPLICATION NUMBER: GB 0016702.3  
PRIOR FILING DATE: 2000-07-08  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 6  
LENGTH: 1461  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
US-10-332-282-6

Query Match 100.0%; Score 57; DB 6; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57

DB 996 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1052

RESULT 6  
US-10-442-502-4  
Sequence 4, Application US/10442502  
Publication No. US2004009945A1  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PUSHKO, PETER  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135B  
CURRENT APPLICATION NUMBER: US/10/442,502  
CURRENT FILING DATE: 2003-05-21  
PRIOR APPLICATION NUMBER: 09/350,729  
PRIOR FILING DATE: 1999-07-09  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1710  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-10-442-502-4

Query Match 100.0%; Score 57; DB 6; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
498 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 554

RESULT 7  
US-10-402-466A-21  
Sequence 21, Application US/10402466A  
Publication No. US20040028695A1  
GENERAL INFORMATION:  
APPLICANT: Park, Sukjeon  
APPLICANT: Grl, Lillian  
TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTIN  
FILE REFERENCE: 18933-00005  
CURRENT APPLICATION NUMBER: US/10/402,466A  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: 60/372,152  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 34  
SEQ ID NO 21  
LENGTH: 1722  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION:  
OTHER INFORMATION: DNA coding sequence from pBP111 for a PA deletion mutant PA64.  
US-10-402-466A-21

Query Match 100.0%; Score 57; DB 7; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57  
510 CGCAATTGATCATTCACATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 566

RESULT 8



```
US-10-332-282-12
; Sequence 12, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 11
US-10-332-282-12

Query Match          100.0%; Score 57; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 996 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052

RESULT 9
US-09-848-909-22
; Sequence 22, Application US/09848909
; Publication No. US20020039568A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Sellman, Brett R.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; FILE REFERENCE: 00742/060002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; OTHER INFORMATION:
US-09-848-909-22

Query Match          100.0%; Score 57; DB 3; Length 2208;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 996 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052

RESULT 10
US-10-332-282-14
; Sequence 14, Application US/10332282
```

```
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 13
US-10-332-282-14

Query Match          100.0%; Score 57; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 996 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052

RESULT 11
US-10-402-466A-8
; Sequence 8, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Girl, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 8
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence for B. anthracis PA.
US-10-402-466A-8

Query Match          100.0%; Score 57; DB 7; Length 2208;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57
DB 996 CGCAATTGATCATTCTATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1052

RESULT 12
US-10-402-466A-11
```



```
; Sequence 11, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gil, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 11
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP105 for B. anthracis PA. The DNA cod
; OTHER INFORMATION: sequences for rPA (2208 bases) is identical to Sequence 8.
US-10-402-466A-11
```

```
Query Match          100.0%; Score 57; DB 7; Length 2208;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57
Db 996 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1052
```

```
RESULT 13
US-10-442-502-2
; Sequence 2, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: MELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-2
```

```
Query Match          100.0%; Score 57; DB 6; Length 2211;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57
Db 999 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1055
```

```
RESULT 14
US-10-638-006-3
; Sequence 3, Application US/10638006
; Publication No. US20040171121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA as
; APPLICANT: represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Roosevelt, Mary Jo
; APPLICANT: Hsu, S. Dana
; TITLE OF INVENTION: METHODS FOR PREPARING BACILLUS ANTHRACIS SPOULATION DEFICIENT
; TITLE OF INVENTION: MUTANTS AND FOR PRODUCING RECOMBINANT BACILLUS ANTHRACIS
; FILE REFERENCE: 4239-66891
; CURRENT APPLICATION NUMBER: US/10/638,006
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,285
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mature double mutant protective antigen
US-10-638-006-3
```

```
Query Match          100.0%; Score 57; DB 7; Length 2235;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57
Db 1023 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1079
```

```
RESULT 15
US-10-442-502-3
; Sequence 3, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: MELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2232
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-3
```

```
Query Match          100.0%; Score 57; DB 6; Length 2232;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 57
Db 1080 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAACAATGGG 1136
```

```
RESULT 16
US-09-747-521-3
; Sequence 3, Application US/09747521
; Patent No. US20020051791A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Galloway, Darrel
; APPLICANT: Mateczun, Alfred
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04079
; CURRENT APPLICATION NUMBER: US/09/747,521
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; US-09-747-521-3

Query Match          100.0%; Score 57; DB 3; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57
DB 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 1139

RESULT 17
US-10-106-014-3
; Sequence 3, Application US/10106014
; Publication No. US20020142002A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106,014
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
; US-10-106-014-3

Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57
DB 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 1139

RESULT 18
US-10-105-695-3
; Sequence 3, Application US/10105695
; Publication No. US20020197272A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04115
; CURRENT APPLICATION NUMBER: US/10/105,695
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
```

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
; US-10-105-695-3

Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57
DB 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 1139

RESULT 19
US-10-105-694-3
; Sequence 3, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus An
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
; US-10-105-694-3

Query Match          100.0%; Score 57; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.5e-22;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 57
DB 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGCTGAAACATGGG 1139

RESULT 20
US-10-442-502-1
; Sequence 1, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
```



NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 2295  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-10-442-502-1

Query Match 100.0%; Score 57; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 1083 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 1139

RESULT 21  
US-10-751-103-3

Sequence 3, Application US/10751103  
Publication No. US20050148529A1  
GENERAL INFORMATION:  
APPLICANT: Schmaljohn, Connie S.  
APPLICANT: Fuller, James T.  
TITLE OF INVENTION: Nucleic Acid Immunization  
FILE REFERENCE: 033267-021  
CURRENT APPLICATION NUMBER: US/10/751,103  
CURRENT FILING DATE: 2004-01-05  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 2605  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (174)...(2465)  
US-10-751-103-3

Query Match 100.0%; Score 57; DB 9; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 1.5e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 1256 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 1312

RESULT 22  
US-10-410-647-29

Sequence 29, Application US/10410647  
Publication No. US20030235818A1  
GENERAL INFORMATION:  
APPLICANT: PLEXUS VACCINE, INC.  
APPLICANT: Kattitch, Vsevolod  
APPLICANT: Bortner, Andrew  
APPLICANT: Deans, Robert  
APPLICANT: Sumner, Mary  
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME  
FILE REFERENCE: PLEX110-1  
CURRENT APPLICATION NUMBER: US/10/410,647  
CURRENT FILING DATE: 2003-04-08  
PRIOR APPLICATION NUMBER: US 60/373,668  
PRIOR FILING DATE: 2002-04-17  
PRIOR APPLICATION NUMBER: US 60/371,256  
PRIOR FILING DATE: 2002-04-08  
PRIOR APPLICATION NUMBER: US 60/371,250  
PRIOR FILING DATE: 2002-04-08  
NUMBER OF SEQ ID NOS: 46  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 29  
LENGTH: 4235  
TYPE: DNA

ORGANISM: Bacillus anthracis  
US-10-410-647-29

Query Match 100.0%; Score 57; DB 6; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 2886 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 2942

RESULT 23  
US-10-402-466A-7

Sequence 7, Application US/10402466A  
Publication No. US20040028695A1  
GENERAL INFORMATION:  
APPLICANT: Park, Sukjoon  
APPLICANT: Giri, Laljan  
TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTIN  
FILE REFERENCE: 18933-00005  
CURRENT APPLICATION NUMBER: US/10/402,466A  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: 60/372,152  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 34  
SEQ ID NO 7  
LENGTH: 8198  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY:  
LOCATION:  
OTHER INFORMATION: Expression vector for B. anthracis Protective Antigen (PA). E  
OTHER INFORMATION: sequence is shown since the vector sequence is different from  
OTHER INFORMATION: of the pBP vectors. The PA coding sequence is from 3735 to 59  
US-10-402-466A-7

Query Match 100.0%; Score 57; DB 7; Length 8198;  
Best Local Similarity 100.0%; Pred. No. 1.6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 57  
DB 4730 CGCAATTGATCATTCATCTCTGACGAGGGGAAAGAACTTGCGCTGAACAATGGG 4786

RESULT 24  
US-10-402-466A-10

Sequence 10, Application US/10402466A  
Publication No. US20040028695A1  
GENERAL INFORMATION:  
APPLICANT: Park, Sukjoon  
APPLICANT: Giri, Laljan  
TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTIN  
FILE REFERENCE: 18933-00005  
CURRENT APPLICATION NUMBER: US/10/402,466A  
CURRENT FILING DATE: 2003-03-20  
PRIOR APPLICATION NUMBER: 60/372,152  
PRIOR FILING DATE: 2002-04-12  
NUMBER OF SEQ ID NOS: 34  
SEQ ID NO 10  
LENGTH: 9286  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY:  
LOCATION:  
OTHER INFORMATION: Dual expression vector pBP105 for B. anthracis PA and LF30. B.  
OTHER INFORMATION: sequence is shown since the vector sequence contains two codin  
OTHER INFORMATION: regions. The coding region for PA is from 3735 to 5942 and th



OTHER INFORMATION: region for LFP3 is from 6391 to 7161.  
US-10-402-466A-10

Query Match 100.0%; Score 57; DB 7; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 1,6e-22;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCAATTGATCATCTACTCTCTAGCAGGAGGAAGAACTTGAGGCTGAAACATGGG 57  
DB 4730 CGCAATTGATCATCTACTCTCTAGCAGGAGGAAGAACTTGAGGCTGAAACATGGG 4786

RESULT 25  
US-10-798-949A-9/c  
; Sequence 9, Application US/10798949A  
; Publication No. US20050064450A1  
; GENERAL INFORMATION:  
; APPLICANT: A.L. Tech Biomedical, Inc.  
; APPLICANT: University of Utah  
; APPLICANT: Joe N. Lucas  
; APPLICANT: Zhong Chen

TITLE OF INVENTION: Methods Of Making Repetitive Sequences  
FILE REFERENCE: 44222-002Pc1  
CURRENT APPLICATION NUMBER: US/10/798,949A  
CURRENT FILING DATE: 2004-03-12  
PRIOR APPLICATION NUMBER: US 60/453,962  
PRIOR FILING DATE: 2003-03-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer

US-10-798-949A-9

Query Match 33.3%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAGCAGGAGGAAGAACTTG 42  
DB 19 TAGCAGGAGGAAGAACTTG 1

RESULT 26  
US-10-798-949A-11/c

; Sequence 11, Application US/10798949A  
; Publication No. US20050064450A1  
; GENERAL INFORMATION:  
; APPLICANT: A.L. Tech Biomedical, Inc.  
; APPLICANT: University of Utah  
; APPLICANT: Joe N. Lucas  
; APPLICANT: Zhong Chen  
TITLE OF INVENTION: Methods Of Making Repetitive Sequences  
FILE REFERENCE: 44222-002Pc1  
CURRENT APPLICATION NUMBER: US/10/798,949A  
CURRENT FILING DATE: 2004-03-12  
PRIOR APPLICATION NUMBER: US 60/453,962  
PRIOR FILING DATE: 2003-03-13  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 19  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: primer

US-10-798-949A-11

Query Match 33.3%; Score 19; DB 9; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TAGCAGGAGGAAGAACTTG 42  
DB 19 TAGCAGGAGGAAGAACTTG 1

RESULT 27  
US-10-068-238-6/c

; Sequence 6, Application US/10068238  
; Publication No. US20030082563A1  
; GENERAL INFORMATION:  
; APPLICANT: Bell, Constance A.  
; APPLICANT: Uhl, James  
; APPLICANT: Cockerill, Franklin  
TITLE OF INVENTION: Detection of Bacillus Anthracis  
FILE REFERENCE: 07039-372001  
CURRENT APPLICATION NUMBER: US/10/068,238  
CURRENT FILING DATE: 2002-02-05  
PRIOR APPLICATION NUMBER: US 60/329,826  
PRIOR FILING DATE: 2001-10-15  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: oligonucleotide

US-10-068-238-6

Query Match 31.6%; Score 18; DB 5; Length 18;  
Best Local Similarity 100.0%; Pred. No. 4.1;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 AAAGAACTTGGGTGAAA 50  
DB 18 AAAGAACTTGGGTGAAA 1

RESULT 28  
US-09-925-065A-401809

; Sequence 401809, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 401809  
LENGTH: 570  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-401809

Query Match 31.6%; Score 18; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5;



Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAATGGG 57  
|||  
Db 22 TTGGGCTGAACAATGGG 39

## RESULT 29

US-09-925-065A-401810  
; Sequence 401810, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 401810  
; LENGTH: 570  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-401810

Query Match 31.6%; Score 18; DB 4; Length 570;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAATGGG 57  
|||  
Db 22 TTGGGCTGAACAATGGG 39

## RESULT 30

US-09-925-065A-903116  
; Sequence 903116, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 903116  
; LENGTH: 574  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-903116

Query Match 31.6%; Score 18; DB 4; Length 574;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAATGGG 57  
|||  
Db 395 TTGGGCTGAACAATGGG 412

## RESULT 31

US-09-925-065A-588142/C  
; Sequence 588142, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 588142  
; LENGTH: 595  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-588142

Query Match 31.6%; Score 18; DB 4; Length 595;  
Best Local Similarity 100.0%; Pred. No. 5;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAATGGG 57  
|||  
Db 280 TTGGGCTGAACAATGGG 263

## RESULT 32

US-09-925-065A-588143/C  
; Sequence 588143, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 588143  
; LENGTH: 595



```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-588143

Query Match      31.6%; Score 18; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 TTGGGCTGAACAATGGG 57
Db      280 TTGGGCTGAACAATGGG 263

RESULT 33
US-09-925-065A-868337/c
; Sequence 868337, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US 09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 868337
; LENGTH: 602
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-868337

Query Match      31.6%; Score 18; DB 4; Length 602;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 TTGGGCTGAACAATGGG 57
Db      417 TTGGGCTGAACAATGGG 400

RESULT 34
US-10-027-632-228164/c
; Sequence 228164, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358

; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 228164
; LENGTH: 633
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-228164

Query Match      31.6%; Score 18; DB 6; Length 633;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      40 TTGGGCTGAACAATGGG 57
Db      231 TTGGGCTGAACAATGGG 214

RESULT 36
US-09-925-065A-872665
; Sequence 872665, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
```



```
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 872665
; LENGTH: 670
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-872665
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Best Local Similarity 100.0%; Pred. No. 5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      40 TTGGGCTGAACATGGG 57
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Db      225 TTGGGCTGAACATGGG 242
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RESULT 37
US-09-925-065A-872666
; Sequence 872666, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
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; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: Nucleotide Polymorphisms in the Human Genome
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 872666
; LENGTH: 670
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-872666
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Query Match          31.6%; Score 18; DB 4; Length 670;
Best Local Similarity 100.0%; Pred. No. 5;
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QY      40 TTGGGCTGAACATGGG 57
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RESULT 38
US-10-450-763-6904/C
; Sequence 6904, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
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; CURRENT APPLICATION NUMBER: US/10/450,763
; CURRENT FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 6904
; LENGTH: 1305
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1)..(1133)
; OTHER INFORMATION: 90% homologous to Homo sapiens unknown protein, accession
; US-10-450-763-6904
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Query Match          31.6%; Score 18; DB 9; Length 1305;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      40 TTGGGCTGAACATGGG 57
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Db      1290 TTGGGCTGAACATGGG 1273
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RESULT 39
US-10-685-837-1
; Sequence 1, Application US/10685837
; Publication No. US20050071893A1
; GENERAL INFORMATION:
; APPLICANT: Seibler, Jost
; APPLICANT: Schwenk, Frieder
; APPLICANT: Kuhn, Ralf
; TITLE OF INVENTION: siRNA mediated gene silencing in transgenic animals
; FILE REFERENCE: 022698us JH/BM
; CURRENT APPLICATION NUMBER: US/10/685,837
; CURRENT FILING DATE: 2003-10-15
; PRIOR APPLICATION NUMBER: US60/420,476
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US60/467,814
; PRIOR FILING DATE: 2003-05-03
; PRIOR APPLICATION NUMBER: US60/485,969
; PRIOR FILING DATE: 2003-07-03
; PRIOR APPLICATION NUMBER: 02023283.1
; PRIOR FILING DATE: 2002-10-17
; NUMBER OF SEQ ID NOS: 220
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 13139
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Rosa26 locus
; OTHER INFORMATION: sequence
US-10-685-837-1
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Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      34 AAGAACTGGGCTGAAC 51
      |||||
Db      10044 AAGAACTGGGCTGAAC 10061
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RESULT 40
US-10-617-320-1352/C
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; Sequence 1352, Application US/10617320  
; Publication No. US20050136404A1  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/617,320  
; FILING DATE: 10-Jul-2003  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Ariniello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: CTC-011  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (781)893-5007  
; TELEFAX: (781)893-8277  
; INFORMATION FOR SEQ ID NO: 1352:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 327 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: circular  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pneumoniae  
; FEATURE:  
; NAME/KEY: misc feature  
; LOCATION: (8) LOCATION 1...327  
; SEQUENCE DESCRIPTION: SEQ ID NO: 1352:  
US-10-617-320-1352  
  
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Best Local Similarity 100.0%; Pred. No. 18;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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|||  
DB 296 GGAAAGAACTGGGCTG 280

Search completed: April 12, 2006, 06:04:28  
Job time : 174.397 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 05:20:02 ; Search time 232.795 Seconds  
(without alignments)  
986.217 Million cell updates/sec

Title: US-10-712-654-22

Perfect score: 57

Sequence: 1 cgcacatgcattccactatc.....actgggctgaacaatggg 57

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 9281099 seqs, 2013915447 residues

Word size : 1

Total number of hits satisfying chosen parameters: 18561424

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications NA New:\*  
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4: /SIDS5/ptodata/2/pubphn/PCT\_NEW\_PUB.seq:\*  
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11: /SIDS5/ptodata/2/pubphn/US11\_NEW\_PUB.seq:\*  
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13: /SIDS5/ptodata/2/pubphn/US11\_NEW\_PUB.seq3:\*  
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15: /SIDS5/ptodata/2/pubphn/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	57	100.0	2295	14 US-11-055-557-11	Sequence 11, Appl
2	57	100.0	2295	14 US-11-055-557-15	Sequence 15, Appl
3	57	100.0	2295	14 US-11-055-557-19	Sequence 19, Appl
4	57	100.0	2304	14 US-11-055-557-1	Sequence 1, Appl
5	57	100.0	2304	14 US-11-055-557-9	Sequence 9, Appl
6	57	100.0	2304	14 US-11-055-557-13	Sequence 13, Appl
7	57	100.0	2307	14 US-11-055-557-3	Sequence 3, Appl
8	57	100.0	2307	14 US-11-055-557-5	Sequence 5, Appl
9	57	100.0	2307	14 US-11-055-557-7	Sequence 7, Appl
10	57	100.0	2307	14 US-11-055-557-17	Sequence 17, Appl
11	57	100.0	2307	14 US-11-055-557-17	Sequence 17, Appl
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13	18	31.6	574	6 US-09-925-065A-401810	Sequence 401810,
14	18	31.6	595	6 US-09-925-065A-588142	Sequence 588142,
15	18	31.6	595	6 US-09-925-065A-588143	Sequence 588143,
16	18	31.6	602	6 US-09-925-065A-868337	Sequence 868337,
17	18	31.6	670	6 US-09-925-065A-872665	Sequence 872665,
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19	17	29.8	579	6 US-09-925-065A-5048	Sequence 5048, Ap
20	17	29.8	579	9 US-10-301-480-106285	Sequence 106285,
21	17	29.8	579	10 US-10-301-480-719694	Sequence 719694,
22	17	29.8	1137	6 US-09-925-065A-546147	Sequence 546147,
23	17	29.8	1137	10 US-10-301-480-524097	Sequence 524097,
24	17	29.8	1137	10 US-10-301-480-1137506	Sequence 1137506,
25	17	29.8	4802	8 US-10-750-185-29644	Sequence 29644, A
26	17	29.8	4802	8 US-10-750-653-29644	Sequence 29644, A
27	17	29.8	61487	14 US-11-124-367A-5103	Sequence 5103, Ap
28	17	29.8	62224	14 US-11-124-367A-5066	Sequence 5066, Ap
29	17	28.1	201	8 US-10-995-561-26689	Sequence 26689, A
30	16	28.1	201	14 US-11-124-368A-155226	Sequence 15526, A
31	16	28.1	456	10 US-10-301-480-523568	Sequence 523568,
32	16	28.1	456	10 US-10-301-480-1116977	Sequence 1116977,
33	16	28.1	490	6 US-09-925-065A-468074	Sequence 468074,
34	16	28.1	510	6 US-09-925-065A-406203	Sequence 406203,
35	16	28.1	539	10 US-10-301-480-472902	Sequence 472902,
36	16	28.1	539	10 US-10-301-480-1086311	Sequence 1086311,
37	16	28.1	544	6 US-09-925-065A-436554	Sequence 436554,
38	16	28.1	544	6 US-09-925-065A-436555	Sequence 436555,
39	16	28.1	544	10 US-10-301-480-498221	Sequence 498221,
40	16	28.1	544	10 US-10-301-480-498222	Sequence 498222,
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42	16	28.1	544	10 US-10-301-480-1111631	Sequence 1111631,
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44	16	28.1	563	6 US-09-925-065A-6450	Sequence 6450, Ap
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56	16	28.1	603	10 US-10-301-480-924405	Sequence 924905,
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62	16	28.1	631	6 US-09-925-065A-736347	Sequence 736347,
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64	16	28.1	675	9 US-10-932-182A-82586	Sequence 82586, A
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66	16	28.1	970	6 US-09-925-065A-86642	Sequence 86642, A
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68	16	28.1	970	10 US-10-301-480-801291	Sequence 801291,
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70	16	28.1	1074	9 US-10-301-480-192256	Sequence 192256,
71	16	28.1	1074	10 US-10-301-480-805655	Sequence 805655,
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75	16	28.1	1479	11 US-11-096-568A-15251	Sequence 15251, A
76	16	28.1	1517	11 US-11-096-568A-18517	Sequence 18517, A
77	16	28.1	1576	8 US-10-750-185-19827	Sequence 19827, A
78	16	28.1	1576	8 US-10-750-185-15581	Sequence 15581, A
79	16	28.1	1602	8 US-10-750-653-55581	Sequence 35581, A
80	16	28.1	1602	8 US-10-750-653-55581	Sequence 35581, A
81	16	28.1	1682	8 US-10-750-185-61942	Sequence 61942, A
82	16	28.1	1682	8 US-10-750-653-61942	Sequence 61942, A
83	16	28.1	1762	6 US-09-925-065A-685993	Sequence 685993,
84	16	28.1	2180	8 US-10-750-653-25643	Sequence 25643, A
85	16	28.1	2180	8 US-10-750-653-25643	Sequence 25643, A
86	16	28.1	2635	11 US-11-072-512-635	Sequence 635, App
87	16	28.1	27615	14 US-11-136-527-514	Sequence 514, App
88	16	28.1	305312	9 US-10-995-561-13226	Sequence 13236, A
89	16	28.1	341511	9 US-10-472-808A-3	Sequence 3, Appl1
90	15	26.3	25	9 US-10-934-048A-86452	Sequence 86452, A
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C 93	15	26.3	201	8	US-10-995-561-43251	Sequence 43251, A	15	26.3	768	6	US-09-925-0655A-5508	Sequence 5508, Ap
C 94	15	26.3	201	8	US-10-995-561-43254	Sequence 43254, A	15	26.3	768	6	US-09-925-0655A-5509	Sequence 5509, Ap
C 95	15	26.3	201	14	US-11-124-368A-14797	Sequence 14797, A	15	26.3	768	9	US-10-301-480-10673	Sequence 10673, A
C 96	15	26.3	201	14	US-11-124-367A-28798	Sequence 28798, A	15	26.3	768	9	US-10-301-480-10674	Sequence 10674, A
C 97	15	26.3	201	14	US-11-124-367A-28799	Sequence 28799, A	15	26.3	768	9	US-10-301-480-10675	Sequence 10675, A
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C 99	15	26.3	380	6	US-09-925-065A-47617	Sequence 47617, A	15	26.3	768	10	US-10-301-480-120152	Sequence 76015, A
C 100	15	26.3	405	6	US-09-925-065A-141559	Sequence 141559, A	15	26.3	768	10	US-10-301-480-120152	Sequence 76015, A
C 101	15	26.3	425	9	US-10-301-480-42869	Sequence 42869, A	15	26.3	768	10	US-10-301-480-120154	Sequence 72015, A
C 102	15	26.3	425	9	US-10-301-480-42869	Sequence 42869, A	15	26.3	768	10	US-10-301-480-120155	Sequence 72015, A
C 103	15	26.3	427	6	US-09-925-065A-474778	Sequence 474778, A	15	26.3	840	10	US-10-301-480-573305	Sequence 573305, A
C 104	15	26.3	440	9	US-10-301-480-23710	Sequence 23710, A	15	26.3	840	10	US-10-301-480-1186714	Sequence 1186714, A
C 105	15	26.3	440	10	US-10-301-480-637119	Sequence 637119, A	15	26.3	991	10	US-10-301-480-595119	Sequence 595119, A
C 106	15	26.3	450	6	US-09-925-065A-221537	Sequence 221537, A	15	26.3	992	10	US-10-301-480-595120	Sequence 595120, A
C 107	15	26.3	455	10	US-10-301-480-306821	Sequence 306821, A	15	26.3	992	10	US-10-301-480-595120	Sequence 595120, A
C 108	15	26.3	455	10	US-10-301-480-920230	Sequence 920230, A	15	26.3	992	10	US-10-301-480-595120	Sequence 595120, A
C 109	15	26.3	457	6	US-09-925-065A-842357	Sequence 842357, A	15	26.3	996	10	US-10-301-480-536838	Sequence 536838, A
C 110	15	26.3	457	6	US-09-925-065A-842358	Sequence 842358, A	15	26.3	996	10	US-10-301-480-1150247	Sequence 1150247, A
C 111	15	26.3	465	6	US-09-925-065A-164561	Sequence 164561, A	15	26.3	1058	8	US-10-750-185-57381	Sequence 57381, A
C 112	15	26.3	469	10	US-10-301-480-256905	Sequence 256905, A	15	26.3	1058	8	US-10-750-623-57381	Sequence 57381, A
C 113	15	26.3	469	10	US-10-301-480-870314	Sequence 870314, A	15	26.3	1161	9	US-10-301-480-95759	Sequence 95759, A
C 114	15	26.3	472	10	US-10-301-480-256906	Sequence 256906, A	15	26.3	1161	9	US-10-301-480-95760	Sequence 95760, A
C 115	15	26.3	472	10	US-10-301-480-870315	Sequence 870315, A	15	26.3	1161	9	US-10-301-480-95761	Sequence 95761, A
C 116	15	26.3	475	6	US-09-925-065A-164560	Sequence 164560, A	15	26.3	1161	9	US-10-301-480-95762	Sequence 95762, A
C 117	15	26.3	480	10	US-10-301-480-244538	Sequence 244538, A	15	26.3	1161	10	US-10-301-480-709168	Sequence 709168, A
C 118	15	26.3	480	10	US-10-301-480-857947	Sequence 857947, A	15	26.3	1161	10	US-10-301-480-709169	Sequence 709169, A
C 119	15	26.3	481	6	US-09-925-065A-470488	Sequence 470488, A	15	26.3	1161	10	US-10-301-480-709170	Sequence 709170, A
C 120	15	26.3	484	6	US-09-925-065A-886559	Sequence 886559, A	15	26.3	1161	10	US-10-301-480-709171	Sequence 709171, A
C 121	15	26.3	506	6	US-09-925-065A-150588	Sequence 150588, A	15	26.3	1161	6	US-09-925-065A-74833	Sequence 74833, A
C 122	15	26.3	510	6	US-09-925-065A-606973	Sequence 606973, A	15	26.3	1172	6	US-09-925-065A-74834	Sequence 74834, A
C 123	15	26.3	524	6	US-09-925-065A-501053	Sequence 501053, A	15	26.3	1172	6	US-09-925-065A-74835	Sequence 74835, A
C 124	15	26.3	520	6	US-09-925-065A-501054	Sequence 501054, A	15	26.3	1172	6	US-09-925-065A-74836	Sequence 74836, A
C 125	15	26.3	520	6	US-09-925-065A-501055	Sequence 501055, A	15	26.3	1172	9	US-10-301-480-176072	Sequence 176072, A
C 126	15	26.3	520	6	US-09-925-065A-501056	Sequence 501056, A	15	26.3	1172	9	US-10-301-480-176073	Sequence 176073, A
C 127	15	26.3	521	10	US-10-301-480-495469	Sequence 495469, A	15	26.3	1172	9	US-10-301-480-176074	Sequence 176074, A
C 128	15	26.3	521	10	US-10-301-480-1108878	Sequence 1108878, A	15	26.3	1172	9	US-10-301-480-176075	Sequence 176075, A
C 129	15	26.3	522	6	US-09-925-065A-169339	Sequence 169339, A	15	26.3	1172	10	US-10-301-480-789481	Sequence 789481, A
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C 133	15	26.3	547	6	US-09-925-065A-259820	Sequence 259820, A	15	26.3	1333	8	US-10-750-185-33980	Sequence 33980, A
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C 136	15	26.3	550	6	US-09-925-065A-33419	Sequence 33419, A	15	26.3	1794	8	US-10-750-185-54523	Sequence 54523, A
C 137	15	26.3	550	9	US-10-301-480-134657	Sequence 134657, A	15	26.3	1794	8	US-10-750-623-54523	Sequence 54523, A
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282	14	24.6	201	8	US-10-995-561-83159	Sequence 83159, A	355	14	24.6	354	11	US-11-199-739-207	Sequence 207, App
283	14	24.6	201	8	US-10-995-561-83160	Sequence 83160, A	356	14	24.6	354	11	US-11-199-739-251	Sequence 251, App
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407	14	24.6	357	11	US-11-199-739-535	Sequence 535, App	480	14	24.6	363	14	US-11-049-536-623	Sequence 623, App
408	14	24.6	357	11	US-11-199-739-539	Sequence 539, App	481	14	24.6	363	14	US-11-049-536-683	Sequence 683, App
409	14	24.6	357	11	US-11-199-739-543	Sequence 543, App	482	14	24.6	363	14	US-11-049-536-695	Sequence 695, App
410	14	24.6	357	11	US-11-199-739-551	Sequence 551, App	483	14	24.6	366	11	US-11-199-739-187	Sequence 187, App
411	14	24.6	357	11	US-11-199-739-563	Sequence 563, App	484	14	24.6	366	11	US-11-199-739-279	Sequence 279, App
412	14	24.6	357	11	US-11-199-739-567	Sequence 567, App	485	14	24.6	366	11	US-11-199-739-303	Sequence 303, App
413	14	24.6	357	11	US-11-199-739-571	Sequence 571, App	486	14	24.6	366	11	US-11-199-739-375	Sequence 375, App
414	14	24.6	357	11	US-11-199-739-571	Sequence 571, App	487	14	24.6	366	14	US-11-049-536-187	Sequence 187, App
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416	14	24.6	357	11	US-11-199-739-651	Sequence 651, App	489	14	24.6	366	14	US-11-049-536-303	Sequence 303, App
417	14	24.6	357	11	US-11-199-739-663	Sequence 663, App	490	14	24.6	366	14	US-11-049-536-575	Sequence 575, App
418	14	24.6	357	14	US-11-049-536-247	Sequence 247, App	491	14	24.6	369	9	US-10-993-543-91	Sequence 91, Appl
419	14	24.6	357	14	US-11-049-536-263	Sequence 263, App	492	14	24.6	369	9	US-10-993-543-111	Sequence 111, Appl
420	14	24.6	357	14	US-11-049-536-283	Sequence 283, App	493	14	24.6	369	11	US-11-199-739-59	Sequence 59, Appl
421	14	24.6	357	14	US-11-049-536-307	Sequence 307, App	494	14	24.6	369	11	US-11-199-739-239	Sequence 239, App
422	14	24.6	357	14	US-11-049-536-315	Sequence 315, App	495	14	24.6	369	11	US-11-199-739-291	Sequence 291, App
423	14	24.6	357	14	US-11-049-536-331	Sequence 331, App	496	14	24.6	369	11	US-11-199-739-379	Sequence 379, App
424	14	24.6	357	14	US-11-049-536-363	Sequence 363, App	497	14	24.6	369	11	US-11-199-739-399	Sequence 399, App
425	14	24.6	357	14	US-11-049-536-371	Sequence 371, App	498	14	24.6	369	11	US-11-199-739-407	Sequence 407, App
426	14	24.6	357	14	US-11-049-536-395	Sequence 395, App	499	14	24.6	369	11	US-11-199-739-411	Sequence 411, App
427	14	24.6	357	14	US-11-049-536-419	Sequence 419, App	500	14	24.6	369	11	US-11-199-739-511	Sequence 511, App
428	14	24.6	357	14	US-11-049-536-451	Sequence 451, App	501	14	24.6	369	14	US-11-049-536-59	Sequence 59, Appl
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437	14	24.6	357	14	US-11-049-536-535	Sequence 535, App	510	14	24.6	372	11	US-11-199-739-299	Sequence 299, App
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439	14	24.6	357	14	US-11-049-536-543	Sequence 543, App	512	14	24.6	372	11	US-11-199-739-359	Sequence 359, App
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442	14	24.6	357	14	US-11-049-536-567	Sequence 567, App	515	14	24.6	372	14	US-11-049-536-299	Sequence 299, App
443	14	24.6	357	14	US-11-049-536-571	Sequence 571, App	516	14	24.6	372	14	US-11-049-536-311	Sequence 311, App
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447	14	24.6	360	11	US-11-199-739-231	Sequence 231, App	520	14	24.6	375	11	US-11-199-739-43	Sequence 43, Appl
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449	14	24.6	360	11	US-11-199-739-463	Sequence 463, App	522	14	24.6	375	11	US-11-199-739-175	Sequence 175, App
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455	14	24.6	360	11	US-11-199-739-667	Sequence 667, App	528	14	24.6	375	11	US-11-199-739-479	Sequence 479, App
456	14	24.6	360	14	US-11-049-536-231	Sequence 231, App	529	14	24.6	375	11	US-11-199-739-487	Sequence 487, App



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539	14	24.6	375	14	US-11-049-536-479	Sequence 479, App	612	14	24.6	396	14	US-11-199-739-31	Sequence 31, Appl
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542	14	24.6	378	9	US-10-993-543-95	Sequence 95, Appl	615	14	24.6	396	14	US-11-049-536-31	Sequence 31, Appl
543	14	24.6	378	11	US-11-199-739-255	Sequence 255, App	616	14	24.6	398	9	US-10-993-543-175	Sequence 175, App
544	14	24.6	378	11	US-11-199-739-323	Sequence 323, App	617	14	24.6	399	9	US-10-993-543-3	Sequence 3, Appl
545	14	24.6	378	11	US-11-199-739-343	Sequence 343, App	618	14	24.6	399	9	US-10-993-543-123	Sequence 123, App
546	14	24.6	378	11	US-11-199-739-423	Sequence 375, App	619	14	24.6	399	9	US-10-993-543-183	Sequence 183, App
547	14	24.6	378	11	US-11-199-739-475	Sequence 423, App	620	14	24.6	402	9	US-10-993-543-23	Sequence 23, Appl
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549	14	24.6	378	14	US-11-049-536-255	Sequence 325, App	622	14	24.6	402	9	US-10-993-543-135	Sequence 135, App
550	14	24.6	378	14	US-11-049-536-323	Sequence 323, App	623	14	24.6	402	9	US-10-993-543-171	Sequence 171, App
551	14	24.6	378	14	US-11-049-536-343	Sequence 343, App	624	14	24.6	405	9	US-10-993-543-35	Sequence 35, Appl
552	14	24.6	378	14	US-11-049-536-375	Sequence 375, App	625	14	24.6	405	9	US-10-993-543-43	Sequence 43, Appl
553	14	24.6	378	14	US-11-049-536-423	Sequence 423, App	626	14	24.6	405	9	US-10-993-543-59	Sequence 59, Appl
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555	14	24.6	381	9	US-10-993-543-153	Sequence 153, App	628	14	24.6	405	9	US-10-993-543-119	Sequence 119, App
556	14	24.6	381	11	US-11-199-739-595	Sequence 325, App	629	14	24.6	411	9	US-10-993-543-75	Sequence 75, Appl
557	14	24.6	381	11	US-11-199-739-527	Sequence 327, App	630	14	24.6	411	9	US-10-993-543-99	Sequence 99, Appl
558	14	24.6	381	11	US-11-199-739-447	Sequence 447, App	631	14	24.6	412	11	US-11-199-739-35	Sequence 35, Appl
559	14	24.6	381	11	US-11-199-739-455	Sequence 455, App	632	14	24.6	412	14	US-11-049-536-35	Sequence 35, Appl
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562	14	24.6	381	14	US-11-049-536-447	Sequence 447, App	635	14	24.6	413	11	US-11-199-739-71	Sequence 71, Appl
563	14	24.6	383	11	US-11-049-536-455	Sequence 455, App	636	14	24.6	413	11	US-11-199-739-79	Sequence 79, Appl
564	14	24.6	383	11	US-11-199-739-63	Sequence 63, Appl	637	14	24.6	413	11	US-11-199-739-87	Sequence 87, Appl
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566	14	24.6	384	9	US-10-993-543-71	Sequence 71, Appl	639	14	24.6	413	14	US-11-049-536-67	Sequence 67, Appl
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569	14	24.6	384	11	US-11-199-739-579	Sequence 579, App	642	14	24.6	413	14	US-11-049-536-87	Sequence 87, Appl
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575	14	24.6	387	14	US-11-049-536-101	Sequence 101, App	648	14	24.6	425	14	US-11-049-536-113	Sequence 113, App
576	14	24.6	387	9	US-10-993-543-7	Sequence 7, Appl	649	14	24.6	426	9	US-10-993-543-131	Sequence 131, App
577	14	24.6	387	9	US-10-993-543-27	Sequence 27, Appl	650	14	24.6	429	11	US-11-199-739-27	Sequence 27, Appl
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592	14	24.6	390	14	US-11-049-536-887	Sequence 387, App	665	14	24.6	458	10	US-10-301-480-630021	Sequence 630021, A
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598	14	24.6	393	9	US-10-993-543-127	Sequence 127, App	671	14	24.6	474	6	US-09-925-065A-459129	Sequence 459129, A
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969 14 24.6 632 6 US-09-925-065A-798352 Sequence 798352,
970 14 24.6 632 6 US-09-925-065A-805081 Sequence 805081,
971 14 24.6 632 9 US-10-301-480-42639 Sequence 42639, A
972 14 24.6 632 9 US-10-301-480-42640 Sequence 42640, A
973 14 24.6 632 9 US-10-301-480-42641 Sequence 42641, A
974 14 24.6 632 10 US-10-301-480-656048 Sequence 656048,
975 14 24.6 632 10 US-10-301-480-656049 Sequence 656049,
976 14 24.6 632 10 US-10-301-480-656050 Sequence 656050,
977 14 24.6 633 6 US-09-925-065A-522719 Sequence 522719,
978 14 24.6 633 6 US-09-925-065A-522720 Sequence 522720,
979 14 24.6 633 6 US-09-925-065A-749638 Sequence 749638,
980 14 24.6 633 6 US-09-925-065A-756429 Sequence 756429,
981 14 24.6 633 6 US-09-925-065A-793578 Sequence 793578,
982 14 24.6 633 6 US-09-925-065A-826491 Sequence 826491,
983 14 24.6 634 6 US-09-925-065A-762980 Sequence 762980,
984 14 24.6 634 6 US-09-925-065A-830876 Sequence 830876,
985 14 24.6 635 6 US-09-925-065A-800526 Sequence 800526,
986 14 24.6 638 6 US-09-925-065A-833901 Sequence 833901,
987 14 24.6 638 6 US-09-925-065A-833901 Sequence 833901,
988 14 24.6 639 6 US-09-925-065A-617388 Sequence 617388,
989 14 24.6 639 6 US-09-925-065A-617389 Sequence 617389,
990 14 24.6 639 9 US-10-301-480-28697, A Sequence 28697, A
991 14 24.6 639 10 US-10-301-480-642106 Sequence 642106,
992 14 24.6 642 6 US-09-925-065A-719595 Sequence 719595,
993 14 24.6 642 6 US-09-925-065A-719596 Sequence 719596,
994 14 24.6 642 6 US-09-925-065A-719597 Sequence 719597,
995 14 24.6 642 6 US-09-925-065A-719598 Sequence 719598,
996 14 24.6 642 6 US-09-925-065A-719599 Sequence 719599,
997 14 24.6 642 6 US-09-925-065A-887736 Sequence 887736,
998 14 24.6 644 6 US-09-925-065A-872748 Sequence 872748,
999 14 24.6 644 6 US-09-925-065A-872749 Sequence 872749,
c1000 14 24.6 644 6 US-09-925-065A-872750 Sequence 872750,
```

## ALIGNMENTS

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RESULT 1
US-11-055-557-11
; Sequence 11, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; OTHER INFORMATION: wild-type homo-oligomeric anthrax toxin protective
; OTHER INFORMATION: antigen (PrAg)
US-11-055-557-11
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Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 6,8e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACATGGG 57
|||||
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```
Db 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACATGGG 1139
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RESULT 2
US-11-055-557-15
; Sequence 15, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-R200A
US-11-055-557-15
```

```
Query Match 100.0%; Score 57; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 6,8e-23;
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACATGGG 57
|||||
Db 1083 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGGGCTGAAACATGGG 1139
```

```
RESULT 3
US-11-055-557-19
; Sequence 19, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; TITLE OF INVENTION: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-I210A
US-11-055-557-19
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```
Query Match 100.0%; Score 57; DB 14; Length 2295;
```







LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-L1-1210A (PA-M-1210A)  
US-11-055-557-3

Query Match 100.0%; Score 57; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 6.8e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1095 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1151

RESULT 8  
US-11-055-557-5  
Sequence 5, Application US/11055557  
Publication No. US20050255083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT APPLICATION NUMBER: US/11/055,557  
CURRENT FILING DATE: 2005-02-09  
PRIOR APPLICATION NUMBER: US 60/543,417  
PRIOR FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-L1-K214A (PA-M-K214A)  
US-11-055-557-5

Query Match 100.0%; Score 57; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 6.8e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1095 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1151

RESULT 9  
US-11-055-557-7  
Sequence 7, Application US/11055557  
Publication No. US20050255083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT APPLICATION NUMBER: US/11/055,557  
CURRENT FILING DATE: 2005-02-09

PRIOR APPLICATION NUMBER: US 60/543,417  
PRIOR FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-L1-R178A (PA-M-R178A)  
US-11-055-557-7

Query Match 100.0%; Score 57; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 6.8e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1095 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1151

RESULT 10  
US-11-055-557-17  
Sequence 17, Application US/11055557  
Publication No. US20050255083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT APPLICATION NUMBER: US/11/055,557  
CURRENT FILING DATE: 2005-02-09  
PRIOR APPLICATION NUMBER: US 60/543,417  
PRIOR FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-L1  
US-11-055-557-17

Query Match 100.0%; Score 57; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 6.8e-23;  
Matches 57; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 57  
Db 1095 CGCAATTGATCATTCATCTCTAGCAGGGGAAAGAACTTGCGCTGAAACAATGGG 1151

RESULT 11  
US-09-925-065A-401809  
Sequence 401809, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08



```

; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 401809
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-401809

Query Match      31.6%; Score 18; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      22 TTGGGCTGAACAATGGG 39

RESULT 12
US-09-925-065A-401810
; Sequence 401810, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 401810
; LENGTH: 570
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-401810

Query Match      31.6%; Score 18; DB 6; Length 570;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      22 TTGGGCTGAACAATGGG 39

RESULT 13
US-09-925-065A-903116
; Sequence 903116, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903116
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-903116

Query Match      31.6%; Score 18; DB 6; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      395 TTGGGCTGAACAATGGG 412

RESULT 14
US-09-925-065A-588142/c
; Sequence 588142, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588142
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-588142

Query Match      31.6%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      280 TTGGGCTGAACAATGGG 263

RESULT 15
US-09-925-065A-588143/c
; Sequence 588143, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 903116
; LENGTH: 574
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-903116

Query Match      31.6%; Score 18; DB 6; Length 574;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      395 TTGGGCTGAACAATGGG 412

RESULT 14
US-09-925-065A-588142/c
; Sequence 588142, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 588142
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-588142

Query Match      31.6%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      40 TTGGGCTGAACAATGGG 57
      |||||
Db      280 TTGGGCTGAACAATGGG 263

RESULT 15
US-09-925-065A-588143/c
; Sequence 588143, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 588143
LENGTH: 595
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-588143
```

```
Query Match 31.6%; Score 18; DB 6; Length 595;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 40 TTGGGCTGAACAATGGG 57
|||||
Db 280 TTGGGCTGAACAATGGG 263
```

```
RESULT 16
US-09-925-065A-868337/c
Sequence 868337, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 868337
LENGTH: 602
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-868337
```

```
Query Match 31.6%; Score 18; DB 6; Length 602;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 40 TTGGGCTGAACAATGGG 57
|||||
Db 417 TTGGGCTGAACAATGGG 400
```

```
RESULT 17
US-09-925-065A-872665
```

```
Sequence 872665, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 872665
LENGTH: 670
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-872665
```

```
Query Match 31.6%; Score 18; DB 6; Length 670;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 40 TTGGGCTGAACAATGGG 57
|||||
Db 225 TTGGGCTGAACAATGGG 242
```

```
RESULT 18
US-09-925-065A-872666
Sequence 872666, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 872666
LENGTH: 670
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-872666
```

```
Query Match 31.6%; Score 18; DB 6; Length 670;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 40 TTGGGCTGAACAATGGG 57
|||||
Db 225 TTGGGCTGAACAATGGG 242
```



```
RESULT 19
US-09-925-065A-5048
; Sequence 5048, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5048
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-5048
```

Query Match 29.8%; Score 17; DB 6; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 18 TATCTTAGCAGGGGAA 34
Db 229 TATCTTAGCAGGGGAA 245
```

```
RESULT 20
US-10-301-480-106285
; Sequence 106285, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 106285
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-106285
```

Query Match 29.8%; Score 17; DB 9; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 18 TATCTTAGCAGGGGAA 34
Db 229 TATCTTAGCAGGGGAA 245
```

RESULT 21  
US-10-301-480-719694

```
; Sequence 719694, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 719694
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-719694
```

Query Match 29.8%; Score 17; DB 10; Length 579;  
Best Local Similarity 100.0%; Pred. No. 9.1;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 18 TATCTTAGCAGGGGAA 34
Db 229 TATCTTAGCAGGGGAA 245
```

```
RESULT 22
US-09-925-065A-546147
; Sequence 546147, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 546147
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-546147
```

Query Match 29.8%; Score 17; DB 6; Length 1137;  
Best Local Similarity 100.0%; Pred. No. 9.7;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy 25 AGCAGGGGAAGAAGCTT 41
Db 200 AGCAGGGGAAGAAGCTT 216
```

RESULT 23  
US-10-301-480-524097  
; Sequence 524097, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:



```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524097
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-524097

Query Match          29.8%; Score 17; DB 10; Length 1137;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      25 AGCAGGGGAAAGAACTT 41
      |||
Db      200 AGCAGGGGAAAGAACTT 216

RESULT 24
US-10-301-480-1137506
; Sequence 1137506, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1137506
; LENGTH: 1137
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1137506

Query Match          29.8%; Score 17; DB 10; Length 1137;
Best Local Similarity 100.0%; Pred. No. 9.7;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      25 AGCAGGGGAAAGAACTT 41
      |||
Db      200 AGCAGGGGAAAGAACTT 216

RESULT 25
US-10-750-185-29644
; Sequence 29644, Application US/10750185
; Publication No. US2005026063A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
```

```
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29644
; LENGTH: 4802
; TYPE: DNA
; ORGANISM: Bovine 1986688055549
US-10-750-185-29644

Query Match          29.8%; Score 17; DB 8; Length 4802;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 TCTAGCAGGGGAAAGAA 38
      |||
Db      2744 TCTAGCAGGGGAAAGAA 2760

RESULT 26
US-10-750-623-29644
; Sequence 29644, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; PRIOR FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29644
; LENGTH: 4802
; TYPE: DNA
; ORGANISM: Bovine 1986688055549
US-10-750-623-29644

Query Match          29.8%; Score 17; DB 8; Length 4802;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      22 TCTAGCAGGGGAAAGAA 38
      |||
Db      2744 TCTAGCAGGGGAAAGAA 2760

RESULT 27
US-11-124-367A-5103/C
; Sequence 5103, Application US/11124367A
; Publication No. US20060024700A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: Hongjin Huang
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; FILE REFERENCE: CL001519.ORD
; CURRENT APPLICATION NUMBER: US/11/124,367A
; PRIOR FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,846
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/582,609
; PRIOR FILING DATE: 2004-06-25
; PRIOR APPLICATION NUMBER: US 60/599,554
```



;; PRIOR FILING DATE: 2004-08-09  
;; NUMBER OF SEQ ID NOS: 34460  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 5103  
;; LENGTH: 61487  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-11-124-367A-5103

Query Match 29.8%; Score 17; DB 14; Length 61487;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 TTGGGCTGAACAATGG 56  
Db 28719 TTGGGCTGAACAATGG 28703

RESULT 28  
US-11-124-367A-5066/c  
; Sequence 5066, Application US/11124367A  
; Publication No. US20060024700A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: Hongjin Huang  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: C1001519.ORD  
; CURRENT APPLICATION NUMBER: US/11/124,367A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,846  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/582,609  
; PRIOR FILING DATE: 2004-06-25  
; PRIOR APPLICATION NUMBER: US 60/599,554  
; PRIOR FILING DATE: 2004-08-09  
; NUMBER OF SEQ ID NOS: 34460  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 5066  
; LENGTH: 66224  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-367A-5066

Query Match 29.8%; Score 17; DB 14; Length 66224;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 TTGGGCTGAACAATGG 56  
Db 42705 TTGGGCTGAACAATGG 42689

RESULT 29  
US-10-995-561-26689/c  
; Sequence 26689, Application US/10995561  
; Publication No. US20050272054A1  
; GENERAL INFORMATION:  
; APPLICANT: CARGILL, Michele et al.  
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH  
; TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF  
; TITLE OF INVENTION: DETECTION AND USES THEREOF  
; FILE REFERENCE: C1001559  
; CURRENT APPLICATION NUMBER: US/10/995,561  
; CURRENT FILING DATE: 2004-11-24  
; NUMBER OF SEQ ID NOS: 85702  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26689  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-995-561-26689

Query Match 28.1%; Score 16; DB 8; Length 201;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 25 AGCAGGGGAAAGAACT 40  
Db 154 AGCAGGGGAAAGAACT 139

RESULT 30  
US-11-124-368A-15526/c  
; Sequence 15526, Application US/11124368A  
; Publication No. US20050287559A1  
; GENERAL INFORMATION:  
; APPLICANT: Michele Cargill  
; APPLICANT: James J. Devlin  
; APPLICANT: May Luke  
; TITLE OF INVENTION: Genetic Polymorphisms Associated with  
; FILE REFERENCE: C1001524  
; CURRENT APPLICATION NUMBER: US/11/124,368A  
; PRIOR FILING DATE: 2005-05-09  
; PRIOR APPLICATION NUMBER: US 60/568,845  
; PRIOR FILING DATE: 2004-05-07  
; PRIOR APPLICATION NUMBER: US 60/625,936  
; PRIOR FILING DATE: 2004-11-09  
; NUMBER OF SEQ ID NOS: 21112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 15526  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-11-124-368A-15526

Query Match 28.1%; Score 16; DB 14; Length 201;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 GGGGAAAGAACTTGGG 44  
Db 194 GGGGAAAGAACTTGGG 179

RESULT 31  
US-10-301-480-523568  
; Sequence 523568, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 523568  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-523568

Query Match 28.1%; Score 16; DB 10; Length 456;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 CTAGCAGGGGAAAGAA 38  
Db 419 CTAGCAGGGGAAAGAA 434



## RESULT 32

US-10-301-480-1136977  
; Sequence 1136977, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1136977  
; LENGTH: 456  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1136977

Query Match 28.1%; Score 16; DB 10; Length 456;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAGCAGGGGAAAGAA 38  
DB 419 CTAGCAGGGGAAAGAA 434

## RESULT 33

US-09-925-065A-468074  
; Sequence 468074, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 468074  
; LENGTH: 490  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-468074

Query Match 28.1%; Score 16; DB 6; Length 490;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 CTAGCAGGGGAAAGAA 38  
DB 419 CTAGCAGGGGAAAGAA 434

## RESULT 34

US-09-925-065A-406203/C  
; Sequence 406203, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 406203  
; LENGTH: 510  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-406203

Query Match 28.1%; Score 16; DB 6; Length 510;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAATTGATCATTCAC 17  
DB 432 GCAATTGATCATTCAC 417

RESULT 35  
US-10-301-480-472902/C  
; Sequence 472902, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 472902  
; LENGTH: 539  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-472902

Query Match 28.1%; Score 16; DB 10; Length 539;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GCAATTGATCATTCAC 17  
DB 432 GCAATTGATCATTCAC 417

RESULT 36  
US-10-301-480-1086311/C  
; Sequence 1086311, Application US/10301480  
; Publication No. US20060057564A1



1 APPLICANT: Wang, David G.  
2 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
3  
4 TITLE OF INVENTION: In the Human Genome  
5  
6 FILE REFERENCE: 108827.137  
7  
8 CURRENT APPLICATION NUMBER: US/10/301,480



; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 122618  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 498222  
; LENGTH: 544  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-498222

Query Match 28.1%; Score 16; DB 10; Length 544;  
Best Local Similarity 100.0%; Pred.No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 24 TAGCAGGGGGAAGAAC 39  
Db 54 TAGCAGGGGGAAGAAC 69

Search completed: April 12, 2006, 07:07:36  
Job time : 237.795 secs







C 96	17	29.8	653	3	BM08105	603617886	C 169	16	28.1	312	9	AO055444	AO055444	CIT-HSP-2
C 97	17	29.8	655	5	BU674014	BU674014	C 170	16	28.1	313	9	BJ211499	BJ211499	BJ211499
C 98	17	29.8	655	10	AG080733	AG080733	C 171	16	28.1	316	1	AI273099	AI273099	AI273099
C 99	17	29.8	659	5	BU619042	BU619042	C 172	16	28.1	321	1	AI276352	AI276352	AI276352
C 100	17	29.8	659	10	CZ779252	CZ779252	C 173	16	28.1	321	1	AM357363	AM357363	AM357363
C 101	17	29.8	664	9	CC154327	CC154327	C 174	16	28.1	325	5	C21519	C21519	HUMG001051
C 102	17	29.8	668	2	BF584986	BF584986	C 175	16	28.1	328	1	AM328167	AM328167	AM328167
C 103	17	29.8	668	10	AG041183	AG041183	C 176	16	28.1	354	5	BY396433	BY396433	BY396433
C 104	17	29.8	668	10	AG119953	AG119953	C 177	16	28.1	356	1	AM034287	AM034287	AM034287
C 105	17	29.8	685	8	DN621159	DN621159	C 178	16	28.1	356	1	AM034934	AM034934	AM034934
C 106	17	29.8	692	6	CF146550	CF146550	C 179	16	28.1	357	8	T79113	T79113	Yd69f06.r1
C 107	17	29.8	694	7	CV272277	CV272277	C 180	16	28.1	358	9	AO567519	AO567519	AO567519
C 108	17	29.8	697	2	BF697214	BF697214	C 181	16	28.1	359	6	CB370319	CB370319	CB370319
C 109	17	29.8	699	2	BE393129	BE393129	C 182	16	28.1	363	9	AO012670	AO012670	CIT-HSP-2
C 110	17	29.8	705	5	BU339958	BU339958	C 183	16	28.1	363	9	AZ506438	AZ506438	IM0347004
C 111	17	29.8	705	6	CA430126	CA430126	C 184	16	28.1	370	6	CD290978	CD290978	ST-Pu538
C 112	17	29.8	708	8	CX757682	CX757682	C 185	16	28.1	372	1	AM348893	AM348893	EST55420
C 113	17	29.8	710	5	BU676144	BU676144	C 186	16	28.1	373	8	W19563	W19563	Zb31d03.r1
C 114	17	29.8	713	10	CE614930	CE614930	C 187	16	28.1	376	10	C2066106	C2066106	OM_Ba006
C 115	17	29.8	720	7	CN832566	CN832566	C 188	16	28.1	380	1	AJ574539	AJ574539	AJ574539
C 116	17	29.8	747	11	CR138004	CR138004	C 189	16	28.1	384	1	AI273082	AI273082	Y62H07.x
C 117	17	29.8	759	5	BQ774186	BQ774186	C 190	16	28.1	392	3	BM692459	BM692459	UI-E-CX1-
C 118	17	29.8	760	1	BB025429	BB025429	C 191	16	28.1	392	5	BK331533	BK331533	BK331533
C 119	17	29.8	767	10	AG494501	AG494501	C 192	16	28.1	394	8	RE4142	RE4142	Y121B04.r1
C 120	17	29.8	786	8	CV817806	CV817806	C 193	16	28.1	395	9	BH349894	BH349894	CH230-65G
C 121	17	29.8	790	10	CZ689343	CZ689343	C 194	16	28.1	396	10	BX098721	BX098721	BX098721
C 122	17	29.8	812	10	CL677670	CL677670	C 195	16	28.1	399	5	CZ087998	CZ087998	OM_Ba009
C 123	17	29.8	823	5	BU748060	BU748060	C 196	16	28.1	400	1	AA089981	AA089981	ch2125.r8
C 124	17	29.8	833	8	CX046391	CX046391	C 197	16	28.1	403	6	CD990173	CD990173	CAVAC05.y
C 125	17	29.8	852	8	CX045954	CX045954	C 198	16	28.1	405	1	AA831613	AA831613	OC80005.r8
C 126	17	29.8	879	8	CX046390	CX046390	C 199	16	28.1	406	2	BF585762	BF585762	FMI_24.CO
C 127	17	29.8	882	10	CG825675	CG825675	C 200	16	28.1	410	9	AZ482908	AZ482908	IM0308C16
C 128	17	29.8	884	11	EC4542887	EC4542887	C 201	16	28.1	411	6	CG691979	CG691979	341490.BA
C 129	17	29.8	885	5	BK420983	BK420983	C 202	16	28.1	411	2	CF111956	CF111956	Shultzom1
C 130	17	29.8	897	2	BG870190	BG870190	C 203	16	28.1	412	1	A1554784	A1554784	cn30906.x
C 131	17	29.8	917	6	CD048194	CD048194	C 204	16	28.1	414	10	CB416358	CB416358	nt4D07.r8
C 132	17	29.8	917	6	CF615761	CF615761	C 205	16	28.1	420	1	AA482850	AA482850	nt4D07.r8
C 133	17	29.8	925	6	CD795189	CD795189	C 206	16	28.1	424	5	BO533897	BO533897	LEAF1.28
C 134	17	29.8	949	2	BE968158	BE968158	C 207	16	28.1	430	5	BX917478	BX917478	BE917478
C 135	17	29.8	951	5	BU911705	BU911705	C 208	16	28.1	431	1	AM512828	AM512828	xm04607.x
C 136	17	29.8	960	6	CD796426	CD796426	C 209	16	28.1	432	1	BP625678	BP625678	BP625678
C 137	17	29.8	962	2	BG292227	BG292227	C 210	16	28.1	432	5	BY452394	BY452394	BY452394
C 138	17	29.8	976	10	CZ936361	CZ936361	C 211	16	28.1	434	1	AA088659	AA088659	z1B3602.r8
C 139	17	29.8	996	2	BF209106	BF209106	C 212	16	28.1	435	6	CB793368	CB793368	AMGNUNC.N
C 140	17	29.8	1002	10	CL460590	CL460590	C 213	16	28.1	436	8	L31980	L31980	HUM21HSU.Hu
C 141	17	29.8	1125	3	BQ220255	BQ220255	C 214	16	28.1	442	1	AI271775	AI271775	q182807.x
C 142	17	29.8	1231	8	DR154070	DR154070	C 215	16	28.1	443	1	AI186557	AI186557	q021408.x
C 143	17	29.8	1398	2	BG848695	BG848695	C 216	16	28.1	445	1	AA312934	AA312934	EST18362
C 144	16	28.1	130	2	BG565658	BG565658	C 217	16	28.1	446	1	AM144895	AM144895	707013E08
C 145	16	28.1	143	10	CM406349	CM406349	C 218	16	28.1	447	6	CF193895	CF193895	17b21j2.r
C 146	16	28.1	143	10	CZ713576	CZ713576	C 219	16	28.1	448	3	BP585154	BP585154	BP585154
C 147	16	28.1	158	7	CN859072	CN859072	C 220	16	28.1	449	1	AM358682	AM358682	43410.MAR
C 148	16	28.1	185	9	BZ840987	BZ840987	C 221	16	28.1	450	9	CC574876	CC574876	CH240.452
C 149	16	28.1	208	1	AA731934	AA731934	C 222	16	28.1	452	1	AI001762	AI001762	CT3805.r8
C 150	16	28.1	209	1	AI494787	AI494787	C 223	16	28.1	452	10	C2637413	C2637413	OM_Ba018
C 151	16	28.1	210	9	AY759017	AY759017	C 224	16	28.1	453	5	BY621185	BY621185	BY621185
C 152	16	28.1	225	9	AZ724774	AZ724774	C 225	16	28.1	455	1	AA604990	AA604990	ng73610.r8
C 153	16	28.1	229	1	AI473527	AI473527	C 226	16	28.1	456	1	AA627253	AA627253	ng68C04.r8
C 154	16	28.1	237	1	AI473527	AI473527	C 227	16	28.1	459	9	AO971060	AO971060	PCCT-23-2
C 155	16	28.1	259	1	AI362631	AI362631	C 228	16	28.1	460	3	BI788466	BI788466	1639B09.x
C 156	16	28.1	265	2	BB598088	BB598088	C 229	16	28.1	461	2	BF077284	BF077284	227125.NA
C 157	16	28.1	266	1	AM628507	AM628507	C 230	16	28.1	467	9	AO708013	AO708013	5570.A
C 158	16	28.1	268	10	CE638103	CE638103	C 231	16	28.1	469	9	AZ998710	AZ998710	2M0285J17
C 159	16	28.1	270	9	CE212990	CE212990	C 232	16	28.1	470	2	AZ051812	AZ051812	RCCT-23-4
C 160	16	28.1	272	9	BH031425	BH031425	C 233	16	28.1	471	2	BG102891	BG102891	RH122.34
C 161	16	28.1	279	1	AI439517	AI439517	C 234	16	28.1	471	9	AO885377	AO885377	HS_5552.B
C 162	16	28.1	281	9	BZ758474	BZ758474	C 235	16	28.1	471	9	AO443565	AO443565	HS_3069.B
C 163	16	28.1	282	1	AA909084	AA909084	C 236	16	28.1	471	9	AO448978	AO448978	mgXB0022F
C 164	16	28.1	284	10	CZ708842	CZ708842	C 237	16	28.1	473	2	BG048871	BG048871	CV1.24.BO
C 165	16	28.1	291	6	CD319015	CD319015	C 238	16	28.1	474	1	AI129552	AI129552	GC34E07.x
C 166	16	28.1	301	1	AA908749	AA908749	C 239	16	28.1	476	6	CF032079	CF032079	OCB13F08
C 167	16	28.1	304	9	CE028569	CE028569	C 240	16	28.1	476	6	CF036212	CF036212	OCG29B11
C 168	16	28.1	310	3	BI309752	BI309752	C 241	16	28.1	477	1	AA737955	AA737955	nx11C02.r8



C 242	16	28.1	479	6	CA234166	SCCCCL6C0	315	16	28.1	565	8	DR900933
C 243	16	28.1	481	2	BE328569	htc01b07.x	316	16	28.1	566	6	CD225675
C 244	16	28.1	481	10	CM333345	CM333345_104_831_1	317	16	28.1	567	2	BG465768
C 245	16	28.1	482	10	C2636330	OM_Ba017	318	16	28.1	567	2	A2075788
C 246	16	28.1	484	1	AA937704	oJ04h09.s	319	16	28.1	569	2	BG560193
C 247	16	28.1	484	9	AO699359	HS_5567_A	320	16	28.1	569	2	BE207803
C 248	16	28.1	485	5	BY275563	BY275563	321	16	28.1	569	9	A2711893
C 249	16	28.1	485	9	BI6901	BI6901_343M12.TVB	322	16	28.1	570	2	BG560346
C 250	16	28.1	487	1	AI124067	AI124067_qa99g12.s	323	16	28.1	572	10	CE426222
C 251	16	28.1	487	6	CF034065	CF034065_QCF23f08.	324	16	28.1	576	5	BW530164
C 252	16	28.1	490	2	BF604350	BF604350_270149_MA	325	16	28.1	576	5	AO822161
C 253	16	28.1	490	6	CF349032	EST0598.Z	326	16	28.1	577	6	CA578704
C 254	16	28.1	492	6	CD513608	CD513608_AGENCOURT	327	16	28.1	577	9	A2497756
C 255	16	28.1	493	9	AZ886668	RPCI-23-1	328	16	28.1	577	9	BH113076
C 256	16	28.1	496	9	AI687755	AI687755_cp83a08.x	329	16	28.1	579	3	BP133669
C 257	16	28.1	498	1	AO761643	AO761643_HS_3132_B	330	16	28.1	579	7	CK898823
C 258	16	28.1	499	1	AI784414	AI784414_tw68a09.x	331	16	28.1	581	5	BU826160
C 259	16	28.1	499	6	CA098566	CA098566_SCMCCL605	332	16	28.1	582	2	BF616793
C 260	16	28.1	500	1	AUI58417	AUI58417_AUI58417	333	16	28.1	582	3	BP293708
C 261	16	28.1	501	1	AUI51909	AUI51909_AUI51909	334	16	28.1	584	1	AI889893
C 262	16	28.1	501	2	BF077044	BF077044_226837_MA	335	16	28.1	585	5	CS5322
C 263	16	28.1	506	9	AQ182048	AQ182048_HS_3226_B	336	16	28.1	586	1	AI739017
C 264	16	28.1	509	1	AI093202	AI093202_qa98c09.x	337	16	28.1	587	6	CF759265
C 265	16	28.1	510	9	AO728055	AO728055_HS_5447_B	338	16	28.1	587	8	CX184212
C 266	16	28.1	510	9	AO880620	AO880620_HS_5047_B	339	16	28.1	588	7	CV522476
C 267	16	28.1	511	1	AM929017	AM929017_EST337721	340	16	28.1	591	6	CD442728
C 268	16	28.1	511	2	BG241848	BG241848_RH122_51_	341	16	28.1	592	3	BM941897
C 269	16	28.1	514	10	CL572178	CL572178_OB_Ba001	342	16	28.1	592	6	CF442089
C 270	16	28.1	516	6	CA578792	CA578792_K0728F02-	343	16	28.1	592	10	CM010646
C 271	16	28.1	519	6	CA197897	CA197897_SCAGAD107	344	16	28.1	593	10	CG291968
C 272	16	28.1	519	6	CD055420	CD055420_H009C22S	345	16	28.1	594	10	CL246032
C 273	16	28.1	520	6	CA577179	CA577179_K0705F09-	346	16	28.1	594	1	AA573891
C 274	16	28.1	520	6	AZ328792	AZ328792_479_.dlf18	347	16	28.1	596	10	CM254110
C 275	16	28.1	521	10	CL596513	CL596513_OB_Ba005	348	16	28.1	601	5	BU356211
C 276	16	28.1	523	10	CG978865	CG978865_CH240_170	349	16	28.1	602	9	BE799569
C 277	16	28.1	526	1	AA589914	AA589914_aea1c0f.s	350	16	28.1	602	9	BZ799574
C 278	16	28.1	527	1	AI869688	AI869688_wm02e05.x	351	16	28.1	602	2	BE510438
C 279	16	28.1	527	1	AM089697	AM089697_xd07d07.x	352	16	28.1	606	9	CC059699
C 280	16	28.1	527	8	CD057192	CD057192_H014H02S	353	16	28.1	606	10	AL765762
C 281	16	28.1	527	8	RS4818	RS4818_y987f02_.81	354	16	28.1	607	6	CA166223
C 282	16	28.1	528	2	BF428966	BF428966_WHE1712_E	355	16	28.1	609	9	BH628134
C 283	16	28.1	528	2	BE593490	BE593490_WSI_98_E0	356	16	28.1	611	1	AM147152
C 284	16	28.1	528	5	BM560243	BM560243_BW560243	357	16	28.1	611	10	CM981110
C 285	16	28.1	529	6	CA650560	CA650560_wre1n.pk0	358	16	28.1	612	1	AA573802
C 286	16	28.1	530	5	BU678698	BU678698_UI-CF-D01	359	16	28.1	612	8	DR432318
C 287	16	28.1	530	10	CM226355	CM226355_104_664_1	360	16	28.1	616	9	BH624661
C 288	16	28.1	531	1	AM659422	AM659422_9657g_MAR	361	16	28.1	617	1	AV913178
C 289	16	28.1	532	2	AI248855	AI248855_qh72h11.x	362	16	28.1	619	1	AJ436604
C 290	16	28.1	536	1	AM005183	AM005183_wz84c03.x	363	16	28.1	619	6	CA745151
C 291	16	28.1	539	9	CC167950	CC167950_1j78d12.g	364	16	28.1	619	9	AT760432
C 292	16	28.1	540	1	AA913701	AA913701_o134h10.s	365	16	28.1	621	2	BF112096
C 293	16	28.1	541	1	AUI52176	AUI52176_AUI52176	366	16	28.1	621	7	CM009023
C 294	16	28.1	542	1	AI018624	AI018624_ou47g04.x	367	16	28.1	622	10	CZ854626
C 295	16	28.1	543	5	BY532238	BY532238_BY532238	368	16	28.1	624	1	AL855641
C 296	16	28.1	545	7	CF898090	CF898090_A0234A08-	369	16	28.1	625	11	CR116817
C 297	16	28.1	549	3	BI886053	BI886053_ZF637-1-0	370	16	28.1	627	9	A2710654
C 298	16	28.1	549	9	CD678256	CD678256_hp04g07.y	371	16	28.1	628	10	CG868256
C 299	16	28.1	550	10	CZ650214	CZ650214_OM_Ba019	372	16	28.1	630	10	CM401050
C 300	16	28.1	551	3	BM661345	BM661345_9520f6H09	373	16	28.1	631	6	CA181637
C 301	16	28.1	551	3	BM664767	BM664767_UI-E-CL1-	374	16	28.1	631	5	BY740741
C 302	16	28.1	551	6	CA577098	CA577098_K0704E11-	375	16	28.1	636	1	AA911217
C 303	16	28.1	552	1	AA633442	AA633442_hp62a05.s	376	16	28.1	636	1	AM144940
C 304	16	28.1	556	1	AM331448	AM331448_707013E08	377	16	28.1	638	6	CD884355
C 305	16	28.1	558	6	CA138450	CA138450_SCEQRT202	378	16	28.1	641	1	AA424401
C 306	16	28.1	559	2	AM144896	AM144896_707013E08	379	16	28.1	641	10	CM319950
C 307	16	28.1	559	2	BE443788	BE443788_WHE1122.C	380	16	28.1	642	10	CZ642055
C 308	16	28.1	559	8	CD861997	CD861997_AZ01_10Tb	381	16	28.1	644	2	BB654553
C 309	16	28.1	559	8	DR800640	DR800640_ZM_BFB002	382	16	28.1	644	2	BE443407
C 310	16	28.1	560	6	CA197850	CA197850_SCAGAD107	383	16	28.1	647	1	AM514428
C 311	16	28.1	560	6	CA257046	CA257046_SCGSFL419	384	16	28.1	647	3	BM995903
C 312	16	28.1	561	3	BI714379	BI714379_1e33b02.Y	385	16	28.1	647	6	CA176045
C 313	16	28.1	561	9	AZ711523	AZ711523_RPCI-24-1	386	16	28.1	647	10	CZ678341
C 314	16	28.1	561	9	AZ711523	AZ711523_RPCI-24-1	387	16	28.1	647	10	CZ678341

DR900933	JGI_XZT55
CD225675	CCCT_40.C
BG465768	RH122_48_
AZ075788	RPCI-23-4
BG560193	BH122_71
BE207803	lb09d09.x
A2711893	RPCI-24-1
BG560346	RH122_73_
CE426222	CL1gF-988-
BM530164	BM530164
AO822161	HS_5494_A
CA578704	K0727E04-
BU826160	UK117TC09
BF616793	HVSMBC001
BP293708	BP293708
AI889893	wm64g02.x
CS5322	CS5322_M0u8
AI739017	w134c05.x
CF759265	DSAP1_43
CX184212	F12_45--28
CV522476	RP-106.Tr
CD442728	ELI01N047
BM941897	UI-M-CG0P
CF442089	EST678434
CM010646	ZMMBBD030
CG291968	CG291968_OGYAV637P
CL246032	ZMMBBD039
AA573891	nk08h12_.8
CM254110	104_718_1
BU356211	603474083
BZ799569	PUGCY687B
BZ799574	PUGCY687D
BE510438	946052H08
CC059699	i126e08_b
AL765762	ATRAD1d0p8
CA166223	SCURR2310
BH628134	1007080E0
AM147152	707013E08
CM981110	KbH0005J0
AA573802	nk07g07.s
DR432318	441E-1064
BH624661	100707980
AV913178	AV913178
AJ436604	AJ436604
CA745151	wr13g.PK0
AT760432	RP43-164F
CC161915	1180D12.g
BF112096	7140b11.x
CM009023	WHE2647_H
CZ854626	OC_Ba024
AL855641	AL855641
CR116817	Reveree.s
A2710654	RPCI-24-1
CG868256	ZMMBBD036
CA401050	FEBD001F0
AM424401	707013E08
CM319950	104_812_1
CZ642055	OM_Ba018
BB654553	BB654553
BE443407	WHE1104_E
AM514428	hd76h09.x
BM995903	UI-H-DT1-
CA176045	SCUJST102
CZ678341	OM_Ba023



C 388	16	28.1	647	11	CR186286	CR186286 Forward B	461	16	28.1	733	10	CE272142	CE272142 t1gr-g88-
C 389	16	28.1	649	1	AI796150	AI796150 wh3a12.x	C 462	16	28.1	734	10	C2276546	C2276546 ZMMBFD0059
C 390	16	28.1	650	6	CA438912	CA438912 UT-H-DHO-	C 463	16	28.1	734	10	CL288837	CL288837 ZMMBFD064
C 391	16	28.1	650	0	AQ447837	AQ447837 mgx500110	C 464	16	28.1	735	6	CA427152	CA427152 UT-H-DFO-
C 392	16	28.1	651	6	CF448056	CF448056 EST684401	C 465	16	28.1	735	10	C2832689	C2832689 OC-Ba021
C 393	16	28.1	651	10	C2847141	C2847141 OC-Ba023	C 466	16	28.1	736	5	A2870274	A2870274 ZM0182N08
C 394	16	28.1	656	6	CD223741	CD223741 CCC1_29 G	C 467	16	28.1	741	5	BW754521	BW754521 BW754521
C 395	16	28.1	659	3	BM918553	BM918553 AGENCOURT	C 468	16	28.1	741	5	BX386720	BX386720 BX386720
C 396	16	28.1	660	3	BM998128	BM998128 UT-H-DT1-	C 469	16	28.1	742	3	BM981477	BM981477 UT-CF-EN1
C 397	16	28.1	660	6	CA218083	CA218083 SCSGAD114	C 470	16	28.1	743	10	CG467854	CG467854 ZMMBBD025
C 398	16	28.1	661	2	BG261300	BG261300 602373048	C 471	16	28.1	744	8	CX610661	CX610661 ANR1_20.C
C 399	16	28.1	663	3	B06582	B06582 CSRL-82d-u	C 472	16	28.1	746	10	CR386371	CR386371 FBBD001f0
C 400	16	28.1	664	6	CA502652	CA502652 WBR4338.A	C 473	16	28.1	749	8	DR810877	DR810877 ZM-FBD003
C 401	16	28.1	664	10	CW537197	CW537197 OP-Ba003	C 474	16	28.1	752	10	CL550733	CL550733 OC-Ba009
C 402	16	28.1	665	7	CK966711	CK966711 4081705.B	C 475	16	28.1	754	6	CF344312	CF344312 AGENCOURT
C 403	16	28.1	667	9	AZ998221	AZ998221 2M0285M04	C 476	16	28.1	754	9	CC344010	CC344010 OGRB31TV
C 404	16	28.1	669	6	CA075640	CA075640 SCUTLAMI06	C 477	16	28.1	756	6	CD526005	CD526005 AGENCOURT
C 405	16	28.1	669	10	CW013473	CW013473 ZMMBLC000	C 478	16	28.1	758	9	BH177071	BH177071 008.M.24-
C 406	16	28.1	671	2	BG223347	BG223347 naF79h01.	C 479	16	28.1	758	11	CNS07JP7	CC147313 ZMMBB001
C 407	16	28.1	672	10	CW329581	CW329581 104.826.1	C 480	16	28.1	759	10	CL265696	CL265696 OC-Ba000
C 408	16	28.1	673	9	CE064878	CE064878 t1gr-g88-	C 481	16	28.1	761	3	B3578143	B3578143 BJ578143
C 409	16	28.1	674	9	AZ243015	AZ243015 RPCI_23-3	C 482	16	28.1	762	6	CF480107	CF480107 POLI_63.F
C 410	16	28.1	677	7	CK962025	CK962025 4076508.B	C 483	16	28.1	767	9	AQ740863	AQ740863 HS_2274.A
C 411	16	28.1	680	2	BB540625	BB540625 BB540625	C 484	16	28.1	767	9	CC961347	CC961347 B01G067TF
C 412	16	28.1	680	10	CW213158	CW213158 104.644.1	C 485	16	28.1	770	3	BQ213275	BQ213275 AGENCOURT
C 413	16	28.1	681	5	CA100255	CA100255 SCVPC1606	C 486	16	28.1	771	2	BG477227	BG477227 602524235
C 414	16	28.1	683	5	BM718527	BM718527 BW718527	C 487	16	28.1	774	10	CL304317	CL304317 ZMMBBD008
C 415	16	28.1	683	8	CX866568	CX866568 HBSC4_11	C 488	16	28.1	775	9	CG303873	CG303873 SUB_BCF04
C 416	16	28.1	683	10	CL578005	CL578005 OB-Ba003	C 489	16	28.1	776	8	CA417055	CA417055 JGI_XZG64
C 417	16	28.1	684	6	CA171530	CA171530 SCSEB105	C 490	16	28.1	777	11	CR875610	CR875610 SUB_BCF04
C 418	16	28.1	684	10	AG050516	AG050516 Pan t1crg1	C 491	16	28.1	779	6	CA221183	CA221183 SCBEFL404
C 419	16	28.1	684	10	AG088522	AG088522 Pan t1crg1	C 492	16	28.1	779	2	BG529943	BG529943 602560768
C 420	16	28.1	686	10	CZ619221	CZ619221 OM-Ba014	C 493	16	28.1	781	2	CL581270	CL581270 OB-Ba004
C 421	16	28.1	690	6	CA814493	CA814493 CA481N091	C 494	16	28.1	782	10	B0625594	B0625594 UT-H-PCI-
C 422	16	28.1	690	10	C2812478	C2812478 OC-Ba018	C 495	16	28.1	783	5	BW233360	BW233360 BW723360
C 423	16	28.1	691	2	C2851516	C2851516 OC-Ba024	C 496	16	28.1	785	5	BK455144	BK455144 BX455144
C 424	16	28.1	691	10	BB298271	BB298271 BB298271	C 497	16	28.1	785	10	CG381688	CG381688 OGYA0713
C 425	16	28.1	693	1	CZ608875	CZ608875 OM-Ba013	C 498	16	28.1	786	10	CG601784	CG601784 OA_Aba013
C 426	16	28.1	694	1	AV909477	AV909477 AV905477	C 499	16	28.1	787	6	CD052845	CD052845 LITTF000
C 427	16	28.1	694	6	CA140227	CA140227 SCEZRT202	C 500	16	28.1	790	10	CZ791229	CZ791229 OC-Ba015
C 428	16	28.1	695	7	CN138939	CN138939 OX1_15.CO	C 501	16	28.1	792	5	BX433438	BX433438 BX433438
C 429	16	28.1	695	10	CW208354	CW208354 104_637_1	C 502	16	28.1	792	6	CD917603	CD917603 G608_106A
C 430	16	28.1	698	10	CW749484	CW749484 OP-Ba006	C 503	16	28.1	792	11	CR185901	CR185901 Reverse B
C 431	16	28.1	698	10	CW889165	CW889165 RPCI42_11	C 504	16	28.1	792	11	CR186567	CR186567 Reverse B
C 432	16	28.1	701	6	CF432860	CF432860 NITL_19.C	C 505	16	28.1	793	11	CR186570	CR186570 Reverse B
C 433	16	28.1	701	7	COS54394	COS54394 AGENCOURT	C 506	16	28.1	794	1	AV723478	AV723478 BHS2Kd28-
C 434	16	28.1	701	6	CA944840	CA944840 UT-CF-FNO	C 507	16	28.1	794	10	CO386278	CO386278 AGENCOURT
C 435	16	28.1	705	9	BH579096	BH579096 BQCK242TF	C 508	16	28.1	795	7	CO380779	CO380779 OGYAUV36TC
C 436	16	28.1	709	10	CW222025	CW222025 104.657.1	C 509	16	28.1	795	9	BZ411414	BZ411414 OGYAUV36TC
C 437	16	28.1	711	9	BH860542	BH860542 OBNL013_B	C 510	16	28.1	798	11	CR269051	CR269051 Reverse B
C 438	16	28.1	711	3	BP125473	BP125473 BP125473	C 511	16	28.1	802	6	CA239151	CA239151 SCRFPL503
C 439	16	28.1	715	6	CD442773	CD442773 EL01N0417	C 512	16	28.1	802	4	CL598140	CL598140 OB-Ba006
C 440	16	28.1	716	10	CZ742841	CZ742841 OC-Ba008	C 513	16	28.1	803	4	AY067815	AY067815 schmidtdea
C 441	16	28.1	718	11	CR104540	CR104540 Reverse B	C 514	16	28.1	803	5	B0222921	B0222921 603946855
C 442	16	28.1	718	8	CX623069	CX623069 GABRI_67	C 515	16	28.1	806	10	CG239609	CG239609 OGYAUV37TH
C 443	16	28.1	719	10	CA319949	CA319949 104.812.1	C 516	16	28.1	809	6	CB310160	CB310160 AGENCOURT
C 444	16	28.1	720	5	BQ743332	BQ743332 WMR4102_G	C 517	16	28.1	810	10	CZ833198	CZ833198 OC-Ba021
C 445	16	28.1	720	1	AI924553	AI924553 WRI604.X	C 518	16	28.1	811	11	CR209680	CR209680 Reverse B
C 446	16	28.1	722	10	CW295334	CW295334 104_776_1	C 519	16	28.1	815	6	CA294778	CA294778 SCQIV101
C 447	16	28.1	723	3	BI933288	BI933288 EST553177	C 520	16	28.1	815	7	CO454156	CO454156 M2CCL1020
C 448	16	28.1	723	5	BM933206	BM933206 BM933206	C 521	16	28.1	815	11	CR040256	CR040256 Reverse B
C 449	16	28.1	723	5	BM932846	BM932846 BM932846	C 522	16	28.1	819	9	BZ547179	BZ547179 OGYAUV30TM
C 450	16	28.1	726	5	BZ785057	BZ785057 PUGAC49TB	C 523	16	28.1	822	11	CR201461	CR201461 Reverse B
C 451	16	28.1	726	9	BH455083	BH455083 BQGS146TR	C 524	16	28.1	826	6	CA227168	CA227168 SCVPL304
C 452	16	28.1	727	5	BM455083	BM455083 OGYAUV37TV	C 525	16	28.1	829	9	CG565522	CG565522 OGYAUV37TV
C 453	16	28.1	727	10	CW559915	CW559915 OA_Aba008	C 526	16	28.1	833	10	CG294863	CG294863 OGYAUV37TV
C 454	16	28.1	728	1	AL813252	AL813252 1005139.R	C 527	16	28.1	837	8	AL562799	AL562799 Reverse B
C 455	16	28.1	729	1	BM990558	BM990558 UT-H-DHO-	C 528	16	28.1	844	5	BK455475	BK455475 Reverse B
C 456	16	28.1	730	3	BE258029	BE258029 601110395	C 529	16	28.1	850	1	AD814794	AD814794 Reverse B
C 457	16	28.1	733	2	BU218680	BU218680 603755286	C 530	16	28.1	850	6	CD644221	CD644221 AGENCOURT
C 458	16	28.1	733	2	BU218680	BU218680 603755286	C 531	16	28.1	850	6	CD644221	CD644221 AGENCOURT
C 459	16	28.1	733	2	BU218680	BU218680 603755286	C 532	16	28.1	850	6	CD644221	CD644221 AGENCOURT
C 460	16	28.1	733	2	BU218680	BU218680 603755286	C 533	16	28.1	850	6	CD644221	CD644221 AGENCOURT



C 534	16	28.1	851	5	BUS62423	BUS62423	AGENCOURT	607	16	28.1	1447	9	BZ572022	BZ572022	mh2.234.
C 536	16	28.1	851	11	CR233494	CR233494	Reverse s	608	16	28.1	1471	9	CC253589	CC253589	CH26T-175
C 537	16	28.1	855	5	BX372659	BX372659	BX372659	609	16	28.1	1535	4	AT109823	AT109823	Zea maye
C 538	16	28.1	856	2	BG675684	BG675684	602621904	C 610	16	28.1	1659	2	BG910999	BG910999	602809563
C 539	16	28.1	858	10	CZ369144	CZ369144	ZMMBPF0150	C 611	16	28.1	1838	4	AK053549	AK053549	Mus muscu
C 540	16	28.1	862	7	CO447959	CO447959	MZCC1011	C 612	16	28.1	2045	1	AW730497	AW730497	GA_Ea002
C 541	16	28.1	862	10	CG130425	CG130425	PURDV48TD	C 613	16	28.1	2306	4	AK014195	AK014195	Mus muscu
C 542	16	28.1	866	10	CG380456	CG380456	OGXAE19TH	C 614	16	28.1	3052	4	BC050476	BC050476	Mus muscu
C 543	16	28.1	867	9	BH128490	BH128490	G-3916 Ma	C 615	16	28.1	3313	4	AK050752	AK050752	Mus muscu
C 544	16	28.1	868	10	CG380465	CG380465	OGXAE19TV	C 616	16	28.1	3838	4	AK037555	AK037555	Mus muscu
C 545	16	28.1	879	10	DU005723	DU005723	301465 To	C 617	16	28.1	5248	4	CR749266	CR749266	Mus muscu
C 546	16	28.1	881	5	AG103263	AG103263	Pan. trogl	C 618	16	26.3	135	9	BZ762976	BZ762976	SAUK 1106
C 547	16	28.1	884	5	BX374170	BX374170	BX374170	C 619	15	26.3	135	10	CM839212	CM839212	CT7894.D8
C 548	16	28.1	891	10	CZ528292	CZ528292	SRNA-aacs	C 620	15	26.3	139	9	BH813174	BH813174	SAUK_0637
C 549	16	28.1	891	2	BE739602	BE739602	601593191	C 621	15	26.3	143	5	BQ966177	BQ966177	QB824K22.
C 550	16	28.1	893	8	DN806748	DN806748	76859243	C 622	15	26.3	148	9	BE674526	BE674526	PUBRT02TD
C 551	16	28.1	896	2	BG254865	BG254865	602369306	C 623	15	26.3	153	11	CR358374	CR358374	Arabidops
C 552	16	28.1	897	5	BX387904	BX387904	BX387904	C 624	15	26.3	153	11	CR358375	CR358375	Arabidops
C 553	16	28.1	900	10	CG130423	CG130423	PURDV48TB	C 625	15	26.3	160	11	CR358428	CR358428	Arabidops
C 554	16	28.1	903	5	B0849596	B0849596	AGENCOURT	C 626	15	26.3	171	5	BX485076	BX485076	DKF2p686L
C 555	16	28.1	904	5	BO721400	BO721400	AGENCOURT	C 628	15	26.3	176	10	BX945557	BX945557	Arabidops
C 556	16	28.1	904	7	CN247820	CN247820	EST013718	C 629	15	26.3	182	2	BB310835	BB310835	Arabidops
C 557	16	28.1	907	5	BX433716	BX433716	BX433716	C 630	15	26.3	185	5	CA035846	CA035846	4001806.B
C 558	16	28.1	909	3	BQ226961	BQ226961	AGENCOURT	C 631	15	26.3	189	6	CD201870	CD201870	MS1-0130U
C 559	16	28.1	909	5	BU119797	BU119797	603143485	C 632	15	26.3	198	9	AZ721447	AZ721447	RPC1-24-1
C 560	16	28.1	912	2	BE381341	BE381341	601271226	C 633	15	26.3	200	3	BI386641	BI386641	603089356
C 561	16	28.1	914	5	BX412948	BX412948	BX412948	C 634	15	26.3	213	1	AV142017	AV142017	AV142017
C 562	16	28.1	917	7	CO440306	CO440306	MZCC1001	C 635	15	26.3	217	1	AM897764	AM897764	CM1-NN006
C 563	16	28.1	921	5	B0682289	B0682289	AGENCOURT	C 636	15	26.3	219	1	AV038519	AV038519	AV038519
C 564	16	28.1	932	5	BD916456	BD916456	AGENCOURT	C 637	15	26.3	219	1	AV134412	AV134412	AV134412
C 565	16	28.1	932	10	CG239618	CG239618	OGXAL57TV	C 638	15	26.3	220	11	CR068167	CR068167	Reverse s
C 566	16	28.1	933	10	AG897940	AG897940	Oryza sat	C 639	15	26.3	234	2	BI185178	BI185178	UNL-P-FN-
C 567	16	28.1	938	6	CD000524	CD000524	AGENCOURT	C 640	15	26.3	235	7	CR521665	CR521665	CR521665
C 568	16	28.1	938	10	CL503555	CL503555	SAIT.725	C 641	15	26.3	243	1	AV367243	AV367243	AV367243
C 569	16	28.1	939	8	DN785023	DN785023	OC_Ba000	C 642	15	26.3	243	6	CP210033	CP210033	CAB30005
C 570	16	28.1	959	8	DN785023	DN785023	92237511	C 643	15	26.3	245	1	AV292751	AV292751	AV292751
C 571	16	28.1	962	8	DN562316	DN562316	88066745	C 644	15	26.3	245	8	DR661596	DR661596	EST105171
C 572	16	28.1	967	1	AL562891	AL562891	AL562891	C 645	15	26.3	253	1	BB112027	BB112027	BB112027
C 573	16	28.1	969	5	BX385660	BX385660	BX385660	C 646	15	26.3	253	1	BB112027	BB112027	BB112027
C 574	16	28.1	972	10	CG969445	CG969445	MBEMO64TR	C 647	15	26.3	260	2	BB523022	BB523022	BB523022
C 575	16	28.1	986	10	DU017076	DU017076	239686 To	C 648	15	26.3	262	1	AV013506	AV013506	AV013506
C 576	16	28.1	990	10	CL993698	CL993698	ZMMBHf000	C 649	15	26.3	264	10	BX892151	BX892151	Arabidops
C 577	16	28.1	997	10	CL461346	CL461346	SAIT.1145	C 650	15	26.3	267	1	AV351065	AV351065	AV351065
C 578	16	28.1	1009	3	BQ230580	BQ230580	AGENCOURT	C 651	15	26.3	269	6	CD785255	CD785255	EST556616
C 579	16	28.1	1012	2	BF607808	BF607808	MY1_00075	C 652	15	26.3	270	9	BH074510	BH074510	AV074510
C 580	16	28.1	1013	10	CL988303	CL988303	ZMMBHf000	C 653	15	26.3	270	9	BH074510	BH074510	SAUK_0383
C 581	16	28.1	1014	1	AL573430	AL573430	AL573430	C 654	15	26.3	271	5	BY424202	BY424202	BY424202
C 582	16	28.1	1014	2	BR421342	BR421342	HWM008.C1	C 655	15	26.3	274	10	BX892150	BX892150	Arabidops
C 583	16	28.1	1014	10	CU114814	CU114814	ISB1-60L2	C 656	15	26.3	275	2	BB277724	BB277724	BB277724
C 584	16	28.1	1028	1	AL518698	AL518698	AL518698	C 657	15	26.3	279	1	AA689627	AA689627	VB08h11.r
C 585	16	28.1	1032	8	DN786072	DN786072	90199709	C 658	15	26.3	279	2	BB599233	BB599233	BB599233
C 586	16	28.1	1045	1	AL576683	AL576683	AL576683	C 659	15	26.3	279	11	DO031224	DO031224	Hom sapi
C 587	16	28.1	1049	4	CR623820	CR623820	full-1eng	C 660	15	26.3	279	11	DO031225	DO031225	Hom sapi
C 588	16	28.1	1056	8	DR739680	DR739680	FGAS08489	C 661	15	26.3	280	2	BB360632	BB360632	BB360632
C 589	16	28.1	1067	1	AL578740	AL578740	AL578740	C 662	15	26.3	281	1	AM561258	AM561258	AV561258
C 590	16	28.1	1071	10	CL083290	CL083290	ISB1-LK16	C 663	15	26.3	281	1	AM561258	AM561258	AV561258
C 591	16	28.1	1079	9	CC286123	CC286123	CH261-29C	C 664	15	26.3	282	1	AT1822623	AT1822623	LO-1138T3
C 592	16	28.1	1113	5	BO918481	BO918481	AGENCOURT	C 665	15	26.3	282	2	BB521809	BB521809	BB521809
C 593	16	28.1	1129	10	CM952416	CM952416	TCB38.1.G	C 666	15	26.3	284	9	BH692554	BH692554	BOHYK34TR
C 594	16	28.1	1129	10	CU066413	CU066413	CH216-108	C 667	15	26.3	286	10	CZ655672	CZ655672	OM_Ba020
C 595	16	28.1	1133	6	CA124380	CA124380	SCQGM202	C 668	15	26.3	289	10	BX651358	BX651358	Arabidops
C 596	16	28.1	1135	7	CK168046	CK168046	FGAS05253	C 669	15	26.3	292	1	AV168665	AV168665	AV168665
C 597	16	28.1	1167	9	CC301784	CC301784	CH261-29H	C 670	15	26.3	292	9	CC808154	CC808154	ZMMB6C046
C 598	16	28.1	1170	1	AL573512	AL573512	AL573512	C 671	15	26.3	294	6	CP757358	CP757358	DSAP1.17
C 599	16	28.1	1187	10	AG441746	AG441746	Mus muscu	C 672	15	26.3	294	2	AZ211810	AZ211810	Sheared_D
C 600	16	28.1	1201	4	CR619865	CR619865	full-1eng	C 673	15	26.3	296	2	BB527673	BB527673	BB527673
C 601	16	28.1	1204	3	BZ694377	BZ694377	SP_Ba004	C 674	15	26.3	298	9	AZ487686	AZ487686	IM0317H01
C 602	16	28.1	1220	3	BO070167	BO070167	AGENCOURT	C 675	15	26.3	300	1	AV176738	AV176738	AV176738
C 603	16	28.1	1237	9	CC209662	CC209662	CH261-14K	C 676	15	26.3	300	1	BB175776	BB175776	BB175776
C 604	16	28.1	1284	10	CL645426	CL645426	CH213-94K	C 677	15	26.3	300	3	BM1031657	BM1031657	MCR049602
C 605	16	28.1	1323	10	AG289702	AG289702	Mus muscu	C 678	15	26.3	300	5	CO7281	CO7281	Yuj1
C 606	16	28.1	1350	5	BX898660	BX898660	BX898660	C 679	15	26.3	300	5	CO7814	CO7814	Yuj1



680	15	26.3	300	5	C34291	C34291 C34291 Yuii	753	15	26.3	400	6	CF511106	CF511106 Cabud0001
681	15	26.3	300	10	CB375011	CB375011 t1gr-g88-	754	15	26.3	401	9	B2837760	B2837760 CH240_261
682	15	26.3	303	5	BM242847	BM242847 BM242847	755	15	26.3	403	3	BP777206	BP777206 BP777206
683	15	26.3	308	7	CK517459	CK517459 t8wjb0_00	756	15	26.3	405	8	CV888791	CV888791 LR888068
684	15	26.3	312	9	CO182895	CO182895 EC24233_5	757	15	26.3	406	3	B1678852	B1678852 SMS754_5M
685	15	26.3	312	7	A2838207	A2838207 2M0133L16	758	15	26.3	406	5	BQ597963	BQ597963 MI-P-A2-A
686	15	26.3	316	6	CF760291	CF760291 DSAF1_57	759	15	26.3	407	5	BY371764	BY371764 BY371764
687	15	26.3	316	6	CF760292	CF760292 DSAF1_57	760	15	26.3	407	9	AQ949279	AQ949279 Sheared_D
688	15	26.3	316	10	AC205829	AC205829 Oryza_Bat	761	15	26.3	408	1	AV805247	AV805247 AV805247
689	15	26.3	317	1	BB132467	BB132467 BB132467	762	15	26.3	408	6	BY802026	BY802026 BY802026
690	15	26.3	317	5	BM839485	BM839485 BM839485	763	15	26.3	408	5	CB771224	CB771224 AMGNNUC:S
691	15	26.3	322	1	AV009832	AV009832 AV009832	764	15	26.3	408	10	CE518427	CE518427 t1gr-g88-
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695	15	26.3	326	1	AA611944	AA611944 v086C02_1	768	15	26.3	411	5	BY185213	BY185213 BY185213
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701	15	26.3	332	1	AZ745673	AZ745673 RPCI-24-1	774	15	26.3	416	9	B27895	B27895 T20E7TRB_TA
702	15	26.3	335	1	AA981588	AA981588 ua23d06_00	775	15	26.3	417	7	CJ373362	CJ373362 CJ373362
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704	15	26.3	337	7	CR521746	CR521746 CR521746	777	15	26.3	418	3	BQ235732	BQ235732 h885a01.g
705	15	26.3	342	3	BM060047	BM060047 KS01008D0	778	15	26.3	419	10	CM872648	CM872648 she35-91
706	15	26.3	343	6	CB893270	CB893270 AMGNNUC:N	779	15	26.3	422	9	AO679833	AO679833 HS_5457_A
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## ALIGNMENTS

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RESULT 1
BU838287 802 bp mRNA linear EST 16-OCT-2002
LOCUS BU838287/c
DEFINITION AGENCOURT 8071679 NIH_MGC_112 Homo sapiens CDNA clone IMAGE:6088520
5' mRNA sequence.
ACCESSION BU838287
VERSION BU838287.1 GI:24022682
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens

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REFERENCE
AUTHORS NIH-MGC http://img.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-r@mail.nih.gov
Tissue Procurement: DCTD/DRP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLCM2326 row: n column: 09
High quality sequence stop: 558.
Location/Qualifiers
1..802

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FEATURES
source

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:6088520"
/cisue_type="melanotic melanoma, cell line"
/lab_host="PH10B (phage-resistant)"
/clone_idb="NIH MGC 112"
/notes="Organ: skin; Vector: pOT7; Site 1: XhoI; Site 2:
EcoRI; CDNA made by oligo-dT priming. Directionally cloned

```

```

into EcoRI/XhoI sites using the following 5' adaptor:
GGCAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH_MGC Library."

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Query Match 35 1%; Score 20; DB 5; Length 802;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 26 GCAGGGGAAGACTTGGGC 45
Db 616 GCAGGGGAAGACTTGGGC 597

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RESULT 2
AV338469 300 bp mRNA linear EST 11-NOV-1999
LOCUS AV338469/c
DEFINITION AV338469 RIKEN full-length enriched, adult male olfactory bulb Mus
musculus CDNA clone 6430409L15 3', mRNA sequence.
ACCESSION AV338469
VERSION AV338469.1 GI:6378521
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus

```

```

REFERENCE
AUTHORS Kono H, Aizawa K, Akahira S, Akiyama J, Carninci P, Endo T,
Fukuda S, Fukunishi Y, Hara A, Hayatsu N, Hirozane T, Hori F,
Ishii Y, Ishikawa T, Itoh M, Izawa M, Kadota K, Kagawa I,
Kai C, Kawai J, Kikuchi N, Kojima Y, Koya S, Kusakabe M,
Matsumura T, Miki R, Mizuno Y, Nakamura M, Oda H, Okazaki Y,
Owa C, Ozawa Y, Saito H, Sano M, Sato K, Shibata K,
Shibata Y, Shigemoto Y, Shiraki T, Sogabe Y, Suganaga Y,
Suzuki H, Suzuki H, Takahashi F, Tateno M, Tomihara N,
Tsunoda Y, Watanabe S, Yamamura T, Yasunishi A,
Yokota T, Yoshiki A, Yoshino M, Yamamoto M, and Hayashizaki Y.
RIKEN Mouse ESTs (Kono H, et al. 1999)
Unpublished (1999)

```

```

TITLE
JOURNAL
COMMENT Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
Saeki N, Izawa M, Watanabe M, Ozawa K, Tanaka T, Yoneda Y,
Matsumura S, Carninci P, Muramatsu M, Okazaki Y, and
Hayashizaki Y.

```

```

Transcriptional sequencing: A method for DNA sequencing using RNA
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3453-3460 (1998)
Itoh M, Kikuchi T, Akiyama J, Shibata K, Izawa M, Kawai J,
Tomaru Y, Carninci P, Shibata Y, Ozawa Y, Muramatsu M,
Okazaki Y, and Hayashizaki Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci P, and Hayashizaki Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (http://genome.rtc.riken.go.jp) for
further details.
Location/Qualifiers
1..300

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FEATURES
source
/organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="6430409L15"

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Gm-cl036-1486.5' similar to TR:P93103 P93103 CYCLIN-D LIKE PROTEIN.  
 : mRNA sequence.  
 ACCESSION AM756140  
 VERSION AM756140.1 GI:7685492  
 KEYWORDS EST.  
 SOURCE Glycine max (soybean)  
 ORGANISM Glycine max  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
 Glycine.  
 REFERENCE 1 (bases 1 to 577)  
 AUTHORS Shoemaker R., Kelm P., Vodkin L., Erpelting J., Corvelli V.,  
 Khanna A., Bolla B., Marra M., Hillier L., Kucaba T., Martin J.,  
 Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M.,  
 Bowers Y., Person B., Swaller T., Gibbons M., Page D., Harvey N.,  
 Schurk R., Ritzer E., Kohn S., Shin T., Jackson Y., Cardenas M.,  
 McCann R., Waterston R. and Wilson R.  
 TITLE Public Soybean EST Project  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shoemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: est@watson.wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. Trace  
 considered overall poor quality This clone is available through:  
 Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone:  
 800 423 4163; email: info@biogeneticservices.com)  
 Insert length: 938 Std Error: 0.00  
 High quality sequence stop: 1.  
 Location/Qualifiers  
 1..577  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Jack"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl036-1486"  
 /tissue\_type="somatic embryos cultured on MSD 20"  
 /lab\_host="DH10B"  
 /clone\_1lb="Gm-cl036"  
 /note="Vector: pSPORT1. Site 1: NotI. Site 2: SalI. This  
 cDNA library was constructed from mRNA isolated from  
 somatic embryos (age ranging from 2 months to 9 months)  
 cultured on MSD 20. The library was prepared using the  
 Life Technologies pSuperScript cDNA library construction  
 kit. Complementary DNA was synthesized from mRNA using a  
 poly (dT) sequence with a NotI restriction site. SalI  
 linkers adapters were ligated to the blunt-ended cDNA  
 fragments followed by NotI digestion. The cDNA fragments  
 were directionally cloned into the NotI-SalI restriction  
 site of the pSPORT1 vector. The ligated cDNA fragments  
 were transformed into E.coli Electromax DH10B host cells.  
 This library was constructed in the laboratory of Dr. Lila  
 Vodkin by Anu Khanna at the University of Illinois at  
 Urbana-Champaign. e-mail: l-vodkin@uiuc.edu"

ORIGIN  
 Query Match 33.3%; Score 19; DB 1; Length 577;  
 Best Local Similarity 100.0%; Pred.No. 9.1;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 GAACCTGGGCTGAACAAT 54  
 |||||  
 DB 103 GAACCTGGGCTGAACAAT 85

RESULT 6  
 CL789551  
 LOCUS CL789551 614 bp DNA linear GSS 30-JUL-2004

DEFINITION OR\_BBa0108G12.r OR\_BBa Oryza nivara genomic clone OR\_BBa0108G12.3',  
 genomic survey sequence.  
 ACCESSION CL789551  
 VERSION CL789551.1 GI:50869202  
 KEYWORDS GSS.  
 SOURCE Oryza nivara  
 ORGANISM Oryza nivara  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 614)  
 AUTHORS Kim H., Yu Y., Stum D., Yost D., Rao K., Luo M., Jetty R.,  
 Kudrna D., Muller C., Hatfield J., Soderlund C. and Wing R.  
 TITLE OMAP Project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 PCR Primers  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Insert Length: 161 Std Error: 0.00  
 Plate: 0108 row: G column: 12  
 Seq primer: CAC TCA TTA GGC ACC CCA  
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 /clone="OR\_BBa0108G12"  
 /tissue\_type="young leaves"  
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 /note="Vector: pGIBAC1, site\_1: HindIII, site\_2: HindIII"

ORIGIN  
 Query Match 33.3%; Score 19; DB 10; Length 614;  
 Best Local Similarity 100.0%; Pred.No. 9.1;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 AGCAGCGGAAAGAACTGG 43  
 |||||  
 DB 492 AGCAGCGGAAAGAACTGG 510

RESULT 7  
 CL805426  
 LOCUS CL805426 622 bp DNA linear GSS 09-AUG-2004  
 DEFINITION OR\_CBa0018M23.r OR\_CBa Oryza rufipogon genomic clone OR\_CBa0018M23  
 3', genomic survey sequence.  
 ACCESSION CL805426  
 VERSION CL805426.1 GI:51043007  
 KEYWORDS GSS.  
 SOURCE Oryza rufipogon  
 ORGANISM Oryza rufipogon  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzaceae; Oryza.  
 REFERENCE 1 (bases 1 to 622)  
 AUTHORS Kim H., Yu Y., Wabsoetaki M., Yost D., Stum D., Rao K., Luo M.,  
 Jetty R., Kudrna D., Muller C., Hatfield J., Soderlund C. and  
 Wing R.  
 TITLE OMAP project  
 JOURNAL Unpublished (2004)  
 COMMENT Contact: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA



Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0018 row: M column: 23  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.  
Location/Qualifiers  
1..622  
/organism="Oryza rufipogon"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4529"  
/clone="OR\_CBa0018M23"  
/tissue\_type="young leaves"  
/dev\_stage="2 week old seedlings"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OR\_CBa"  
/note="Vector: pAG1BAC1, Site\_1: HindIII, Site\_2: HindIII;  
dir treated 36 hrs before harvest"

ORIGIN  
Query Match 33.3%; Score 19; DB 10; Length 622;  
Best Local Similarity 100.0%; Pred. No. 9.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 25 AGCAGGGGAGAAAGACTTGG 43  
|||||  
Db 491 AGCAGGGGAGAAAGACTTGG 509

RESULT 8  
CZ771457/c 648 bp DNA linear GSS 26-JUL-2005  
LOCUS OC\_Ba0128021.f OC\_Ba Oryza coarctata genomic clone OC\_Ba0128021  
DEFINITION 5' genomic survey sequence.  
ACCESSION CZ771457  
VERSION CZ771457.1 GI:71211308  
KEYWORDS GSS.  
SOURCE Oryza coarctata (Porteresia coarctata)  
ORGANISM Oryza coarctata  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretoidae; Oryzaceae; Oryza.  
1 (bases 1 to 648)  
Kim,H., Collura,K., Wisoetaki,M., Byrne,M., Stum,D., Rao,K.,  
Wing,R., Luo,M., Jetty,R., Kudrna,D., Muller,C., Soderlund,C. and  
OMP (Oryza Map Alignment Project) - Arizona Genomics Institute  
TITLE OMP (Oryza Map Alignment Project) - Arizona Genomics Institute  
JOURNAL Unpublished (2005)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0128 row: O column: 21  
Seq primer: TAA TAC GAC TCA CTA TAG GG  
Class: BAC ends.  
Location/Qualifiers  
1..648  
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/db\_xref="taxon:77588"  
/clone="OC\_Ba0128021"  
/tissue\_type="leaves"  
/dev\_stage="mature"  
/lab\_host="DH10B"

FEATURES  
source

/clone\_lib="OC\_Ba"  
/note="Vector: pAG1BAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN  
Query Match 33.3%; Score 19; DB 10; Length 648;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 6 TTGATCATTCACATCTCT 24  
|||||  
Db 104 TTGATCATTCACATCTCT 86

RESULT 9  
Cw689465 657 bp DNA linear GSS 01-NOV-2004  
LOCUS OG\_BBa0049009.r OG\_BBa Oryza glaberrima genomic clone OG\_BBa0049009  
DEFINITION 3' genomic survey sequence.  
ACCESSION Cw689465  
VERSION Cw689465.1 GI:55160899  
KEYWORDS GSS.  
SOURCE Oryza glaberrima (African rice)  
ORGANISM Oryza glaberrima  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehretoidae; Oryzaceae; Oryza.  
1 (bases 1 to 657)  
Kim,H., Yu,Y., Wisoetaki,M., Byrne,M., Stum,D., Rao,K.,  
Luo,M., Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C.  
and Wing,R.  
OMP  
TITLE Unpublished (2004)  
JOURNAL Contact: Rod A. Wing  
COMMENT Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0049 row: O column: 09  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:4538"  
/clone="OG\_BBa0049009"  
/tissue\_type="young leaves"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OG\_BBa"  
/note="Vector: pAG1BAC1, Site\_1: HindIII, Site\_2: HindIII"

ORIGIN  
Query Match 33.3%; Score 19; DB 10; Length 657;  
Best Local Similarity 100.0%; Pred. No. 9.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 25 AGCAGGGGAGAAAGACTTGG 43  
|||||  
Db 290 AGCAGGGGAGAAAGACTTGG 308

RESULT 10  
CL815149 684 bp DNA linear GSS 09-AUG-2004  
LOCUS CL815149 684 bp DNA linear GSS 09-AUG-2004  
DEFINITION OR\_CBa0031P09.r OR\_CBa Oryza rufipogon genomic clone OR\_CBa0031P09  
ACCESSION CL815149  
VERSION CL815149.1 GI:51058875



KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
REFERENCE 1 (bases 1 to 684)  
AUTHORS Kim,H., Yu,Y., Misotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,  
Jecty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and  
Wing,R.  
TITLE OMAP project  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0031 row: F column: 09  
Seq primer: CAC TCA TTA GGC ACC CCA  
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/tissue\_type="young leaves"  
/dev\_stage="2 week old seedlings"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OR\_CBA"  
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Best Local Similarity 100.0%; Pred.No. 9.2; 0; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;  
Qy 25 AGCAGCGGAAAGAACTTGG 43  
|||||  
Db 491 AGCAGCGGAAAGAACTTGG 509  
RESULT 11  
LOCUS CL801207 710 bp DNA linear GSS 06-AUG-2004  
DEFINITION OR\_CBA0013B04.f OR\_CBA Oryza rufipogon genomic clone OR\_CBA0013B04  
3', genomic survey sequence.  
ACCESSION CL801207  
VERSION CL801207.1 GI:51026887  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
REFERENCE 1 (bases 1 to 710)  
AUTHORS Kim,H., Yu,Y., Misotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,  
Jecty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and  
Wing,R.  
TITLE OMAP project  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259

Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0013 row: B column: 04  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.  
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/tissue\_type="young leaves"  
/dev\_stage="2 week old seedlings"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OR\_CBA"  
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Best Local Similarity 100.0%; Pred.No. 9.2; 0; Indels 0; Gaps 0;  
Matches 19; Conservative 0; Mismatches 0;  
Qy 25 AGCAGCGGAAAGAACTTGG 43  
|||||  
Db 606 AGCAGCGGAAAGAACTTGG 588  
RESULT 12  
LOCUS CL794245 754 bp DNA linear GSS 06-AUG-2004  
DEFINITION OR\_CBA0003K07.f OR\_CBA Oryza rufipogon genomic clone OR\_CBA0003K07  
5', genomic survey sequence.  
ACCESSION CL794245  
VERSION CL794245.1 GI:51016261  
KEYWORDS GSS.  
SOURCE Oryza rufipogon  
ORGANISM Oryza rufipogon  
REFERENCE 1 (bases 1 to 754)  
AUTHORS Kim,H., Yu,Y., Misotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,  
Jecty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and  
Wing,R.  
TITLE OMAP project  
JOURNAL Unpublished (2004)  
COMMENT Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu  
PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Plate: 0003 row: K column: 07  
Seq primer: TAA TAC GAC TCA CTA TAG GG  
Class: BAC ends.  
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/db\_xref="taxon:4529"  
/clone="OR\_CBA0003K07"  
/tissue\_type="young leaves"  
/dev\_stage="2 week old seedlings"  
/lab\_host="DH10B T1 phage resistant"  
/clone\_lib="OR\_CBA"  
/note="Vector: PACIBAC1; Site\_1: HindIII; Site\_2: HindIII;



ORIGIN                    dirk treated 36 hrs before harvest"

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 Best Local Similarity    100.0%; Pred. No. 9.2;  
 Matches    19; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY                    25 AGCAGGGGAAAGAACTTG3 43  
 DB                    492 AGCAGGGGAAAGAACTTG3 510

RESULT 13  
 CL799200/c  
 LOCUS                    CL799200                    833 bp    DNA                    linear    GSS 06-AUG-2004  
 DEFINITION    OR\_CBA0010F02.f OR\_CBA Oryza rufipogon genomic clone OR\_CBA0010F02  
 5', genomic survey sequence.  
 ACCESSION    CL799200  
 VERSION    CL799200.1 GI:51022846  
 KEYWORDS    GSS.

SOURCE  
 ORGANISM    Oryza rufipogon  
 Oryza rufipogon  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Ehrhartoideae; Oryzoae; Oryza.  
 1 (bases 1 to 833)  
 Kim,H., Yu,Y., Wlasotski,M., Yost,D., Stum,D., Rao,K., Luo,M.,  
 Jetty,R., Kudrna,D., Muller,C., Hatfield,J., Soderlund,C. and  
 Wing,R.  
 OMAP project  
 Unpublished (2004)  
 CONTACT: Rod A. Wing  
 Arizona Genomics Institute  
 University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9595  
 Fax: 520 621 1259  
 Email: rwing@genome.arizona.edu  
 PCR PRIMERs  
 FORWARD: TAA TAC GAC TCA CTA TAG GG  
 BACKWARD: CAC TCA TTA GGC ACC CCA  
 Plate: 0010 row: F column: 02  
 Seq primer: TAA TAC GAC TCA CTA TAG GG  
 Class: BAC ends.

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                   /db\_xref="taxon:4529"  
                   /clone="OR\_CBA0010F02"  
                   /tissue\_type="young leaves"  
                   /dev\_stage="2 week old seedlings"  
                   /lab\_host="DH10B T1 phage resistant"  
                   /clone\_lib="OR\_CBA"  
                   /note="Vector: PACIBAC1, Site\_1: HindIII; Site\_2: HindIII;  
                   dirk created 36 hrs before harvest"

ORIGIN

Query Match                    33.3%; Score 19; DB 10; Length 833;  
 Best Local Similarity    100.0%; Pred. No. 9.3;  
 Matches    19; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY                    25 AGCAGGGGAAAGAACTTG3 43  
 DB                    607 AGCAGGGGAAAGAACTTG3 589

RESULT 14  
 AV026006/c  
 LOCUS                    AV026006                    144 bp    mRNA                    linear    EST 31-AUG-1999  
 DEFINITION    AV026006 Mus musculus adult C57BL/6J lung Mus musculus cDNA clone  
 1200017E21, mRNA sequence.  
 ACCESSION    AV026006

VERSION                    AV026006.1 GI:4802998  
 KEYWORDS    EST.  
 SOURCE    Mus musculus (house mouse)  
 ORGANISM    Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS    1 (bases 1 to 144)  
                   Carninci,P., Shibata,K., Ozawa,Y., Konno,H., Itoh,M., Aizawa,K.,  
                   Akahira,S., Akiyama,J., Fukuda,S., Fukunishi,Y., Funayama,T.,  
                   Hara,A., Hayatsu,N., Hori,F., Ishikawa,T., Itoh,M., Izawa,M.,  
                   Kawai,J., Kikuchi,N., Kojima,Y., Matsuyama,T., Nitsuma,H., Oda,H.,  
                   Owa,C., Sato,K., Shibata,Y., Shigemoto,Y., Shiraki,T., Sogabe,Y.,  
                   Sugahara,Y., Suzuki,H., Suzuki,H., Tateo,M., Tomaru,Y.,  
                   Tomioka,N., Watanabe,S., Yagame,M., Yamamura,T., Yokota,T.,  
                   Yoshino,M., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.  
 RIKEN Mouse ESTs  
 Unpublished (1999)  
 CONTACT: Chie Owa  
 Genome Science Laboratory  
 RIKEN  
 3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan  
 Tel: 81-298-36-9145  
 Fax: 81-298-36-9098  
 Email: genome-res@rtc.riken.go.jp  
 Thermostabilization and thermoinactivation of thermostable enzymes by  
 trehalose and its application for the synthesis of full length cDNA  
 (Proc. Natl. Acad. Sci. U.S.A. 95(12):520-524 (1998))  
 Transcriptional sequencing: A method for DNA sequencing using RNA  
 polymerase (Proc. Natl. Acad. Sci. U.S.A. 95(7):3455-3460 (1998))  
 Please visit our web site (<http://genome.rtc.riken.go.jp>) for  
 further details.

FEATURES  
 source                    Location/Qualifiers  
                   1..144  
                   /organism="Mus musculus"  
                   /mol\_type="mRNA"  
                   /strain="C57BL/6J"  
                   /db\_xref="taxon:10090"  
                   /clone="1200017E21"  
                   /tissue\_type="lung"  
                   /dev\_stage="adult"  
                   /clone\_lib="Mus musculus adult C57BL/6J lung"

ORIGIN

Query Match                    31.6%; Score 18; DB 1; Length 144;  
 Best Local Similarity    100.0%; Pred. No. 31;  
 Matches    18; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

OY                    34 AAGAACTTGGGCTGAAC 51  
 DB                    100 AAGAACTTGGGCTGAAC 83

RESULT 15  
 BH875745  
 LOCUS                    BH875745                    187 bp    DNA                    linear    GSS 05-AUG-2002  
 DEFINITION    hr26g08.b1 WGS-2mayesf (JMI07 adapted methyl filtered) Zea mays  
 genomic clone hr26g08 5', genomic survey sequence.  
 ACCESSION    BH875745  
 VERSION    BH875745.1 GI:22111642  
 KEYWORDS    GSS.

SOURCE  
 ORGANISM    Zea mays  
 Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.

REFERENCE  
 AUTHORS    1 (bases 1 to 187)  
                   Rabinowicz,P.D., O'Shaughnessy,A.L., Balija,V., Dedhia,N.,  
                   Katzenburger,F., King,L., Miller,B., Muller,S., Nascimento,L.,  
                   Zuberav,T., McCombie,W.R. and Martienssen,R.A.  
 Genomic shotgun sequences from Zea mays (methyl-filtered)  
 Unpublished (2002)  
 CONTACT: W. Richard McCombie



Liita Annenberg Hazen Genome Sequencing Center  
Cold Spring Harbor Laboratory  
PO Box 100, Cold Spring Harbor, NY 11724, USA  
Tel: 516 367 8884  
Fax: 516 367 8874  
Email: mcomblie@cshl.org  
Plate: hr26 row: g column: 08  
Seq primer: -21M13univFwd  
Class: Shotgun  
High quality sequence stop: 187.  
Location/Qualifiers  
1..187  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="hr26g08"  
/lab\_host="JMI07 or DHSa"  
/note="Organ: immature ears; Site\_1: Xba I; Site\_2: Xba I;  
The vector was digested with XbaI and one nucleotide was  
added by fill in in the recessive 3' end. The genomic DNA  
was nebulized, end repaired, adaptor ligated and size  
fractionated using sephadex. The resulting fragments were  
between 0.8 and 3 kb and were cloned into the vector  
(x/y reads in M13mp19, b/g reads in pUC19). The same  
ligation was transformed in either JMI07 or DHSa."

## ORIGIN

Query Match 31.6%; Score 18; DB 9; Length 187;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 26 GCAGGGGAAAGAACTTGG 43  
|||||  
Db 68 GCAGGGGAAAGAACTTGG 85

RESULT 16  
AQ475448 259 bp DNA linear GSS 23-APR-1999  
LOCUS CITBI-EI-2592K1.FR CITBI-EI Homo sapiens genomic clone 2592K1,  
DEFINITION genomic survey sequence.  
ACCESSION AQ475448  
VERSION AQ475448.1 GI:4657567  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 259)  
Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and  
Venter,J.C.  
Use of BAC End Sequences from Caltech Libraries for Sequence-Ready  
Map Building (1997)  
Contact: Shanying Zhao, William Nierman, Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: hbeetlgr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/cdb/humgen/bac\_end\_search/bac\_end\_search.html.  
Seq primer: M13 Reverse  
Class: BAC ends.

## FEATURES

source  
1..259  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"

/db\_xref="taxon:9606"  
/clone="2592K1"  
/sex="male"  
/cell\_type="sperm"  
/clone\_1lb="CITBI-EI"  
/note="Vector: pBelOAC11, Site\_1: EcoRI, Site\_2: EcoRI;  
Caltech Human BAC Library D"

## ORIGIN

Query Match 31.6%; Score 18; DB 9; Length 259;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 TTGGGCTGAACAAATGGG 57  
|||||  
Db 77 TTGGGCTGAACAAATGGG 94

RESULT 17  
CA898982 269 bp mRNA linear EST 27-DEC-2002  
LOCUS PCBP02047 Scarlet Runner Bean Embryo-Propag Region Phaseolus  
DEFINITION coccineus cDNA 5' similar to ISP42-LIKE PROTEIN, mRNA sequence.  
ACCESSION CA898982  
VERSION CA898982.1 GI:27385973  
KEYWORDS EST.  
SOURCE Phaseolus coccineus  
ORGANISM Phaseolus coccineus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;  
Phaseolus.  
1 (bases 1 to 269)  
Bui,A.O., Le,B.H., Weterings,K., Bi,Y.-P., Choi,J.-S.,  
McElroy,K.E., Choi,P.S., Harada,T.J., Fischer,R.L. and  
Goldberg,R.B.  
Gene Activity in Different Regions of a Post-Fertilization Plant  
Embryo by EST Analysis  
Unpublished (2002)  
Contact: Goldberg, R.B.  
Department of Molecular, Cell, & Developmental Biology  
University of California, Los Angeles  
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA  
Tel: 310 825 3270  
Fax: 310 825 8201  
Email: bobg@ucla.edu  
Seq primer: 5' triplex  
POLYA-No.

## JOURNAL

COMMENT  
Unpublished (2002)  
Contact: Goldberg, R.B.  
Department of Molecular, Cell, & Developmental Biology  
University of California, Los Angeles  
621 Charles E. Young Drive South, Los Angeles, CA 90095-1606, USA  
Tel: 310 825 3270  
Fax: 310 825 8201  
Email: bobg@ucla.edu  
Seq primer: 5' triplex  
POLYA-No.

## FEATURES

source  
1..269  
Location/Qualifiers  
/organism="Phaseolus coccineus"  
/mol\_type="mRNA"  
/cultivar="Hammond's Dwarf Scarlet"  
/db\_xref="taxon:3886"  
/dev\_stage="6-days post-pollination"  
/clone\_1lb="Scarlet Runner Bean Embryo-Propag Region"  
/note="Organ: Embryo-Propag Region of Globular-Stage  
Embryos; Vector: triplex2; Site\_1: SfiI; Site\_2: SfiI;  
Embryo-propag regions were micro-dissected from  
globular-stage embryos six days after pollination from  
greenhouse-grown plants [Weterings et al., Plant Cell 13,  
2409-2425 (2001)]. Double-stranded cDNA was synthesized  
from embryo-propag mRNA using the SMART cDNA Library  
Construction Kit according to the manufacturer (Clontech).  
The embryo-propag cDNA fragments were directionally  
ligated into the SfiI restriction site of the lambda  
triplex2 vector (Clontech), and the recombinant cDNAs were  
transformed into E. coli XL1-Blue cells (Clontech).  
Embryo-propag cDNA plasmids used for directional  
sequencing were obtained by in vivo excision from the  
lambda triplex2 recombinants in E. coli BW25.8 cells  
(Clontech)."

## ORIGIN



Query Match	31.6%	Score 18	DB 6	length 269	
Best Local Similarity	100.0%	Pred. No. 32			
Matches	18	Conservative	0	Mismatches 0; Indels 0; Gaps 0	
Db	36	GAAGTTGGGCTGMAACAA	53		
RESULT 18					
BB290745/c					
LOCUS					
DEFINITION	BB290745 RIKEN full-length enriched, 2 cells egg Mus musculus cDNA				
ACCESSION	BB290745	275 bp	mRNA	linear	
VERSION	BB290745.1				
KEYWORDS	EST				
SOURCE	Mus musculus (house mouse)				
ORGANISM	Mus musculus				
REFERENCE	Mumakura, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
AUTHORS	Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T., Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M., Iizawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N., Kiyosawa, H., Kojima, Y., Kondo, S., Koya, S., Kurihara, C., Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K., Shibata, K., Shibata, Y., Shigenoto, Y., Shingawa, A., Shiraki, T., Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A., Takahashi, F., Tominaga, N., Toya, T., Tsunoda, Y., Watanabe, S., Yamamura, T., Yamana, T., Yano, R., Yasunishi, A., Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayaishizaki, Y.				
TITLE	RIKEN Mouse ESTs (Komno, H., et al.)				
JOURNAL	Unpublished (2000)				
COMMENT	Contact: Yoshihide Hayaishizaki Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Shuto-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-res@gs.c.riken.jp, URL: http://genome.gs.c.riken.jp/ Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagakura, S., Sasaki, N., Okazaki, Y., Muramatsu, M. and Hayaishizaki, Y. Thermosensitization and thermocatalysis of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh, M., Katsunari, T., Akiyama, J., Shibata, K., Iizawa, M., Kawai, J., Tomaru, Y., Carninci, P., Shibata, Y., Okazaki, Y., and Hayaishizaki, Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci, P. and Hayaishizaki, Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999) Please visit our web site (http://genome.etc.riken.go.jp) for further details. Location/Qualifiers 1. 275 /organism="Mus musculus" /mol_type="mRNA" /db_xref="taxon:10090" /clone="B020047E03" /tissue_type="egg" /dev_stage="2 cells" /lab_host="DH10B" /clone_1="RIKEN full-length enriched, 2 cells egg" /note="Site_1: Salt; Site_2: BamHI; cDNA library was				

	Query Match	31.6%	Score 18;	DB 2;	Length 275;	
	Best Local Similarity	100.0%	Pred. No. 33;			
	Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
Oy	31 GGAAGAAGACTTGGGCTGA 48             					
Dn	240 GGAAAGAAGCTTGCGCTCA 223					
RESULT 19	AZ706097/c	474 bp	DNA	linear	GSS 24-JAN-2001	
LOCUS	RPCI-23-229B11.TJ RPCI-23 Mus musculus genomic clone					
DEFINITION	RPCI-23-229B11, genomic survey sequence.					
ACCESSION	AZ706097					
VERSION	AZ706097.1 GI:12433220					
KEYWORDS	GSS.					
SOURCE	Mus musculus (house mouse)					
ORGANISM	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 474) Zhao,S., Nierman,W., Feldblum,T., Malek,J., Shatsman,S., Akinret,B., Levins,M., Megann,S., Teegaye,G., Geer,K., Krol,M., de Jong,P. and Fraser,C.M. Mouse BAC End Sequences from Library RPCI-23 Unpublished (1999) Contact: Shaying Zhao Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel.: 301 838 0200 Fax: 301 838 0208 Email: szhao@tigr.org Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pierer de Jong [pdejong@mail.cho.org]. Clones may be purchased from BACPAC Resources ( <a href="http://www.chori.org/bacpac/orderingfrme.htm">http://www.chori.org/bacpac/orderingfrme.htm</a> ). BAC end page: <a href="http://www.tigr.org/tcd/bac_end/mouse/bac_end_intro.html">http://www.tigr.org/tcd/bac_end/mouse/bac_end_intro.html</a> Plate: 229 row: B column: 11 Seq primer: SP6 Class: BAC ends.					
TITLE	Location/Qualifiers					
JOURNAL	1. .474					
COMMENT	/organism="Mus musculus" /mol_type="genomic DNA" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="RPCI-23-229B11" /sex="Female" /lab_host="DH10B" /clone_lib="RPCI-23" /notes="Organ: Kidney/Brain; Vector: pBACe3.6; Site_1: EcoRI_Site_2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Size					



## ORIGIN

selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

Query Match 31.6%; Score 18; DB 9; Length 474;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 AAGAACTTGCGCTGAAA 50  
|||||  
Db 87 AAGAACTTGCGCTGAAA 70

## RESULT 20

CE057757/c 475 bp DNA linear GSS 24-SEP-2003  
LOCUS tigr-gss-dog-17000322454115 Dog library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE057757 GI:35106375  
VERSION CE057757.1 GI:35106375  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris

REFERENCE 1 (bases 1 to 475)  
AUTHORS Kirkeness,E.F., Rafina,V., Halpern,A.L., Levy,S., Remington,K.,  
Ruech,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkeness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville MD 20850, USA  
Tel: 301-838-0208  
Fax: 301-838-0208  
Email: ekirkenes@tigr.org  
Classes: shotgun.

## FEATURES

source location/Qualifiers

1..475  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

## ORIGIN

Query Match 31.6%; Score 18; DB 9; Length 475;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 CATTCACTATCTCTAGCA 28  
|||||  
Db 168 CATTCACTATCTCTAGCA 151

RESULT 21  
LOCUS A1195160 476 bp mRNA linear EST 14-OCT-1998  
DEFINITION u161d04.x1 Sugano mouse liver mla Mus musculus cDNA clone  
IMAGE:186887.3', similar to gb:M28649 Mouse major urinary protein  
mRNA, complete cds (MUSMF), mRNA sequence.

ACCESSION A1195160  
VERSION A1195160.1 GI:3747766  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE

1 (bases 1 to 476)  
AUTHORS Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,  
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,  
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,  
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and  
Waterston,R.

TITLE The WashU-HMI Mouse EST Project  
JOURNAL Unpublished (1996)  
COMMENT Contact: Marra M/Mouse EST Project  
WashU-HMI Mouse EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: mouseest@wustl.edu  
This clone is available royalty-free through LMLT; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
MGI:971211

Seq primer: custom primer used  
High quality sequence stop: 469.  
Location/Qualifiers

1..476  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL"  
/db\_xref="taxon:10090"  
/clone="IMAGE:186887"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="Sugano mouse liver mla"  
/note="Organ: liver; Vector: pHE18-F13; Site\_1: DraIII  
(CAGCTGTG); Site\_2: DraIII (CAGCAATG); 1st strand cDNA  
was primed with an oligo(dT) primer  
(ATGGGCCCTTTTCTTTTCTTTT); double-stranded cDNA was  
ligated to a DraIII adaptor (TTTGGCCCTACTGG) , digested  
and cloned into distinct draIII sites of the pHE18-F13  
vector (5' site CAGCTGTG, 3' site CAGCAATG). xhoI should  
be used to isolate the cDNA insert. Size selection was  
performed to exclude fragments <1.5kb. Library  
constructed by Dr. Sumio Sugano (University of Tokyo  
Institute of Medical Science). Custom primers for  
sequencing: 5' end primer CTTTCGCTCTAAAGCTGG and 3' end  
primer CGACTCGAGCTCGAGCACA."

## ORIGIN

Query Match 31.6%; Score 18; DB 1; Length 476;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 34 AAGAACTTGCGCTGAAC 51  
|||||  
Db 271 AAGAACTTGCGCTGAAC 288

RESULT 22  
LOCUS AQ223774 477 bp DNA linear GSS 20-SEP-1998  
DEFINITION HS 2011.A1.C07 MR CIT Approved Human Genomic Sperm Library D Homo  
sapiens genomic clone Plate=2011 Col=13 Row=E, genomic survey  
sequence.

ACCESSION AQ223774  
VERSION AQ223774.1 GI:3639617  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 477)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurgonathi; Muridae; Muridae; Mus.



AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.

TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)

PUBMED 10449764

COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Sequence Tagged Connector  
Plate: 2011 Row: E Column: 13  
Class: BAC ends  
High quality sequence atop: 477.

FEATURES  
source  
1. 477  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=2011 Col=13 Row=E"  
/sex="male"  
/clone\_lib="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBeloBAC11; BAC Clones in E-Coli DH10B"

ORIGIN  
Query Match 31.6%; Score 18; DB 9; Length 477;  
Best Local Similarity 100.0%; Pred.No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 27 CAGGGGAAAGACTGGG 44  
|||||  
DB 219 CAGGGGAAAGACTGGG 236

RESULT 23  
CES60604 548 bp DNA linear GSS 28-SEP-2003  
LOCUS tigr-gss-dog-17000327486804 dog library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CES60604  
VERSION CES60604.1 GI:36877385  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 548)  
Kirkness,E.F., Bafn,V., Halpern,A.L., Levy,S., Remington,K.,  
Ruech,D.B., Delcher,A.L., Pop,M., Wang,W., Frazer,C.W. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
14512627  
Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
Location/Qualifiers  
1. 548  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"

FEATURES  
source  
1. 548  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"

/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from peripheral blood"

ORIGIN  
Query Match 31.6%; Score 18; DB 10; Length 548;  
Best Local Similarity 100.0%; Pred.No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 37 AACTTGGGCTGAACAAAT 54  
|||||  
DB 81 AACTTGGGCTGAACAAAT 98

RESULT 24  
AQ463454 611 bp DNA linear GSS 23-APR-1999  
LOCUS AQ463454  
DEFINITION HS\_5200\_B2\_E08\_SP6B\_RPCI-11 Human Male BAC library Homo sapiens  
genomic clone Plate=776 Col=16 Row=J, genomic survey sequence.  
ACCESSION AQ463454  
VERSION AQ463454.1 GI:4640549  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Homo.  
1 (bases 1 to 611)  
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and  
Hood,L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCI-11. For BAC  
library availability, please contact pister de Jong  
(pister@jondj.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
or from Resear h Genetics (info@resgen.com). BAC end Web Server:  
http://www.htcsc.washington.edu  
Plate: 776 row: J column: 16  
Seq primer: SP6  
Class: BAC ends  
High quality sequence atop: 611.

FEATURES  
source  
1. 611  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=776 Col=16 Row=J"  
/sex="male"  
/clone\_lib="RPCI-11 Human Male BAC library"  
/note="Vector: pBACe3.6; Site.1: EcoRI; Site.2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

ORIGIN  
Query Match 31.6%; Score 18; DB 9; Length 611;  
Best Local Similarity 100.0%; Pred.No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 32 GAAGAACTGGGCTGAA 49  
|||||



Db 428 GAAGAACTTGCGCTGAA 445

RESULT 25  
CE257607/c 651 bp DNA linear GSS 26-SEP-2003  
LOCUS tigr-gss-dog-17000345854653 dog library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CE257607  
VERSION CE257607.1 GI:35962531  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
1 (bases 1 to 651)  
Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)  
14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
FEATURES  
source Location/Qualifiers  
1..651  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog library"  
/note="Site 1: Becki; Libraries were prepared from  
peripheral blood"

ORIGIN  
Query Match 31.6%; Score 18; DB 9; Length 651;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 30 GCGAAGAACTTGCGCTG 47  
|||||  
Db 107 GCGAAGAACTTGCGCTG 90

RESULT 26  
CR334147/c 655 bp DNA linear GSS 17-NOV-2004  
LOCUS mtel-64M20RM1 BAC end, cultivar Jemalong A17 of Medicago  
DEFINITION truncatula, genomic survey sequence.  
ACCESSION CR334147  
VERSION CR334147.1 GI:44880291  
KEYWORDS GSS.  
SOURCE Medicago truncatula  
ORGANISM Medicago truncatula (barrel medic)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifoliales;  
Medicago.  
1 (bases 1 to 655)  
Genoscope.  
Direct Submission  
Submitted (25-FEB-2004) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr)  
- Web : www.genoscope.cns.fr  
Location/Qualifiers  
1..655  
source

Db 347 GCATTCATTCATTCACCTA 330

ORIGIN  
Query Match 31.6%; Score 18; DB 11; Length 655;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 2 GCATTCATTCATTCACCTA 19  
|||||  
Db 347 GCATTCATTCATTCACCTA 330

RESULT 27  
B16435/c 689 bp DNA linear GSS 04-JUN-1998  
LOCUS 342D19.TPB CTT978SKA1 Homo sapiens genomic clone A-342D19, genomic  
DEFINITION survey sequence.  
ACCESSION B16435  
VERSION B16435.1 GI:2124184  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 689)  
Adams,M.D., Kelley,J.M., Rounsley,S.R. and Venter,J.C.  
Use of a BAC End Sequence Database for Sequence-Ready Map Building  
Unpublished (1997)  
Other GSSs: 342D19.TV 342D19.TVB  
CONTACT: Mark Adams  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: mdadams@tigr.org  
Clones are available from Research Genetics (info@resgen.com). BAC  
end search page:  
http://www.tigr.org/cdb/hungen/bac\_end\_search/bac\_end\_search.html  
Seq primer: SP6  
Class: BAC ends.  
FEATURES  
source Location/Qualifiers  
1..689  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone\_lib="A-342D19"  
/sex="Female"  
/cell\_type="Fibroblast"  
/clone\_lib="CTT978SKA1"  
/note="Vector: pBAC108L; Site\_1: HindIII; Site\_2: HindIII;  
Caltech Human BAC Library A1"

ORIGIN  
Query Match 31.6%; Score 18; DB 9; Length 689;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 40 TTGGGCTGAACATCGG 57  
|||||  
Db 464 TTGGGCTGAACATCGG 447

RESULT 28  
CE062663/c



LOCUS CB062663 691 bp DNA linear GSS 24-SEP-2003  
 DEFINITION tigr-gss-dog-17000322601357 Dog library Canis familiaris genomic,  
 genomic survey sequence.  
 ACCESSION CB062663  
 VERSION CB062663.1 GI:35116196  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.  
 1 (bases 1 to 691)  
 Kirhness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Ruech,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 The dog genome: survey sequencing and comparative analysis  
 Science 301 (5641), 1898-1903 (2003)  
 14512627  
 CONTACT: Kirhness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirhness@tigr.org  
 Class: shotgun.  
 FEATURES  
 source  
 1..691  
 Location/Qualifiers  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BscXI; Libraries were prepared from  
 peripheral blood"  
 ORIGIN  
 Query Match 31.6%; Score 18; DB 9; Length 691;  
 Best Local Similarity 100.0%; Pred.No. 34;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 7 TGATCATTCACATCTCT 24  
 |||||  
 Db 149 TGATCATTCACATCTCT 132  
 RESULT 29  
 AG032453 770 bp DNA linear GSS 01-NOV-2001  
 LOCUS Pan troglodytes DNA, clone: PTB-007D05.F, genomic survey sequence.  
 DEFINITION AG032453  
 ACCESSION AG032453  
 VERSION AG032453.1 GI:16559326  
 KEYWORDS GSS.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan.  
 1  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Torok,Y., Watanabe,H. and Sakaki,Y.  
 BAC end sequences of Library PTB  
 2 (bases 1 to 770)  
 Unpublished  
 Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,  
 Torok,Y., Watanabe,H. and Sakaki,Y.  
 Direct Submission  
 Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical  
 and Chemical Research (RIKEN), Genomic Sciences Center (GSC);  
 1-7-22 Shuohiro-chou,Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 (E-mail:chimbese@sc.riken.go.jp, URL:http://hgp-gssc.riken.go.jp/,  
 Tel:81-45-503-9111, Fax:81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library PTB This BAC end

was generated during the Red process and may have higher chance of  
 clone tracking errors.  
 PRIMERS  
 Sequencing: -21M13  
 LIBRARY  
 Vector : pRS145  
 R.Site 1 : SacI  
 R.Site 2 : SacI.  
 FEATURES  
 source  
 1..770  
 Location/Qualifiers  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /clone="PTB-007D05.F"  
 /sex="male"  
 /cell\_type="lymphoblast"  
 /clone\_lib="PTB Chimpanzee Male BAC library"  
 ORIGIN  
 Query Match 31.6%; Score 18; DB 10; Length 770;  
 Best Local Similarity 100.0%; Pred.No. 34;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 30 GGGAAGAACTTGGGCTG 47  
 |||||  
 Db 410 GGGAAGAACTTGGGCTG 427  
 RESULT 30  
 AG743426 785 bp DNA linear GSS 16-JUL-1999  
 LOCUS HS\_5387\_B1\_F02\_SP6 RPCI-11 Human Male BAC library Homo sapiens  
 DEFINITION genomic clone Plate=963 Col=3 Row=L, genomic survey sequence.  
 ACCESSION AG743426  
 VERSION AG743426.1 GI:5520948  
 KEYWORDS GSS.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 785)  
 Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,  
 Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,W.D. and  
 Hood,L.  
 Sequence-tagged connectors: A sequence approach to mapping and  
 scanning the human genome  
 Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
 10449764  
 CONTACT: Mahairas GG, Wallace JC, Hood L  
 High Throughput Sequencing Center  
 University of Washington  
 401 Queen Anne Avenue North, Seattle, WA 98109, USA  
 Tel: (206) 616-3618  
 Fax: (206) 616-3887  
 Email: jwallace@u.washington.edu  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@dejong.med.buffalo.edu). Clones may be purchased from  
 BACPAC Resources (http://bacpac.med.buffalo.edu/ordering\_bac.htm)  
 or from Research Genetics (info@resgen.com). BAC end Web Server:  
 http://www.husc.washington.edu  
 Seq primer: SP6  
 Plate: 963 row: L column: 3  
 Class: BAC ends  
 High quality sequence stop: 785.  
 FEATURES  
 source  
 1..785  
 Location/Qualifiers  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /clone="Plate=963 Col=3 Row=L"  
 /sex="male"



ORIGIN

/clone\_lib="RPC1-11 Human Male BAC Library"  
/note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"

Query Match 31.6%; Score 18; DB 9; Length 785;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACAATGGG 57  
|||||  
Db 635 TTGGGCTGAACAATGGG 652

RESULT 31  
LOCUS BG444212 854 bp mRNA linear EST 15-MAR-2001  
DEFINITION GA\_Ea0023K06f Gossypium arboreum 7-10 dpa fiber library Gossypium  
arboreum cDNA clone GA\_Ea0023K06f, mRNA sequence.  
ACCESSION BG444212  
VERSION BG444212.1 GI:13353864  
KEYWORDS EST  
SOURCE Gossypium arboreum  
ORGANISM Gossypium arboreum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eustoids II; Malvales; Malvaceae; Malvoideae; Gossypium.  
1 (bases 1 to 854)  
Wing,R.A., Fritsch,D., Yu,Y., Main,D., Rambo,T., Simmons,J.,  
Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.  
An integrated analysis of the genetics, development, and evolution  
of the cotton fiber  
Unpublished (2000)  
Contact: Wing RA  
Clemson University Genomics Institute  
Clemson University  
100 Jordan Hall, Clemson, SC 29634, USA  
Tel: 864 656 7288  
Fax: 864 656 4293  
Email: rwing@clemson.edu  
Seq primer: TAATACGACTCACTATAGG  
High quality sequence stop: 612.  
Location/Qualifiers

FEATURES  
source  
1..854  
/organism="Gossypium arboreum"  
/mol\_type="mRNA"  
/strain="AKA"  
/cultivar="8400"  
/db\_xref="taxon:29729"  
/clone="GA\_Ea0023K06f"  
/tissue\_type="Fibers isolated from bolls harvested 7-10  
dpa"  
/lab\_host="E. coli"  
/clone\_lib="Gossypium arboreum 7-10 dpa fiber library"  
/note="Vector: pBK-CMV; Site\_1: EcoRI; Site\_2: XhoI"

## ORIGIN

Query Match 31.6%; Score 18; DB 2; Length 854;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 AGCGAAGAACTTGGGC 45  
|||||  
Db 511 AGCGAAGAACTTGGGC 528

RESULT 32  
LOCUS CL406370 1067 bp DNA linear GSS 05-MAR-2004  
DEFINITION ZMMBB0412C22r ZMMBB (HindIII) Zea mays genomic clone

ACCESSION ZMMBB0412C22 3', genomic survey sequence.  
LOCUS CL406370  
KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Zea.  
1 (bases 1 to 1067)  
Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,  
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.  
Sequencing of the maize genome at PGR (2003c)  
Unpublished (2003)  
Contact: Bharti,A.K.  
Dr. Joseph Messing's lab  
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers  
University  
190 Frelinghuysen Road, Piscataway, NJ 08854, USA  
Tel: 732 445 3801  
Fax: 732 445 5735  
Email: bharti@waksman.rutgers.edu  
Seq primer: SP6  
Class: BAC ends  
High quality sequence start: 73.  
Location/Qualifiers

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

## FEATURES

source  
1..1067  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/cultivar="B73"  
/db\_xref="taxon:4577"  
/clone="ZMMBB0412C22"  
/lab\_host="E. coli DH10B"  
/clone\_lib="ZMMBB (HindIII)"  
/note="Vector: pCUG1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 31.6%; Score 18; DB 10; Length 1067;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 TATCTCTAGACGGGAAA 35  
|||||  
Db 49 TATCTCTAGACGGGAAA 66

RESULT 33  
LOCUS BU506883 1094 bp mRNA linear EST 12-SEP-2002  
DEFINITION AGENCOURT\_10094884 NIH\_MGC\_71 Homo sapiens cDNA clone IMAGE:6500745  
5', mRNA sequence.  
ACCESSION BU506883  
VERSION BU506883.1 GI:22813116  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
1 (bases 1 to 1094)  
NIH-MGC http://mgs.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: ATCC  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: LLM14054 row: b column: 10

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

http://image.llnl.gov  
Plate: LLM14054 row: b column: 10



```

High quality sequence start: 37
FEATURES
  High quality sequence stop: 202.
  Location/Qualifiers
    1..1094
      /organism="Homo sapiens"
      /mol_type="mRNA"
      /db_xref="taxon:9606"
      /clone_image="5500745"
      /issue_type="leiomysarcoma"
      /lab_host="DH10B (phage-resistant)"
      /clone_1ib="NIH MGc 71"
      /note="Organ: uterus; Vector: pCMV-Sport6; Site 1: NotI;
      Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
      Average insert size 2.1 kb."
ORIGIN

Query Match          31.6%; Score 18; DB 5; Length 1094;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
30 GGGAAAGAACTGGGCTG 47
|||||
727 GGGAAAGAACTGGGCTG 744

RESULT 34
CD780683          102 bp      mRNA      linear      EST 01-JUL-2004
LOCUS             EST652044 RAA Rhipicephalus appendiculatus cDNA clone RAAAM41 3'
DEFINITION        end. mRNA sequence.
ACCESSION         CD780683
VERSION           CD780683.1 GI:49536356
KEYWORDS          EST.
SOURCE            Rhipicephalus appendiculatus
ORGANISM          Rhipicephalus appendiculatus
Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhipicephalus.
1 (bases 1 to 102)
Nene,V., Lee,D., Kang'a,S., Skilton,R., Shah,T., de Villiers,E.,
Mwaura,S., Taylor,D., Quackenbush,J. and Bishop,R.
Genes transcribed in the salivary glands of female Rhipicephalus
appendiculatus ticks infected with Theileria parva
Insect Biochem. Mol. Biol. 34 (10), 1117-1128 (2004)
15475305
Other_ESTs: EST652045
Contact: Vishvanath Nene
Parasite Genomics
The Institute for Genomic Research
9712 Medical Center Drive, Rockville, MD 20850, USA
Tel: 301-610-5968
Fax: 301-838-0208
Email: nene@tigr.org
Seq primer: mixed oligo dT.
FEATURES
  source
    1..102
      /organism="Rhipicephalus appendiculatus"
      /mol_type="mRNA"
      /strain="Muguga"
      /db_xref="taxon:34631"
      /clone_image="RAAM41"
      /dev_stage="Adult"
      /lab_host="E. coli strain DH10B-Tona"
      /note="Organ: Salivary glands; Vector: pCMVSPORT6.0.ccdh;
      Salivary glands were dissected on day four after
      initiation of feeding. Total RNA was prepared using acid
      guanidium thiocyanate-phenol-chloroform extraction. The
      cDNA library was custom prepared by Invitrogen
      Corporation. Briefly, first strand cDNA was primed using
      oligo(dT) containing a NotI site. Size fractionated double
      stranded cDNA was ligated to EcoRV-NotI cleaved vector and
      electroporated into E.coli. Library RAA was made from
      uninfected ticks."

```

```

ORIGIN

Query Match          29.8%; Score 17; DB 6; Length 102;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
5 ATTGATCATTCATCTATC 21
|||||
81 ATTGATCATTCATCTATC 97

RESULT 35
B0569007/c        219 bp      mRNA      linear      EST 19-JUN-2002
LOCUS             g1119h05.x1 Mouse Organ of Corti cDNA plunescrypt Mus musculus cDNA
DEFINITION        clone g1119h05 3', mRNA sequence.
ACCESSION         B0569007
VERSION           B0569007.1 GI:21472324
KEYWORDS          EST.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Muridae; Murinae; Mus.
1 (bases 1 to 219)
Kachar,B.
EST analysis of gene expression in the mouse Organ of Corti at the
onset of hearing
Unpublished (2002)
Contact: Kachar B.
Structural Cell Biology
National Institute of Deafness and other Communication Disorders
50/4249 South Drive, NIH, Bethesda, MD 20892-8027, USA
Tel: 301-402-1599
Fax: 301-402-1765
Email: kachar@nidcd.nih.gov
Plate: 119 row: h column: 05
Seq primer: -21M13 forward primer (ABI).
FEATURES
  source
    1..219
      /organism="Mus musculus"
      /mol_type="mRNA"
      /strain="BALB/c"
      /db_xref="taxon:10090"
      /clone_image="g1119h05"
      /sex="male and female"
      /dev_stage="Post natal day 5 to 13"
      /clone_1ib="Mouse Organ of Corti cDNA plunescrypt"
      /note="Organ: Organ of Corti; Vector: pBluescript; The
      organ of Corti (OC) was fine dissected from a total of 386
      OC as follows: 102 samples from post-natal (P) day 5; 72
      from P6; 60 from P7; 46 from P8; 18 from P9; 20 from P10;
      14 from P12 and 24 from P13. After killing animals by
      cervical dislocation followed by decapitation, the bulla
      was removed and opened in Leibowitz medium. The bony
      capsule of the cochlea was removed and the sensory
      epithelium was carefully dissected out of the modiolus.
      Total RNA was extracted using the micro Fasttrack kit
      (catalog # K1593-02; Invitrogen, Carlsbad, CA), according
      to manufacturer's instructions. Reverse transcription and
      library construction were carried out with the Uni-Zap XR
      vector kit (catalog # 237211, Stratagene) and Uni-Zap XR
      GigaPack III Gold Cloning kit (catalog # 237612), both
      from Stratagene (La Jolla, CA, USA), according to
      manufacturer's instructions. Briefly, 1.5 ug mRNA was
      reverse transcribed using a hybrid oligo(dT) linker-primer
      that contains an Xho I site. First strand synthesis was
      primed with the linker-primer and transcribed using
      Moloney murine leukemia virus reverse transcriptase
      (PMV-RT) and 5-methyl dCTP. The second strand was
      synthesized with DNA polymerase and RNase H. Complementary
      DNA was blunt ended with Pfu DNA polymerase, ligated with

```



BCor I adapters in the presence of ligase and digested with Xho I. The cDNA was sequentially size fractionated over Pharmacia Size Sep400 (Pharmacia, Uppsala, Sweden) and Clontech Chroma Spin-100 (Clontech, Palo Alto, CA) columns to enrich for cDNAs greater than 400bp and 1000 bp, respectively. The cDNA was then directionally ligated to the Uni-ZAP XR vector, which had been predigested with Bcor I and Xho I. The phagemid was packaged with Gigapak III Gold and, upon titration on XL1 Blue MRF<sup>+</sup> cells, the yield of the phage library was estimated to be 11,100,000 recombinants. Stratagene's ExAssist Interference resistance helper phage (catalogue # 211203) was adopted to rescue plasmid DNA from the phages. Upon plating of the rescued library, individual cDNA clones were selected and grown in 96-well, 2 ml growth plate. Plasmid DNA was purified from 200  $\mu$ l of saturated culture with the Concert96 (TM) plasmid purification kit (Invitrogen, Carlsbad, CA) as instructed by the manufacturer. ESTs from the 5' end of the cDNA clones were generated with the universal M13 reverse primer (CAGGAACGCTAAGACC) and 25 $\times$  strength BigDye terminator sequencing chemistry (Applied Biosystems, Foster City, CA). Sequencing reactions were performed on MJ Tetrad thermal cyclers (MJ Research, Waltham, MA), and analyzed on 3700 automated capillary sequencers using POPs polymer (Applied Biosystems, Foster City, CA). The frequency distribution of the library is as follows: 72% of genes have 1 copy; 14.3% 2; 12% 3-10; 1.4% 11-50 and 0.1% 51-150. As to gene function, 45% of genes are present in Genbank and have known function; 23% have hits in Genbank, but do not have assigned function; 12% are uncharacterized ESTs and 20% are unidentified."

## ORIGIN

Query Match 29.8%; Score 17; DB 5; Length 219;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 TTGGGCTGAACATGG 56  
|||  
Db 100 TTGGGCTGAACATGG 84

## RESULT 36

AA842601 232 bp mRNA linear EST 02-MAR-1998  
LOCUS MBATCZ80C0773 Brugia malayi adult female cDNA (SMM96MLM-BMAF) Brugia  
DEFINITION malayi cDNA clone AfcZ8C07 5', mRNA sequence.  
ACCESSION AA842601  
VERSION AA842601.1 GI:2923937  
KEYWORDS EST.  
SOURCE Brugia malayi  
ORGANISM Brugia malayi  
Bukariyota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;  
Onchocercidae; Brugia.  
1 (bases 1 to 232)  
Jones, S. J.  
Blaxter, M. L., Waterfall, M., Daub, J., Lizotte, M., Baron, L. and  
Jones, S. J.  
Genes expressed in adult female Brugia malayi  
Unpublished (1996)  
Contact: Blaxter ML  
Institute of Cell, Animal and Population Biology  
University of Edinburgh  
Ashworth Labs, King's Buildings, West Mains Road, Edinburgh, EH9  
3JT, UK.  
Tel: +44 131 650 6760  
Fax: +44 131 670 5450  
Email: mark.blaxter@ed.ac.uk  
The ABI trace of this sequence can be viewed at  
http://www.sanger.ac.uk/Brugia/AFc/MBATCZ80C0773.html  
Seq primer: T3  
Location/Qualifiers  
1..232  
/organism="Brugia malayi"

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

/mol\_type="mRNA"  
/db\_xref="taxon:6279"  
/clone="AFCZ8C07"  
/sex="female"  
/dev\_stage="adult"  
/lab\_host="XL1-Blue MRF<sup>+</sup>"  
/clone\_1ib="Brugia malayi adult female cDNA  
(SMM96MLM-BMAF)"  
/note="Vector: Lambda Uni-ZAP XR; Site 1: Eco RI; Site 2:  
Xho I; Lymphatic filarial nematode parasite of humans.  
mRNA was prepared from approximately 50 adult females  
isolated from the peritoneal cavity of jirds and  
converted to double-stranded cDNA using reverse  
transcriptase and oligo(dT) followed by RNase H and DNA  
pol I. The library has 5 x 10<sup>6</sup> independent recombinants  
and the average insert size is ~900bp. The library was  
constructed by Michelle Lizotte-Waniewski. The  
library is available from Dr. S.A. Williams, email:  
genome@mith.edu."

## ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 232;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 AACTGGGCTGAACAA 53  
|||  
Db 33 AACTGGGCTGAACAA 17

## RESULT 37

N74556 254 bp mRNA linear EST 19-MAR-1996  
LOCUS za48A07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
DEFINITION IMAGE:295764 3', mRNA sequence.  
ACCESSION N74556  
VERSION N74556.1 GI:1231841  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;  
Homnidae; Homo.  
1 (bases 1 to 254)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marre, M.,  
Parsons, J., Rifkin, L., Rohlffing, I., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGS Consortium (info@image.jini.gov) for further information.  
Seq primer: m3 -40 forward  
High quality sequence stop: 212.  
Location/Qualifiers  
1..254  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1240685"  
/db\_xref="taxon:9606"  
/clone="IMAGE:295764"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_1ib="Soares fetal liver spleen INFLS"  
/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia)

Qy 37 AACTGGGCTGAACAA 53  
|||  
Db 33 AACTGGGCTGAACAA 17

## RESULT 37

N74556 254 bp mRNA linear EST 19-MAR-1996  
LOCUS za48A07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
DEFINITION IMAGE:295764 3', mRNA sequence.  
ACCESSION N74556  
VERSION N74556.1 GI:1231841  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;  
Homnidae; Homo.  
1 (bases 1 to 254)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marre, M.,  
Parsons, J., Rifkin, L., Rohlffing, I., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGS Consortium (info@image.jini.gov) for further information.  
Seq primer: m3 -40 forward  
High quality sequence stop: 212.  
Location/Qualifiers  
1..254  
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/mol\_type="mRNA"  
/db\_xref="GDB:1240685"  
/db\_xref="taxon:9606"  
/clone="IMAGE:295764"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_1ib="Soares fetal liver spleen INFLS"  
/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia)

## RESULT 37

N74556 254 bp mRNA linear EST 19-MAR-1996  
LOCUS za48A07.s1 Soares fetal liver spleen INFLS Homo sapiens cDNA clone  
DEFINITION IMAGE:295764 3', mRNA sequence.  
ACCESSION N74556  
VERSION N74556.1 GI:1231841  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Bukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catherhini;  
Homnidae; Homo.  
1 (bases 1 to 254)  
Hillier, L., Clark, N., Dubuque, T., Elliston, K., Hawking, M.,  
Holman, M., Hultman, M., Kucaba, T., Le, M., Lennon, G., Marre, M.,  
Parsons, J., Rifkin, L., Rohlffing, I., Soares, M., Tan, F.,  
Trevasakis, E., Waterston, R., Williamson, A., Wohldmann, P. and  
Wilson, R.  
The WashU-Merck EST Project  
Unpublished (1995)  
Contact: Wilson RK  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@wustl.edu  
This clone is available royalty-free through LML; contact the  
IMAGS Consortium (info@image.jini.gov) for further information.  
Seq primer: m3 -40 forward  
High quality sequence stop: 212.  
Location/Qualifiers  
1..254  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="GDB:1240685"  
/db\_xref="taxon:9606"  
/clone="IMAGE:295764"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_1ib="Soares fetal liver spleen INFLS"  
/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia)

## FEATURES

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1..254  
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/db\_xref="taxon:9606"  
/clone="IMAGE:295764"  
/sex="male"  
/dev\_stage="20 week-post conception fetus"  
/lab\_host="DH10B (ampicillin resistant)"  
/clone\_1ib="Soares fetal liver spleen INFLS"  
/note="Organ: Liver and spleen; Vector: pT73D (Pharmacia)



with a modified polylinker; Site 1: Pac I; Site 2: Eco RI; 1st strand cDNA was primed with a Pac I - oligo(dT) primer [5', AACGGAAGATTAAATCTTTTCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

## ORIGIN

Query Match 29.8%; Score 17; DB 8; Length 254;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

23 CTAGCAGCGGGAAGAAC 39  
|||||  
178 CTAGCAGCGGGAAGAAC 162

## Db

RESULT 38  
AV236608/c

LOCUS AV236608 261 bp mRNA linear EST 15-NOV-2001  
DEFINITION AV236608 RIKEN full-length enriched, 10 day neonate skin Mus  
musculus cDNA clone 4732414H19 3', mRNA sequence.

## ACCESSION

AV236608

## VERSION

AV236608.1 GI:6189121

## KEYWORDS

EST.

## SOURCE

Mus musculus (house mouse)

## ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridea; Muridae; Murinae; Mus.

## REFERENCE

1 (bases 1 to 261)

Komuro, H., Aizawa, K., Akahira, S., Akiyama, J., Carninci, P., Endo, T.,  
Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N., Hirozane, T., Hori, F.,  
Ishii, Y., Ishikawa, T., Itoh, M., Izawa, M., Kadota, K., Kagawa, I.,  
Kai, C., Kawai, J., Kikuchi, N., Kojima, Y., Koya, S., Kusakabe, M.,  
Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H., Okazaki, Y.,  
Owa, C., Ozawa, Y., Saito, H., Sano, M., Sato, K., Shibata, K.,  
Shibata, Y., Shigemoto, Y., Shiraki, T., Sogabe, Y., Sugahara, Y.,  
Suzuki, H., Suzuki, H., Takahashi, F., Tateo, M., Tomihata, N.,  
Tsunoda, Y., Watanabe, S., Yamamura, T., Yasunishi, A.,  
Yokota, T., Yoshiki, A., Yoshino, M., Muramatsu, M. and Hayashizaki, Y.  
RIKEN Mouse ESTs (Komuro, H., et al. 1999)  
Unpublished (1999)

TITLE  
JOURNAL  
COMMENT

Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic  
Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suenho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@gscc.riken.jp, URL: http://genome.gsc.riken.jp/  
Sasaki, N., Izawa, M., Watabiki, M., Ozawa, K., Tanaka, T., Yoneda, Y.,  
Matsuda, S., Carninci, P., Muramatsu, M., Okazaki, Y. and  
Hayashizaki, Y.  
Transcriptional sequencing: A method for DNA sequencing using RNA  
polymerase. Proc. Natl. Acad. Sci. U.S.A. 95 (7), 3455-3460 (1998)  
Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,  
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,  
Y. and Hayashizaki, Y.  
Automated filtration-based high-throughput plasmid preparation  
system. Genome Res. 9 (5), 463-470 (1999)  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,  
19-44 (1999)  
Please visit our web site (http://genome.gsc.riken.go.jp) for  
further details.

FEATURES  
SOURCE

1. 261  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/strain="C57BL/6J"

## ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 261;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## QY

20 TCTCTAGCAGCGGAAG 36  
|||||  
49 TCTCTAGCAGCGGAAG 33

## Db

RESULT 39  
CD070416/c

LOCUS CD070416 291 bp mRNA linear EST 14-SEP-2003  
DEFINITION MA2-00180-D291-C04-U.B MA2-0018 Schistosoma mansoni cDNA clone  
MA2-00180-D291-C04.B, mRNA sequence.

ACCESSION  
CD070416

VERSION  
CD070416.1 GI:34621496

KEYWORDS  
EST.

SOURCE  
Schistosoma mansoni

ORGANISM  
Schistosoma mansoni

Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigoida; Schistosomatidae; Schistosomatidae; Schistosoma.

1 (bases 1 to 291)

Verjovsky-Almeida, S., DeMarco, R., Martins, B.A.L., Guimaraes, P.E.M.,  
Ojopi, E.P.B., Paquola, A.C.M., Piazza, J.P., Nishiyama, M.Y., Jr.,  
Katajima, J.P., Adamson, R.E., Ashton, P.D., Bonaldo, M.F.,  
Coulson, P.S., Dillon, G.P., Farias, L.P., Gregorio, S.P., Ho, P.L.,  
Leite, R.A., Malgouyres, L.C.C., Marques, R.C.P., Miyasato, P.A.,  
Nascimento, A.L.T.O., Onilweiler, F.P., Reis, B.M., Ribeiro, M.A.,  
Sa, R.G., Stukart, G.C., Soares, M.B., Gargioni, C., Kawano, T.,  
Rodrigues, V., Madeira, A.M.B.N., Wilson, R.A., Menck, C.F.M.,  
Seubald, U.C., Leite, L.C.C. and Dias-Neto, E.  
Transcriptome analysis of the acelomate human parasite Schistosoma  
mansoni  
Nat. Genet. 35 (2), 148-157 (2003)  
12973350

TITLE  
JOURNAL  
PUBMED  
COMMENT

Contact: Dr. Sergio Verjovsky-Almeida  
Departamento de Bioquímica  
Instituto de Química - Universidade de São Paulo  
Av. Prof. Lineu Prestes 748 sala 1200, 05508-900 São Paulo - SP,  
Brasil  
Tel: +55-11-3091-2173  
Fax: +55-11-3091-2186  
Email: verjov@iq.usp.br  
This sequence was derived from the PAPSP Schistosoma mansoni EST  
Genome Project. All sequences in the project were assembled and  
annotated. This entry and all the assembled sequences can be seen



in the following URL: <http://bioinfo.ig.usp.br/schisto/>  
 Plate: MA2-0018U-D291 row: 4 column: C.

## FEATURES

Source

Location/Qualifiers  
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 /organism="Schistosoma mansoni"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6183"  
 /clone="MA2-0018U-D291-C04.B"  
 /sex="mixed pool"  
 /dev\_stage="adult"  
 /lab\_host="Mus musculus"  
 /clone\_1ib="MA2-0018"  
 /note="Vector: pGEM T-easy"

## ORIGIN

Query Match 29.8%; Score 17; DB 6; Length 291;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 AATTGATCATTCACCTAT 20  
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 Db 77 AATTGATCATTCACCTAT 61

## RESULT 40

AI364094/c

LOCUS 296 bp mRNA linear EST 07-JAN-1999  
 DEFINITION qy76a03.x1 NCI\_CGAP\_Brn25 Homo sapiens cDNA clone IMAGE:2017900 3',  
 mRNA sequence.

## ACCESSION

AI364094

## VERSION

AI364094.1 GI:4123783

## KEYWORDS

EST.

## SOURCE

Homo sapiens (human)

## ORGANISM

Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.

## REFERENCE

1 (bases 1 to 296)

NCI/NINDS-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>  
 National Cancer Institute / National Institute of Neurological  
 Disorders and Stroke, Brain Tumor Genome Anatomy Project  
 (CGAP/BRGAP), Tumor Gene Index

Unpublished (1998)

## AUTHORS

Contact: Robert Strausberg, Ph.D.

## TITLE

Unpublished (1998)

## JOURNAL

Email: cgaps-remail.nih.gov

## COMMENT

Tissue Procurement: David N. Louis, M.D., Myrna R. Rosenfeld M.D.,  
 Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima  
 Bonaldo, Ph.D.

CDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center

Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:

[www.bio.11nl.gov/bdip/image/image.html](http://www.bio.11nl.gov/bdip/image/image.html)  
 Seg primer: -40UP from Gibco.

Location/Qualifiers  
 1..296

## FEATURES

Source

/organism="Homo sapiens"  
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 /db\_xref="taxon:9606"  
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 /tissue\_type="anaplastic oligodendroglioma"  
 /lab\_host="DH108"  
 /clone\_1ib="NCI\_CGAP\_Brn25"  
 /note="Organ: Brain; Vector: pTT73D-Pac (Pharmacia) with a  
 modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
 strand cDNA was primed with a Not I - oligo(dT) primer [5'  
 TGTTCACATCTGAGTGGAGCGCGCATGATTTTCTTTTCTTTTCTTTT  
 T 3']; double-stranded cDNA was ligated to Eco RI  
 adaptors (Pharmacia), digested with Not I and cloned into  
 the Not I and Eco RI sites of the modified pTT73 vector.  
 Library is normalized, and was constructed by Bento  
 Soares and M. Fatima Bonaldo."

## ORIGIN

Query Match 29.8%; Score 17; DB 1; Length 296;  
 Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 CTAGCAGGGGAAAGAAC 39  
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 Db 179 CTAGCAGGGGAAAGAAC 163

Search completed: April 11, 2006, 21:46:50  
 Job time : 849.814 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 20.2944 Seconds

(without alignments)  
4379.433 Million cell updates/sec

Title: US-10-712-654-23

Perfect score: 50  
Sequence: 1 gggagcgctccatctacaa.....acgacttcgttagctagg 50

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database : Issued Patents NA:\*

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	50	100.0	2211	3	US-09-350-729A-2
5	50	100.0	2292	3	US-09-350-729A-3
6	50	100.0	2295	3	US-09-350-729A-1
7	50	100.0	2709	2	US-08-021-601-11
8	50	100.0	2709	2	US-08-082-849B-11
9	50	100.0	2709	6	PCT-US94-01624-11
10	50	100.0	4235	2	US-08-021-601-3
11	50	100.0	4235	2	US-08-082-849B-3
12	50	100.0	4235	6	PCT-US94-01624-3
13	16	32.0	414	3	US-09-328-352-687
14	16	32.0	937	3	US-08-393-889-14
15	16	32.0	937	3	US-09-119-900-14
16	16	32.0	937	3	US-08-472-630-14
17	16	32.0	937	6	PCT-US94-09450-14
18	16	32.0	940	3	US-08-393-889-11
19	16	32.0	940	3	US-09-119-900-11
20	16	32.0	940	3	US-08-472-630-11
21	16	32.0	940	6	PCT-US94-09450-11
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27	16	32.0	36620	3	US-09-952-060-31	Sequence 31, Appli
28	16	32.0	37474	3	US-09-952-060-26	Sequence 26, Appli
29	16	32.0	38519	3	US-09-952-060-29	Sequence 29, Appli
30	15	30.0	602	2	US-08-682-218-16	Sequence 16, Appli
31	15	30.0	605	2	US-08-682-218-11	Sequence 11, Appli
32	15	30.0	605	2	US-08-682-218-12	Sequence 12, Appli
33	15	30.0	606	2	US-08-682-218-13	Sequence 13, Appli
34	15	30.0	655	2	US-08-682-218-4	Sequence 4, Appli
35	15	30.0	1209	3	US-08-822-774-18	Sequence 18, Appli
36	15	30.0	1209	3	US-09-632-711-18	Sequence 18, Appli
37	15	30.0	1209	3	US-09-632-703B-18	Sequence 18, Appli
38	15	30.0	1209	3	US-09-632-702-18	Sequence 18, Appli
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40	15	30.0	1986	3	US-09-487-558B-165	Sequence 165, App
41	15	30.0	32768	3	US-08-961-527-71	Sequence 71, Appli
42	15	30.0	42394	3	US-09-949-016-12752	Sequence 12752, A
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45	15	30.0	132438	3	US-09-949-016-14350	Sequence 14350, A
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47	15	30.0	524032	3	US-09-949-016-16928	Sequence 16928, A
48	15	30.0	524032	3	US-09-949-016-16929	Sequence 16929, A
49	15	30.0	524032	3	US-09-949-016-16930	Sequence 16930, A
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52	15	30.0	529885	3	US-09-949-016-14341	Sequence 14341, A
53	15	30.0	529885	3	US-09-949-016-14342	Sequence 14342, A
54	15	30.0	529885	3	US-09-949-016-14343	Sequence 14343, A
55	15	30.0	529885	3	US-09-949-016-14344	Sequence 14344, A
56	15	30.0	529885	3	US-09-949-016-14345	Sequence 14345, A
57	15	30.0	529885	3	US-09-949-016-14346	Sequence 14346, A
58	15	30.0	529885	3	US-09-949-016-14347	Sequence 14347, A
59	14	28.0	237	3	US-09-134-001C-1782	Sequence 1782, Ap
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62	14	28.0	486	3	US-09-406-065-78	Sequence 78, Appli
63	14	28.0	486	3	US-09-790-417-90	Sequence 90, Appli
64	14	28.0	556	3	US-09-710-279-909	Sequence 909, App
65	14	28.0	594	3	US-09-903-814A-7	Sequence 7, Appli
66	14	28.0	594	3	US-10-723-061-7	Sequence 7, Appli
67	14	28.0	601	3	US-09-949-016-171415	Sequence 171415, A
68	14	28.0	618	3	US-09-248-796A-2126	Sequence 2126, Ap
69	14	28.0	777	3	US-09-134-000C-3368	Sequence 3368, Ap
70	14	28.0	810	3	US-09-230-041-1	Sequence 1, Appli
71	14	28.0	816	3	US-09-134-001C-1780	Sequence 1780, Ap
72	14	28.0	912	3	US-09-248-796A-1440	Sequence 440, Ap
73	14	28.0	951	3	US-09-134-000C-1036	Sequence 1036, Ap
74	14	28.0	1080	3	US-09-543-681A-2655	Sequence 2655, Ap
75	14	28.0	1086	3	US-09-902-540-9568	Sequence 9568, Ap
76	14	28.0	1100	3	US-09-270-767-11650	Sequence 11650, A
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78	14	28.0	1155	2	US-08-387-942C-18	Sequence 18, Appli
79	14	28.0	1155	2	US-08-387-942C-20	Sequence 20, Appli
80	14	28.0	1155	2	US-08-387-942C-21	Sequence 21, Appli
81	14	28.0	1253	3	US-09-270-767-12785	Sequence 12785, A
82	14	28.0	1258	3	US-09-710-279-1466	Sequence 3466, Ap
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84	14	28.0	12708	3	US-09-949-016-13216	Sequence 1216, A
85	14	28.0	14823	3	US-09-949-016-10871	Sequence 1087, Ap
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88	14	28.0	55886	3	US-09-949-016-15129	Sequence 15129, A
89	14	28.0	57054	3	US-09-949-016-14159	Sequence 14159, A
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C 102	13	26.0	292	3	US-09-313-294A-529	Sequence 529, App	175	13	26.0	2634	3	US-09-252-991A-8976	Sequence 8976, App
C 103	13	26.0	434	3	US-09-513-999C-21709	Sequence 21709, A	176	13	26.0	2718	3	US-09-717-964A-14	Sequence 14, Appl
C 104	13	26.0	465	3	US-09-252-991A-10129	Sequence 10129, A	177	13	26.0	2726	3	US-09-634-238-13	Sequence 33, Appl
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C 114	13	26.0	601	3	US-09-949-016-66309	Sequence 66309, A	187	13	26.0	4134	3	US-10-141-076-23	Sequence 23, Appl
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C 124	13	26.0	601	3	US-09-949-016-144334	Sequence 144334, A	C 197	13	26.0	6915	3	US-09-902-540-837	Sequence 1, Appl1
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C 131	13	26.0	601	3	US-09-949-016-194234	Sequence 194234, A	C 204	13	26.0	11389	3	US-09-949-016-17463	Sequence 17463, A
C 132	13	26.0	601	3	US-09-949-016-194235	Sequence 194235, A	C 205	13	26.0	11459	3	US-09-462-136-7	Sequence 7, Appl1
C 133	13	26.0	601	3	US-09-949-016-194236	Sequence 194236, A	C 206	13	26.0	11466	3	US-08-956-112E-444	Sequence 444, App
C 134	13	26.0	601	3	US-09-949-016-194237	Sequence 194237, A	C 207	13	26.0	11466	3	US-08-781-966A-444	Sequence 1069, App
C 135	13	26.0	601	3	US-09-949-016-194238	Sequence 194238, A	C 208	13	26.0	11468	3	US-09-902-540-1069	Sequence 11, Appl1
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C 140	13	26.0	601	3	US-09-949-016-203032	Sequence 203032, A	C 213	13	26.0	24428	3	US-09-949-016-11889	Sequence 1, Appl1
C 141	13	26.0	601	3	US-09-949-016-203039	Sequence 203039, A	C 214	13	26.0	26270	3	US-09-717-364A-1	Sequence 15882, A
C 142	13	26.0	601	3	US-09-949-016-203040	Sequence 203040, A	C 215	13	26.0	26552	3	US-09-949-016-15822	Sequence 12407, A
C 143	13	26.0	601	3	US-09-949-016-204132	Sequence 204132, A	C 216	13	26.0	27557	3	US-09-949-016-14407	Sequence 14545, A
C 144	13	26.0	601	3	US-09-949-016-204132	Sequence 204132, A	C 217	13	26.0	27557	3	US-09-949-016-15619	Sequence 12619, A
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C 148	13	26.0	692	3	US-09-533-559-4574	Sequence 4574, App	C 221	13	26.0	36412	3	US-09-902-540-1367	Sequence 1267, App
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C 153	13	26.0	1056	3	US-09-489-039A-6267	Sequence 6267, App	C 226	13	26.0	43018	3	US-09-949-016-15730	Sequence 17530, A
C 154	13	26.0	1101	3	US-09-252-991A-9031	Sequence 9031, App	C 227	13	26.0	43995	3	US-09-676-51A-19	Sequence 19, Appl
C 155	13	26.0	1134	3	US-09-489-039A-5575	Sequence 5375, App	C 228	13	26.0	43976	3	US-09-949-016-15661	Sequence 16651, A
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C 157	13	26.0	1218	3	US-09-328-352-223	Sequence 223, App	C 230	13	26.0	46841	3	US-09-949-016-11466	Sequence 17, Appl
C 158	13	26.0	1242	3	US-09-328-352-101	Sequence 101, App	C 231	13	26.0	56737	3	US-09-782-378A-17	Sequence 17070, A
C 159	13	26.0	1311	2	US-08-899-028A-1	Sequence 1, Appl1	C 232	13	26.0	60589	3	US-09-949-016-11070	Sequence 29, Appl
C 160	13	26.0	1311	2	US-09-210-124-1	Sequence 1, Appl1	C 233	13	26.0	66886	3	US-09-596-002-29	Sequence 13300, A
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C 162	13	26.0	1317	3	US-09-252-991A-9952	Sequence 9952, App	C 235	13	26.0	80411	3	US-09-949-016-15777	Sequence 17397, A
C 163	13	26.0	1338	3	US-09-902-540-6194	Sequence 6194, App	C 236	13	26.0	86639	3	US-09-949-016-17397	Sequence 57, Appl
C 164	13	26.0	1340	3	US-09-902-540-320	Sequence 320, App	C 237	13	26.0	87563	3	US-09-453-702B-57	Sequence 57, Appl
C 165	13	26.0	1341	3	US-09-902-540-8155	Sequence 8155, App	C 238	13	26.0	87563	3	US-10-114-170-57	Sequence 17068, A
C 166	13	26.0	1360	3	US-09-533-029-41	Sequence 41, Appl	C 239	13	26.0	89884	3	US-09-949-016-117068	Sequence 12757, A
C 167	13	26.0	1413	3	US-09-543-681A-1780	Sequence 1780, App	C 240	13	26.0	91993	3	US-09-949-016-12157	Sequence 13950, A
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C 246	13	26.0	120609	3	US-09-949-016-13915	Sequence 13915, A	319	12	24.0	325	3	US-09-513-999C-24632	Sequence 24632, A
C 247	13	26.0	126468	3	US-09-949-016-14418	Sequence 14418, A	320	12	24.0	333	2	US-08-634-797-90	Sequence 30, Appl
C 248	13	26.0	130563	3	US-09-949-016-12273	Sequence 12273, A	321	12	24.0	346	3	US-09-533-559-9879	Sequence 3879, Ap
C 249	13	26.0	131333	3	US-09-949-016-15535	Sequence 15535, A	322	12	24.0	351	3	US-09-902-540-1446	Sequence 3446, Ap
C 250	13	26.0	131374	3	US-09-949-016-16050	Sequence 16050, A	323	12	24.0	367	3	US-09-401-064-468	Sequence 266, Ap
C 251	13	26.0	1313724	3	US-09-949-016-12893	Sequence 12893, A	324	12	24.0	369	3	US-09-248-789-12479	Sequence 12479, A
C 252	13	26.0	142504	3	US-09-949-016-13693	Sequence 13693, A	325	12	24.0	371	3	US-09-270-767-1564	Sequence 1564, Ap
C 253	13	26.0	142506	3	US-09-949-016-1474	Sequence 12474, A	326	12	24.0	371	3	US-09-270-767-16846	Sequence 16846, A
C 254	13	26.0	148567	3	US-09-801-876B-3	Sequence 3, Appl1	327	12	24.0	375	3	US-09-543-661A-1923	Sequence 1923, Ap
C 255	13	26.0	148567	3	US-10-254-869-3	Sequence 3, Appl1	328	12	24.0	383	3	US-08-454-899C-70	Sequence 70, Appl
C 256	13	26.0	148567	3	US-10-667-442-3	Sequence 3, Appl1	329	12	24.0	393	3	US-09-854-133-609	Sequence 609, Ap
C 257	13	26.0	150032	3	US-09-949-016-14321	Sequence 14321, A	330	12	24.0	402	3	US-09-543-661A-3755	Sequence 3755, Ap
C 258	13	26.0	150651	3	US-09-949-016-13447	Sequence 17349, A	331	12	24.0	403	3	US-09-270-767-12237	Sequence 2237, Ap
C 259	13	26.0	171700	3	US-09-949-016-12276	Sequence 12276, A	332	12	24.0	403	3	US-09-270-767-17519	Sequence 17519, Ap
C 260	13	26.0	171701	3	US-09-949-016-15835	Sequence 15835, A	333	12	24.0	408	3	US-09-513-999C-3336	Sequence 3336, Ap
C 261	13	26.0	192956	3	US-09-949-016-14382	Sequence 14382, A	334	12	24.0	422	3	US-09-533-559-3555	Sequence 3555, Ap
C 262	13	26.0	193169	3	US-09-949-016-15091	Sequence 15091, A	335	12	24.0	423	2	US-08-470-179-150	Sequence 150, Ap
C 263	13	26.0	233024	3	US-09-949-016-13477	Sequence 13477, A	336	12	24.0	424	3	US-09-621-976-8360	Sequence 8360, Ap
C 264	13	26.0	237863	3	US-09-949-016-13404	Sequence 13404, A	337	12	24.0	426	3	US-09-397-787-307	Sequence 307, Ap
C 265	13	26.0	240157	3	US-09-949-016-16264	Sequence 16264, A	338	12	24.0	429	3	US-09-489-039A-4010	Sequence 4010, Ap
C 266	13	26.0	276237	3	US-09-949-016-17504	Sequence 17504, A	339	12	24.0	433	3	US-08-956-171E-524	Sequence 524, Ap
C 267	13	26.0	331814	3	US-09-949-016-12008	Sequence 12008, A	340	12	24.0	433	3	US-08-781-986A-524	Sequence 524, Ap
C 268	13	26.0	331814	3	US-09-949-016-17056	Sequence 17056, A	341	12	24.0	435	3	US-09-489-039A-6988	Sequence 6988, Ap
C 269	13	26.0	423592	3	US-09-949-016-14182	Sequence 14182, A	342	12	24.0	436	3	US-09-513-999C-25442	Sequence 25442, A
C 270	13	26.0	536165	3	US-09-214-808-1	Sequence 1, Appl1	343	12	24.0	443	3	US-09-621-976-9887	Sequence 9887, Ap
C 271	13	26.0	786431	3	US-09-751-389-3	Sequence 1, Appl1	344	12	24.0	454	3	US-09-710-279-119	Sequence 119, Ap
C 272	13	26.0	1230025	3	US-09-198-452A-1	Sequence 1, Appl1	345	12	24.0	456	3	US-09-134-001C-2200	Sequence 2200, Ap
C 273	13	26.0	1230230	3	US-09-438-185A-1	Sequence 1, Appl1	346	12	24.0	462	3	US-09-621-976-11757	Sequence 11757, A
C 274	13	26.0	1664976	3	US-08-916-421B-1	Sequence 1, Appl1	347	12	24.0	467	3	US-09-902-540-1371	Sequence 1371, Ap
C 275	13	26.0	1664976	3	US-08-916-421B-1	Sequence 1, Appl1	348	12	24.0	479	3	US-09-270-767-740	Sequence 740, Ap
C 276	13	26.0	1664976	3	US-08-632-570-1	Sequence 1, Appl1	349	12	24.0	479	3	US-09-270-767-16022	Sequence 16022, A
C 277	13	26.0	1664976	3	US-09-692-570-1	Sequence 1, Appl1	350	12	24.0	488	3	US-09-621-976-1616	Sequence 1616, Ap
C 278	13	26.0	1830121	3	US-09-557-884-1	Sequence 1, Appl1	351	12	24.0	488	3	US-09-252-991A-1636	Sequence 1636, Ap
C 279	13	26.0	1830121	3	US-09-643-990A-1	Sequence 1, Appl1	352	12	24.0	498	3	US-09-902-540-1475	Sequence 1475, Ap
C 280	13	26.0	1830121	3	US-10-158-865-1	Sequence 1, Appl1	353	12	24.0	510	3	US-09-902-540-6947	Sequence 6947, Ap
C 281	13	26.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl1	354	12	24.0	510	3	US-10-314-739A-5	Sequence 5, Appl1
C 282	13	26.0	4403765	3	US-09-103-840A-2	Sequence 2, Appl1	355	12	24.0	513	3	US-09-248-796A-5545	Sequence 5545, Ap
C 283	13	26.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1	356	12	24.0	531	3	US-09-902-540-7089	Sequence 7089, Ap
C 284	13	26.0	4411529	3	US-09-103-840A-1	Sequence 1, Appl1	357	12	24.0	539	3	US-09-270-767-6631	Sequence 2631, Ap
C 285	12	24.0	4411529	20	US-09-291-289-18	Sequence 18, Appl1	358	12	24.0	539	3	US-09-270-767-17913	Sequence 17913, A
C 286	12	24.0	24	3	US-08-979-616-6	Sequence 6, Appl1	359	12	24.0	541	3	US-09-878-281A-13	Sequence 13, Appl
C 287	12	24.0	25	3	US-09-396-196G-54702	Sequence 54702, A	360	12	24.0	541	3	US-09-878-281A-17	Sequence 17, Appl
C 288	12	24.0	25	3	US-09-396-196G-102614	Sequence 102614, A	361	12	24.0	541	3	US-09-878-281A-19	Sequence 19, Appl
C 289	12	24.0	50	3	US-08-956-171E-1833	Sequence 1833, Ap	362	12	24.0	541	3	US-09-878-281A-21	Sequence 21, Appl
C 290	12	24.0	50	3	US-08-781-986A-1833	Sequence 5779, Ap	363	12	24.0	541	3	US-09-878-281A-23	Sequence 23, Appl
C 291	12	24.0	50	3	US-10-131-827-5779	Sequence 85, Appl	364	12	24.0	541	3	US-09-878-281A-25	Sequence 25, Appl
C 292	12	24.0	66	3	US-08-454-889G-85	Sequence 86, Appl	365	12	24.0	541	3	US-09-878-281A-27	Sequence 27, Appl
C 293	12	24.0	66	3	US-08-454-889G-86	Sequence 93, Appl	366	12	24.0	541	3	US-09-533-559-358	Sequence 358, Ap
C 294	12	24.0	66	3	US-08-454-889G-93	Sequence 94, Appl	367	12	24.0	549	3	US-09-107-532A-302	Sequence 302, Ap
C 295	12	24.0	86	3	US-08-976-413A-266	Sequence 266, Ap	368	12	24.0	558	3	US-09-710-879-3063	Sequence 3063, Ap
C 296	12	24.0	86	3	US-08-976-413A-283	Sequence 283, Ap	369	12	24.0	567	3	US-09-385-882-425	Sequence 425, Ap
C 297	12	24.0	86	3	US-09-270-767-26461	Sequence 26461, A	370	12	24.0	576	2	US-08-086-428B-35	Sequence 35, Appl
C 298	12	24.0	110	3	US-09-392-184-26	Sequence 26, Appl1	371	12	24.0	576	2	US-08-086-428B-36	Sequence 36, Appl
C 299	12	24.0	118	3	US-09-544-618-2	Sequence 9435, Ap	372	12	24.0	576	2	US-08-086-428B-38	Sequence 38, Appl
C 300	12	24.0	143	3	US-09-902-540-9435	Sequence 28, Appl	373	12	24.0	576	2	US-08-086-428B-39	Sequence 39, Appl
C 301	12	24.0	171	3	US-09-910-430-28	Sequence 1, Appl1	374	12	24.0	576	2	US-08-468-570-36	Sequence 36, Appl
C 302	12	24.0	200	3	US-09-254-023B-1	Sequence 1207, Ap	375	12	24.0	576	2	US-08-468-570-38	Sequence 38, Appl
C 303	12	24.0	254	3	US-09-313-284A-1207	Sequence 8203, Ap	376	12	24.0	576	2	US-08-468-570-39	Sequence 39, Appl
C 304	12	24.0	275	3	US-09-248-786A-8203	Sequence 33, Appl	377	12	24.0	576	2	US-08-290-665A-38	Sequence 38, Appl
C 305	12	24.0	276	3	US-08-634-797-52	Sequence 35, Appl	378	12	24.0	576	2	US-08-290-665A-39	Sequence 39, Appl
C 306	12	24.0	277	2	US-08-634-797-33	Sequence 36, Appl	379	12	24.0	576	2	US-08-466-601A-35	Sequence 35, Appl
C 307	12	24.0	277	2	US-08-634-797-34	Sequence 37, Appl	380	12	24.0	576	2	US-08-466-601A-36	Sequence 36, Appl
C 308	12	24.0	277	2	US-08-634-797-35	Sequence 39, Appl	381	12	24.0	576	2	US-08-466-601A-38	Sequence 38, Appl
C 309	12	24.0	277	2	US-08-634-797-36	Sequence 37, Appl	382	12	24.0	576	2	US-08-466-601A-39	Sequence 39, Appl
C 310	12	24.0	277	2	US-08-634-797-37	Sequence 39, Appl	383	12	24.0	576	2	US-08-466-601A-39	Sequence 39, Appl
C 311	12	24.0	277	2	US-08-634-797-39	Sequence 11069, A	384	12	24.0	576	2	US-08-466-601A-39	Sequence 39, Appl
C 312	12	24.0	277	2	US-08-634-797-39	Sequence 11069, A	385	12	24.0	576	2	US-08-466-601A-39	Sequence 39, Appl
C 313	12	24.0	282	3	US-09-513-999C-11069	Sequence 30514, A	386	12	24.0	576	3	US-08-466-601A-39	Sequence 39, Appl
C 314	12	24.0	287	3	US-09-270-767-70514	Sequence 30514, A	387	12	24.0	576	3	US-08-466-601A-39	Sequence 39, Appl
C 315	12	24.0	296	3	US-09-313-294A-5782	Sequence 5782, Ap	388	12	24.0	576	6	PCT-US95-10398-35	Sequence 35, Appl
C 316	12	24.0	300	3	US-09-313-294A-6696	Sequence 6696, Ap	389	12	24.0	576	6	PCT-US95-10398-36	Sequence 36, Appl



390	12	24.0	576	6	PCT-US95-10398-38	Sequence 38, Appl1	463	12	24.0	637	3	US-09-533-559-5373	Sequence 5373, Ap
391	12	24.0	576	6	PCT-US95-10398-39	Sequence 39, Appl1	464	12	24.0	638	3	US-09-533-559-5992	Sequence 4992, Ap
392	12	24.0	593	3	US-09-533-559-373	Sequence 373, Appl1	465	12	24.0	649	3	US-09-533-559-6475	Sequence 6475, Ap
393	12	24.0	594	3	US-09-248-796A-13033	Sequence 13033, A	466	12	24.0	652	3	US-09-533-559-9-114	Sequence 314, Appl
394	12	24.0	597	3	US-09-270-767-5201	Sequence 5201, Ap	467	12	24.0	654	3	US-09-252-991A-4506	Sequence 4506, Ap
395	12	24.0	597	3	US-09-270-767-5201	Sequence 5201, Ap	468	12	24.0	658	3	US-10-101-664A-184	Sequence 184, Appl
396	12	24.0	597	3	US-09-949-016-19755	Sequence 19755, A	469	12	24.0	660	3	US-09-902-540-6872	Sequence 6872, Ap
397	12	24.0	601	3	US-09-949-016-22747	Sequence 22747, A	470	12	24.0	663	3	US-09-533-559-804	Sequence 804, Appl
398	12	24.0	601	3	US-09-949-016-22747	Sequence 22747, A	471	12	24.0	667	2	US-08-685-764-9	Sequence 9, Appl1
399	12	24.0	601	3	US-09-949-016-22983	Sequence 22983, A	472	12	24.0	667	3	US-09-533-559-1517	Sequence 1517, Appl
400	12	24.0	601	3	US-09-949-016-22984	Sequence 22984, A	473	12	24.0	683	3	US-08-456-2008-1	Sequence 1, Appl1
401	12	24.0	601	3	US-09-949-016-23984	Sequence 23984, A	474	12	24.0	700	3	US-09-735-271-474	Sequence 474, Appl
402	12	24.0	601	3	US-09-949-016-30340	Sequence 30340, A	475	12	24.0	700	3	US-09-735-271-523	Sequence 523, Appl
403	12	24.0	601	3	US-09-949-016-40538	Sequence 40538, A	476	12	24.0	701	3	US-09-533-559-9-216	Sequence 6216, Ap
404	12	24.0	601	3	US-09-949-016-63952	Sequence 63952, A	477	12	24.0	702	3	US-09-533-559-5470	Sequence 5470, Appl
405	12	24.0	601	3	US-09-949-016-63952	Sequence 63952, A	478	12	24.0	726	3	US-08-998-416-892	Sequence 892, Appl
406	12	24.0	601	3	US-09-949-016-65150	Sequence 65150, A	479	12	24.0	726	3	US-09-489-039A-1159	Sequence 1159, Appl
407	12	24.0	601	3	US-09-949-016-65151	Sequence 65151, A	480	12	24.0	726	3	US-09-489-039A-1812	Sequence 1812, Appl
408	12	24.0	601	3	US-09-949-016-65822	Sequence 65822, A	481	12	24.0	740	3	US-09-721-341-10	Sequence 10, Appl1
409	12	24.0	601	3	US-09-949-016-73797	Sequence 73797, A	482	12	24.0	740	3	US-09-721-341-10	Sequence 10, Appl1
410	12	24.0	601	3	US-09-949-016-73797	Sequence 73797, A	483	12	24.0	750	3	US-09-902-540-2476	Sequence 2476, Appl
411	12	24.0	601	3	US-09-949-016-75940	Sequence 75940, A	484	12	24.0	765	3	US-09-248-796A-8429	Sequence 8429, Appl
412	12	24.0	601	3	US-09-949-016-81974	Sequence 81974, A	485	12	24.0	771	3	US-09-252-991A-13613	Sequence 13613, A
413	12	24.0	601	3	US-09-949-016-81974	Sequence 81974, A	486	12	24.0	772	3	US-09-270-767-11350	Sequence 11350, A
414	12	24.0	601	3	US-09-949-016-84407	Sequence 84407, A	487	12	24.0	801	3	US-09-248-796A-4093	Sequence 4093, Appl
415	12	24.0	601	3	US-09-949-016-92631	Sequence 92631, A	488	12	24.0	804	3	US-09-248-796A-3648	Sequence 3648, Appl
416	12	24.0	601	3	US-09-949-016-92631	Sequence 92631, A	489	12	24.0	806	3	US-09-270-767-10964	Sequence 10964, A
417	12	24.0	601	3	US-09-949-016-107871	Sequence 107871, A	490	12	24.0	810	3	US-09-248-796A-2403	Sequence 2403, Appl
418	12	24.0	601	3	US-09-949-016-133805	Sequence 123805, A	491	12	24.0	817	3	US-09-248-796A-6630	Sequence 6630, Appl
419	12	24.0	601	3	US-09-949-016-126543	Sequence 126543, A	492	12	24.0	815	3	US-09-674-741-1	Sequence 1, Appl1
420	12	24.0	601	3	US-09-949-016-127191	Sequence 127191, A	493	12	24.0	815	3	US-10-379-010-1	Sequence 1, Appl1
421	12	24.0	601	3	US-09-949-016-127192	Sequence 127192, A	494	12	24.0	823	3	US-08-998-416-993	Sequence 493, Appl
422	12	24.0	601	3	US-09-949-016-132121	Sequence 132121, A	495	12	24.0	825	3	US-09-270-767-27643	Sequence 27643, Appl
423	12	24.0	601	3	US-09-949-016-139620	Sequence 139620, A	496	12	24.0	844	3	US-08-998-416-349	Sequence 349, Appl
424	12	24.0	601	3	US-09-949-016-139621	Sequence 139621, A	497	12	24.0	853	3	US-09-902-540-6116	Sequence 6116, Appl
425	12	24.0	601	3	US-09-949-016-139622	Sequence 139622, A	498	12	24.0	895	4	US-09-605-703B-927	Sequence 927, Appl
426	12	24.0	601	3	US-09-949-016-147579	Sequence 147579, A	499	12	24.0	900	3	US-09-134-000C-3283	Sequence 3283, Appl
427	12	24.0	601	3	US-09-949-016-150510	Sequence 150510, A	500	12	24.0	907	3	US-09-270-767-4558	Sequence 4558, Appl
428	12	24.0	601	3	US-09-949-016-151703	Sequence 151703, A	501	12	24.0	907	3	US-09-270-767-19840	Sequence 19840, A
429	12	24.0	601	3	US-09-949-016-155344	Sequence 155344, A	502	12	24.0	916	3	US-09-640-211A-220	Sequence 220, Appl
430	12	24.0	601	3	US-09-949-016-155345	Sequence 155345, A	503	12	24.0	918	3	US-09-937-862B-16	Sequence 36, Appl1
431	12	24.0	601	3	US-09-949-016-155346	Sequence 155346, A	504	12	24.0	918	3	US-08-714-918-88	Sequence 88, Appl1
432	12	24.0	601	3	US-09-949-016-159699	Sequence 159699, A	505	12	24.0	954	3	US-09-265-315-88	Sequence 88, Appl1
433	12	24.0	601	3	US-09-949-016-164070	Sequence 164070, A	506	12	24.0	954	3	US-09-265-315-88	Sequence 88, Appl1
434	12	24.0	601	3	US-09-949-016-164071	Sequence 164071, A	507	12	24.0	954	3	US-09-265-315-88	Sequence 88, Appl1
435	12	24.0	601	3	US-09-949-016-165370	Sequence 165370, A	508	12	24.0	954	3	US-09-528-709-88	Sequence 88, Appl1
436	12	24.0	601	3	US-09-949-016-165550	Sequence 165550, A	509	12	24.0	954	3	US-09-527-745-88	Sequence 88, Appl1
437	12	24.0	601	3	US-09-949-016-175219	Sequence 175219, A	510	12	24.0	965	2	US-08-736-361A-3	Sequence 3, Appl1
438	12	24.0	601	3	US-09-949-016-180748	Sequence 180748, A	511	12	24.0	972	3	US-09-248-796A-3053	Sequence 3053, Appl
439	12	24.0	601	3	US-09-949-016-186172	Sequence 186172, A	512	12	24.0	975	3	US-09-365-150-3	Sequence 4, Appl1
440	12	24.0	601	3	US-09-949-016-186779	Sequence 186779, A	513	12	24.0	975	3	US-09-365-150-3	Sequence 4, Appl1
441	12	24.0	601	3	US-09-949-016-186878	Sequence 186878, A	514	12	24.0	990	3	US-09-270-767-11360	Sequence 14360, A
442	12	24.0	601	3	US-09-949-016-192194	Sequence 192194, A	515	12	24.0	993	3	US-09-107-532A-450	Sequence 450, Appl
443	12	24.0	601	3	US-09-949-016-192195	Sequence 192195, A	516	12	24.0	996	4	US-09-605-703B-925	Sequence 925, Appl
444	12	24.0	601	3	US-09-949-016-192196	Sequence 192196, A	517	12	24.0	997	4	US-09-605-703B-925	Sequence 925, Appl
445	12	24.0	601	3	US-09-949-016-192786	Sequence 192786, A	518	12	24.0	1021	3	US-09-221-017B-582	Sequence 582, Appl
446	12	24.0	601	3	US-09-949-016-192787	Sequence 192787, A	519	12	24.0	1027	3	US-09-775-399-51	Sequence 9, Appl1
447	12	24.0	601	3	US-09-949-016-192788	Sequence 192788, A	520	12	24.0	1027	3	US-09-674-741-9	Sequence 9, Appl1
448	12	24.0	601	3	US-09-949-016-195910	Sequence 195910, A	521	12	24.0	1035	3	US-10-379-010-9	Sequence 9, Appl1
449	12	24.0	601	3	US-09-949-016-195911	Sequence 195911, A	522	12	24.0	1035	3	US-09-134-001C-2506	Sequence 2506, Appl
450	12	24.0	601	3	US-09-949-016-198918	Sequence 198918, A	523	12	24.0	1035	3	US-09-579-664B-6	Sequence 6, Appl1
451	12	24.0	601	3	US-09-949-016-205244	Sequence 205244, A	524	12	24.0	1038	3	US-10-355-978A-6	Sequence 6, Appl1
452	12	24.0	601	3	US-09-949-002-1214	Sequence 1214, Appl	525	12	24.0	1044	3	US-09-533-559-4711	Sequence 4711, Appl
453	12	24.0	601	3	US-09-949-002-1215	Sequence 1215, Appl	526	12	24.0	1044	3	US-09-498-520A-21	Sequence 21, Appl1
454	12	24.0	601	3	US-09-949-002-1216	Sequence 1216, Appl	527	12	24.0	1047	3	US-09-221-017B-59	Sequence 59, Appl1
455	12	24.0	601	3	US-09-949-002-8266	Sequence 8266, Appl	528	12	24.0	1050	3	US-09-291-289-13	Sequence 13, Appl1
456	12	24.0	601	3	US-09-949-002-8266	Sequence 8266, Appl	529	12	24.0	1056	3	US-09-270-767-10276	Sequence 10276, Appl
457	12	24.0	602	3	US-09-252-991A-4143	Sequence 4143, Appl	530	12	24.0	1062	3	US-09-248-796A-6028	Sequence 6028, Appl
458	12	24.0	619	3	US-09-328-352-3601	Sequence 3601, Appl	531	12	24.0	1062	3	US-09-802-111-3	Sequence 3, Appl1
459	12	24.0	621	3	US-09-270-767-25319	Sequence 25319, A	532	12	24.0	1062	3	US-10-217-745-3	Sequence 3, Appl1
460	12	24.0	621	3	US-09-533-559-1963	Sequence 1963, Appl	533	12	24.0	1080	3	US-10-324-910-11	Sequence 11, Appl1
461	12	24.0	630	3	US-08-612-973-29	Sequence 29, Appl1	534	12	24.0	1092	3	US-09-793-495-11	Sequence 11, Appl1
462	12	24.0	630	3	US-08-927-597-29	Sequence 29, Appl1	535	12	24.0	1101	3	US-09-252-991A-14951	Sequence 14951, A
					US-08-928-757-29	Sequence 29, Appl1						US-08-979-616-1	Sequence 1, Appl1



C 536	12	24.0	1101	3	US-09-583-110-2144	Sequence 2144, Ap	609	12	24.0	1424	3	US-09-270-767-9997	Sequence 9997, Ap
C 537	12	24.0	1103	3	US-09-270-767-7405	Sequence 7405, Ap	C 610	12	24.0	1425	3	US-09-252-991A-4709	Sequence 4709, Ap
C 538	12	24.0	1103	3	US-09-270-767-22687	Sequence 22687, A	C 611	12	24.0	1428	3	US-09-258-624-3	Sequence 3, Appl1
C 539	12	24.0	1107	3	US-09-902-540-4129	Sequence 4129, Ap	C 612	12	24.0	1437	2	US-08-252-966B-14	Sequence 14, Appl1
C 540	12	24.0	1110	3	US-09-252-991A-3674	Sequence 3674, Ap	C 613	12	24.0	1440	3	US-10-067-422-6	Sequence 6, Appl1
C 541	12	24.0	1110	3	US-09-809-665A-152	Sequence 152, App	C 614	12	24.0	1440	3	US-09-949-016-5423	Sequence 5423, Ap
C 542	12	24.0	1119	3	US-10-162-012-41	Sequence 41, Appl	C 615	12	24.0	1446	3	US-09-252-991A-9015	Sequence 9015, Ap
C 543	12	24.0	1119	3	US-09-710-279-1631	Sequence 1631, Ap	C 616	12	24.0	1454	2	US-08-657-352-1	Sequence 1, Appl1
C 544	12	24.0	1121	3	US-09-270-767-15973	Sequence 15973, A	C 617	12	24.0	1454	6	PCT-US94-02539-1	Sequence 1, Appl1
C 545	12	24.0	1131	3	US-09-248-796A-980	Sequence 980, App	C 618	12	24.0	1455	2	US-08-657-352-26	Sequence 26, Appl
C 546	12	24.0	1137	3	US-09-134-001C-1265	Sequence 1265, Ap	C 619	12	24.0	1455	6	PCT-US94-02539-26	Sequence 26, Appl
C 547	12	24.0	1149	2	US-08-049-282B-1	Sequence 1, Appl1	C 620	12	24.0	1469	2	US-08-053-867A-3	Sequence 3, Appl1
C 548	12	24.0	1149	2	US-08-537-715-1	Sequence 1, Appl1	C 621	12	24.0	1469	2	US-08-053-867A-6	Sequence 6, Appl1
C 549	12	24.0	1149	3	US-09-134-000C-1484	Sequence 2484, Ap	C 622	12	24.0	1470	3	US-09-902-540-79	Sequence 79, Appl
C 550	12	24.0	1149	3	US-09-303-518D-189	Sequence 189, App	C 623	12	24.0	1482	3	US-10-037-417-29	Sequence 29, Appl
C 551	12	24.0	1149	3	US-09-303-518D-191	Sequence 191, App	C 624	12	24.0	1488	3	US-09-107-532A-427	Sequence 427, App
C 552	12	24.0	1149	6	PCT-US94-04173-1	Sequence 1, Appl1	C 625	12	24.0	1491	3	US-09-056-947A-3	Sequence 3, Appl1
C 553	12	24.0	1155	3	US-09-902-540-7881	Sequence 7881, Ap	C 626	12	24.0	1496	3	US-09-857-896A-17	Sequence 17, Appl
C 554	12	24.0	1156	3	US-09-270-767-11379	Sequence 11379, A	C 627	12	24.0	1502	3	US-08-866-373-11	Sequence 11, Appl
C 555	12	24.0	1179	3	US-09-248-796A-12849	Sequence 12849, A	C 628	12	24.0	1504	3	US-10-067-422-8	Sequence 8, Appl1
C 556	12	24.0	1182	3	US-09-165-827C-1	Sequence 1, Appl1	C 629	12	24.0	1506	3	US-09-489-039A-5492	Sequence 5492, Ap
C 557	12	24.0	1185	3	US-09-165-827C-13	Sequence 13, Appl	C 630	12	24.0	1515	3	US-09-252-991A-4123	Sequence 4123, Ap
C 558	12	24.0	1191	3	US-09-902-540-8380	Sequence 8380, Ap	C 631	12	24.0	1518	3	US-09-614-912-191	Sequence 191, App
C 559	12	24.0	1199	2	US-08-053-867A-1	Sequence 1, Appl1	C 632	12	24.0	1522	3	US-09-533-559-5608	Sequence 5608, Ap
C 560	12	24.0	1199	2	US-08-053-867A-7	Sequence 7, Appl1	C 633	12	24.0	1530	3	US-09-252-991A-6770	Sequence 6770, Ap
C 561	12	24.0	1203	3	US-09-902-540-3733	Sequence 3733, Ap	C 634	12	24.0	1537	3	US-09-902-540-222	Sequence 222, App
C 562	12	24.0	1206	3	US-09-107-433-2299	Sequence 2299, Ap	C 635	12	24.0	1548	3	US-08-665-259-28	Sequence 28, Appl
C 563	12	24.0	1212	3	US-09-614-221A-458	Sequence 458, App	C 636	12	24.0	1548	3	US-08-762-500-28	Sequence 28, Appl
C 564	12	24.0	1216	3	US-09-071-035-3	Sequence 3, Appl1	C 637	12	24.0	1559	3	US-09-602-472A-3	Sequence 3, Appl1
C 565	12	24.0	1216	3	US-10-206-576-3	Sequence 3, Appl1	C 638	12	24.0	1567	3	US-08-961-083-119	Sequence 119, App
C 566	12	24.0	1227	3	US-09-248-796A-5935	Sequence 5935, Ap	C 639	12	24.0	1567	3	US-09-536-784-119	Sequence 119, App
C 567	12	24.0	1227	3	US-09-712-363-122	Sequence 122, App	C 640	12	24.0	1567	3	US-09-765-271-119	Sequence 119, App
C 568	12	24.0	1239	3	US-09-252-991A-9961	Sequence 9961, App	C 641	12	24.0	1567	3	US-09-765-271A-119	Sequence 119, App
C 569	12	24.0	1242	3	US-09-902-540-5044	Sequence 5044, Ap	C 642	12	24.0	1576	2	US-08-307-499-50	Sequence 50, Appl
C 570	12	24.0	1245	3	US-09-543-681A-3922	Sequence 3922, Ap	C 643	12	24.0	1593	3	US-08-307-499-50	Sequence 50, Appl
C 571	12	24.0	1245	3	US-09-270-767-4534	Sequence 4534, Ap	C 644	12	24.0	1593	3	US-08-993-359-23	Sequence 23, Appl
C 572	12	24.0	1245	3	US-09-270-767-19816	Sequence 19816, A	C 645	12	24.0	1593	3	US-08-993-359-23	Sequence 23, Appl
C 573	12	24.0	1246	3	US-09-651-656-30	Sequence 30, Appl	C 646	12	24.0	1593	3	US-09-252-991A-3716	Sequence 3716, Ap
C 574	12	24.0	1246	3	US-09-651-656-30	Sequence 30, Appl	C 647	12	24.0	1593	3	US-09-482-558A-23	Sequence 23, Appl
C 575	12	24.0	1254	2	US-08-815-688A-3	Sequence 3, Appl1	C 648	12	24.0	1605	3	US-09-734-217B-74	Sequence 74, Appl
C 576	12	24.0	1266	3	US-09-800-729-15	Sequence 15, Appl1	C 649	12	24.0	1608	2	US-08-815-688A-2	Sequence 2, Appl
C 577	12	24.0	1272	3	US-09-328-325-222	Sequence 222, App	C 650	12	24.0	1611	3	US-09-252-991A-14553	Sequence 14553, A
C 578	12	24.0	1290	3	US-09-252-991A-14811	Sequence 14811, A	C 651	12	24.0	1617	3	US-09-252-991A-788	Sequence 788, App
C 579	12	24.0	1293	3	US-09-902-540-6763	Sequence 5999, Ap	C 652	12	24.0	1617	3	US-09-461-774-1	Sequence 1, Appl1
C 580	12	24.0	1293	3	US-09-902-540-6763	Sequence 6763, Ap	C 653	12	24.0	1630	3	US-10-162-012-39	Sequence 39, Appl
C 581	12	24.0	1301	3	US-09-424-978B-10	Sequence 10, Appl	C 654	12	24.0	1641	3	US-09-252-991A-13507	Sequence 13507, A
C 582	12	24.0	1302	3	US-09-248-796A-10445	Sequence 10445, A	C 655	12	24.0	1662	3	US-09-738-894A-1	Sequence 1, Appl1
C 583	12	24.0	1305	3	US-09-242-859A-3	Sequence 3, Appl1	C 656	12	24.0	1662	3	US-09-802-117-1	Sequence 1, Appl1
C 584	12	24.0	1305	3	US-09-242-859A-7	Sequence 7, Appl1	C 657	12	24.0	1662	3	US-09-964-469-1	Sequence 1, Appl1
C 585	12	24.0	1308	3	US-09-724-864-15	Sequence 15, Appl	C 658	12	24.0	1662	3	US-10-217-745-1	Sequence 1, Appl1
C 586	12	24.0	1313	3	US-09-774-528-51	Sequence 51, Appl	C 659	12	24.0	1666	3	US-09-857-896A-37	Sequence 37, Appl
C 587	12	24.0	1313	3	US-10-120-968-51	Sequence 51, Appl	C 660	12	24.0	1674	3	US-09-902-540-9401	Sequence 9401, Ap
C 588	12	24.0	1319	3	US-09-418-980-9	Sequence 9, Appl1	C 661	12	24.0	1680	3	US-09-487-558B-255	Sequence 255, App
C 589	12	24.0	1320	3	US-09-221-654-1	Sequence 1, Appl1	C 662	12	24.0	1681	3	US-09-270-767-14557	Sequence 14557, A
C 590	12	24.0	1320	3	US-08-989-358A-1	Sequence 1, Appl1	C 663	12	24.0	1686	3	US-10-101-464A-875	Sequence 875, App
C 591	12	24.0	1329	3	US-09-252-991A-4809	Sequence 4809, Ap	C 664	12	24.0	1695	3	US-09-252-991A-6969	Sequence 6969, Ap
C 592	12	24.0	1332	3	US-09-902-540-4672	Sequence 1293, Ap	C 665	12	24.0	1710	3	US-09-912-628-2	Sequence 2, Appl1
C 593	12	24.0	1334	3	US-09-710-279-1293	Sequence 1293, Ap	C 666	12	24.0	1719	3	US-09-543-681A-3966	Sequence 3966, App
C 594	12	24.0	1344	3	US-09-134-000C-1666	Sequence 1666, Ap	C 667	12	24.0	1739	3	US-09-489-039A-876	Sequence 876, App
C 595	12	24.0	1347	3	US-09-071-035-1	Sequence 1, Appl1	C 668	12	24.0	1737	3	US-09-134-000C-854	Sequence 854, App
C 596	12	24.0	1347	3	US-10-206-576-1	Sequence 1, Appl1	C 669	12	24.0	1743	3	US-10-012-631A-235	Sequence 235, App
C 597	12	24.0	1356	2	US-08-317-880-4	Sequence 4, Appl1	C 670	12	24.0	1743	3	US-10-015-389A-235	Sequence 235, App
C 598	12	24.0	1356	2	US-08-782-386-4	Sequence 4, Appl1	C 671	12	24.0	1743	3	US-10-006-768A-235	Sequence 235, App
C 599	12	24.0	1360	2	US-09-856-599-2	Sequence 2, Appl1	C 672	12	24.0	1743	3	US-10-015-671A-235	Sequence 235, App
C 600	12	24.0	1361	3	US-08-979-616-3	Sequence 3, Appl1	C 673	12	24.0	1743	3	US-10-015-393A-235	Sequence 235, App
C 601	12	24.0	1389	3	US-09-252-991A-14801	Sequence 14801, A	C 674	12	24.0	1743	3	US-10-011-833A-235	Sequence 235, App
C 602	12	24.0	1392	3	US-09-489-039A-6234	Sequence 6234, Ap	C 675	12	24.0	1743	3	US-10-006-641A-235	Sequence 235, App
C 603	12	24.0	1402	3	US-08-258-287B-56	Sequence 56, Appl	C 676	12	24.0	1743	3	US-10-012-064A-235	Sequence 235, App
C 604	12	24.0	1402	3	US-08-368-704C-54	Sequence 54, Appl	C 677	12	24.0	1761	3	US-09-950-071-1	Sequence 1, Appl1
C 605	12	24.0	1402	3	US-09-291-289-1	Sequence 1, Appl1	C 678	12	24.0	1761	3	US-09-902-540-7394	Sequence 7394, Ap
C 606	12	24.0	1414	3	US-09-404-296B-9	Sequence 9, Appl1	C 679	12	24.0	1764	3	US-09-252-991A-8779	Sequence 8779, Ap
C 607	12	24.0	1422	3	US-09-387-574-7	Sequence 7, Appl1	C 680	12	24.0	1800	3	US-09-252-991A-3797	Sequence 3797, Ap
C 608	12	24.0	1422	3	US-09-668-096-7	Sequence 7, Appl1	C 681	12	24.0	1800	3	US-09-902-540-281	Sequence 281, App



682	12	24.0	1801	2	US-08-557-917A-1	Sequence 1, Appli	755	12	24.0	2393	3	US-09-393-529-1	Sequence 1, Appli
683	12	24.0	1801	3	US-09-084-153-1	Sequence 1, Appli	C 756	12	24.0	2448	3	US-09-543-681A-4158	Sequence 4158, Ap
684	12	24.0	1801	3	US-09-084-079-1	Sequence 1, Appli	C 757	12	24.0	2524	3	US-08-956-111E-360	Sequence 360, App
C 685	12	24.0	1803	3	US-09-543-681A-1608	Sequence 1608, Ap	C 758	12	24.0	2524	3	US-08-781-986A-360	Sequence 360, App
C 686	12	24.0	1807	3	US-09-058-947A-2	Sequence 2, Appli	759	12	24.0	2525	3	US-08-714-918-84	Sequence 84, Appl
C 687	12	24.0	1809	3	US-09-489-039A-5265	Sequence 5265, Ap	760	12	24.0	2525	3	US-09-265-315-84	Sequence 84, Appl
C 688	12	24.0	1812	3	US-10-117-846-11	Sequence 11, Appl	761	12	24.0	2525	3	US-09-265-315-84	Sequence 84, Appl
C 689	12	24.0	1818	3	US-10-104-047-1943	Sequence 1943, Ap	762	12	24.0	2525	3	US-09-266-417-84	Sequence 84, Appl
C 690	12	24.0	1824	3	US-09-248-796A-3178	Sequence 3178, Ap	763	12	24.0	2525	3	US-09-528-709-84	Sequence 84, Appl
C 691	12	24.0	1827	3	US-09-720-318A-9	Sequence 9, Appli	764	12	24.0	2525	3	US-09-527-745-84	Sequence 84, Appl
C 692	12	24.0	1838	2	US-09-091-433-1	Sequence 1, Appli	765	12	24.0	2533	3	US-09-902-540-5607	Sequence 5607, Ap
C 693	12	24.0	1838	2	US-09-387-663-1	Sequence 1, Appli	766	12	24.0	2543	3	US-09-461-335-57	Sequence 57, Appl
C 694	12	24.0	1838	3	US-09-214-139B-2	Sequence 2, Appli	767	12	24.0	2543	3	US-10-012-542-57	Sequence 57, Appl
C 695	12	24.0	1854	2	US-09-949-016-1931	Sequence 1931, Ap	768	12	24.0	2543	3	US-10-115-133-57	Sequence 57, Appl
C 696	12	24.0	1857	2	US-08-537-715-3	Sequence 3, Appli	769	12	24.0	2550	3	US-10-104-047-387	Sequence 387, App
C 697	12	24.0	1857	6	PCT-US94-04173-3	Sequence 3, Appli	770	12	24.0	2612	3	US-09-495-050A-214	Sequence 214, App
C 698	12	24.0	1859	3	US-10-037-417-27	Sequence 27, Appl	771	12	24.0	2621	3	US-09-270-767-11965	Sequence 11965, A
C 699	12	24.0	1893	3	US-09-328-352-793	Sequence 793, App	772	12	24.0	2631	3	US-09-712-353-97	Sequence 97, Appl
C 700	12	24.0	1954	2	US-08-097-823-3	Sequence 3, Appli	773	12	24.0	2673	3	US-09-902-540-8430	Sequence 4830, Ap
C 701	12	24.0	1954	2	US-08-577-403-3	Sequence 3, Appli	774	12	24.0	2703	3	US-09-482-273-75	Sequence 75, Appl
C 702	12	24.0	1956	3	US-09-724-797-57	Sequence 57, Appl	775	12	24.0	2703	3	US-09-620-312D-152	Sequence 152, App
C 703	12	24.0	1956	3	US-10-152-886-20	Sequence 20, Appl	776	12	24.0	2709	3	US-09-134-001C-2320	Sequence 2320, Ap
C 704	12	24.0	1968	3	US-10-152-886-90	Sequence 90, Appl	777	12	24.0	2709	3	US-09-482-273-101	Sequence 101, App
C 705	12	24.0	1980	3	US-10-152-886-70	Sequence 70, Appl	C 778	12	24.0	2718	3	US-09-248-796A-2230	Sequence 2230, Ap
C 706	12	24.0	1980	3	US-10-152-886-100	Sequence 100, App	C 779	12	24.0	2730	3	US-09-902-540-5705	Sequence 5705
C 707	12	24.0	1983	2	US-08-073-799C-9	Sequence 9, Appli	C 780	12	24.0	2761	3	US-09-743-674-1	Sequence 674-1
C 708	12	24.0	1989	3	US-09-134-000C-2277	Sequence 2277, Ap	781	12	24.0	2794	3	US-09-513-057C-32	Sequence 32, Appl
C 709	12	24.0	2016	3	US-09-843-598-1	Sequence 1, Appli	782	12	24.0	2794	3	US-09-746-801A-32	Sequence 32, Appl
C 710	12	24.0	2016	3	US-09-843-598-2	Sequence 2, Appli	783	12	24.0	2794	3	US-10-719-885-32	Sequence 32, Appl
C 711	12	24.0	2016	3	US-09-843-598-3	Sequence 3, Appli	C 784	12	24.0	2796	3	US-09-949-016-5678	Sequence 5678, Ap
C 712	12	24.0	2031	3	US-10-152-886-60	Sequence 60, Appl	C 785	12	24.0	2818	3	US-09-710-279-4012	Sequence 4012, Ap
C 713	12	24.0	2045	3	US-09-270-767-13760	Sequence 13760, A	C 786	12	24.0	2856	3	US-09-328-352-41	Sequence 41, Appl
C 714	12	24.0	2045	3	US-09-270-767-13760	Sequence 13760, A	787	12	24.0	2886	3	US-09-221-017B-863	Sequence 863, App
C 715	12	24.0	2046	3	US-10-104-047-1468	Sequence 1468, Ap	788	12	24.0	2894	3	US-10-070-634-22	Sequence 22, Appl
C 716	12	24.0	2091	3	US-09-902-540-7268	Sequence 7268, Ap	C 789	12	24.0	2929	3	US-09-710-279-4120	Sequence 4120, Ap
C 717	12	24.0	2094	3	US-09-270-767-13304	Sequence 13304, A	790	12	24.0	2940	3	US-09-703-416-1	Sequence 1, Appli
C 718	12	24.0	2100	2	US-08-264-002-6	Sequence 6, Appli	791	12	24.0	2940	3	US-09-703-416-1	Sequence 1, Appli
C 719	12	24.0	2101	3	US-09-902-540-3956	Sequence 3956, Ap	792	12	24.0	2940	3	US-10-171-229-91	Sequence 1, Appli
C 720	12	24.0	2116	3	US-09-023-655-1256	Sequence 1256, Ap	793	12	24.0	2940	3	US-10-429-398-1	Sequence 12, Appl
C 721	12	24.0	2124	3	US-09-198-122-1	Sequence 1, Appli	794	12	24.0	2980	3	US-08-456-200B-12	Sequence 12, Appl
C 722	12	24.0	2166	2	US-08-408-095-30	Sequence 30, Appl	C 795	12	24.0	2984	3	US-09-701-866-2	Sequence 2, Appli
C 723	12	24.0	2169	2	US-09-252-991A-836	Sequence 836, App	C 796	12	24.0	2984	3	US-09-710-279-4132	Sequence 4132, Ap
C 724	12	24.0	2178	2	US-08-492-027A-2	Sequence 2, Appli	797	12	24.0	3001	3	US-09-710-279-3403	Sequence 3403, Ap
C 725	12	24.0	2190	2	US-08-492-027A-7	Sequence 7, Appli	C 798	12	24.0	3001	3	US-09-539-333D-171	Sequence 171, App
C 726	12	24.0	2190	3	US-10-209-405-4	Sequence 4, Appli	C 799	12	24.0	3029	3	US-09-949-016-3621	Sequence 3621, Ap
C 727	12	24.0	2214	3	US-09-583-110-1377	Sequence 1377, Ap	800	12	24.0	3030	3	US-09-710-279-4001	Sequence 4001, Ap
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## ALIGNMENTS

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RESULT 1
US-09-350-729A-4
; Sequence 4, Application US/09350729A
; Patent No. 6770479
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSKHO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135
; CURRENT APPLICATION NUMBER: US/09/350,729A
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-09-350-729A-4
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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 2
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; Sequence 30, Application US/08082849B
; Patent No. 5672274
; GENERAL INFORMATION:
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atoria, Naveen
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; APPLICANT: Singh, Yogendra
; APPLICANT: Nicholas, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; TITLE OF INVENTION: Related Methods
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
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; TELEPHONE: (415) 576-0200
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; INFORMATION FOR SEQ ID NO: 30:
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; LENGTH: 2160 base pairs
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; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
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Qy 1 GGGACGGCTCCAAATCTACACGTTGTTACCAAGACTTGGTTAGTGG 50
Db 1120 GGGACGGCTCCAAATCTACACGTTGTTACCAAGACTTGGTTAGTGG 1169
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RESULT 3
PCT-US94-01624-30
; Sequence 30, Application PC/TUS9401624
; GENERAL INFORMATION:
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atoria, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nicholas, Peter J.
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESS: TOWNSEND AND TOWNSEND KHOURIE AND CREW
; STREET: Stewart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
```



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/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US94/01624
/ FILING DATE: June 25, 1993
/ CLASSIFICATION:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Weber, Kenneth A.
/ REGISTRATION NUMBER: 31,677
/ REFERENCE/DOCKET NUMBER: 15280-115
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 543-9600
/ TELEFAX: (415) 543-5043
/ INFORMATION FOR SEQ ID NO: 30:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 2160 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: DNA (genomic)
/ HYPOTHEetical: NO
/ ORIGINAL SOURCE:
/ ORGANISM: Bacillus anthracis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: 1..2157
/ OTHER INFORMATION: /product= "PAHIV#2"
PCT-US94-01624-30

Query Match
Best Local Similarity 100.0%; Score 50; DB 6; Length 2160;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 50
Db 1120 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 1169

RESULT 4
US-09-350-729A-2
/ Sequence 2, Application US/09350729A
/ Patent No. 6770479
/ GENERAL INFORMATION:
/ APPLICANT: LEE, JOHN SCOTT
/ APPLICANT: PUSHKO, PETER
/ APPLICANT: PARKER, MICHAEL D.
/ APPLICANT: SMITH, JONATHAN F.
/ APPLICANT: WELKOS, SUSAN L.
/ TITLE OF INVENTION: ANTHRAX VACCINES
/ FILE REFERENCE: ARMY135
/ CURRENT APPLICATION NUMBER: US/09/350,729A
/ CURRENT FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: 60/092,416
/ PRIOR FILING DATE: 1998-07-10
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 2
/ LENGTH: 2211
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
US-09-350-729A-2

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 2211;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 50

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Db 1111 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 1160

RESULT 5
US-09-350-729A-3
/ Sequence 3, Application US/09350729A
/ Patent No. 6770479
/ GENERAL INFORMATION:
/ APPLICANT: LEE, JOHN SCOTT
/ APPLICANT: PUSHKO, PETER
/ APPLICANT: PARKER, MICHAEL D.
/ APPLICANT: SMITH, JONATHAN F.
/ APPLICANT: WELKOS, SUSAN L.
/ TITLE OF INVENTION: ANTHRAX VACCINES
/ FILE REFERENCE: ARMY135
/ CURRENT APPLICATION NUMBER: US/09/350,729A
/ CURRENT FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: 60/092,416
/ PRIOR FILING DATE: 1998-07-10
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2292
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
US-09-350-729A-3

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 2292;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 50
Db 1192 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 1241

RESULT 6
US-09-350-729A-1
/ Sequence 1, Application US/09350729A
/ Patent No. 6770479
/ GENERAL INFORMATION:
/ APPLICANT: LEE, JOHN SCOTT
/ APPLICANT: PUSHKO, PETER
/ APPLICANT: PARKER, MICHAEL D.
/ APPLICANT: SMITH, JONATHAN F.
/ APPLICANT: WELKOS, SUSAN L.
/ TITLE OF INVENTION: ANTHRAX VACCINES
/ FILE REFERENCE: ARMY135
/ CURRENT APPLICATION NUMBER: US/09/350,729A
/ CURRENT FILING DATE: 2001-06-20
/ PRIOR APPLICATION NUMBER: 60/092,416
/ PRIOR FILING DATE: 1998-07-10
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 1
/ LENGTH: 2295
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
US-09-350-729A-1

Query Match
Best Local Similarity 100.0%; Score 50; DB 3; Length 2295;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 50
Db 1195 GGAGCGGCTCCAAATCTACCAACGCTGTACCAACGACTTGTAGTTAGG 1244

RESULT 7
US-08-021-601-11
/ Sequence 11, Application US/08021601
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```

; Patent No. 5591631
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Nichols, Peter J.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 133 Carnegie Way, Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,601
; FILING DATE: 19930212
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-0770
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2709 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2709
; US-08-021-601-11

Query Match          100.0%; Score 50; DB 2; Length 2709;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGACGGCTCCCAATCTACACGCTGTACCAAGCACTTCGTTAGTGTAGG 50
DB      1108 GGGACGGCTCCCAATCTACACGCTGTACCAAGCACTTCGTTAGTGTAGG 1157

RESULT 8
US-08-082-849B-11
; Sequence 11, Application US/08082849B
; Patent No. 5677274
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; TITLE OF INVENTION: Related Methods
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-161-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2709
; OTHER INFORMATION: /product= "PA(1-725)-Human CD4
; OTHER INFORMATION: residues (1-178)"
; US-08-082-849B-11

Query Match          100.0%; Score 50; DB 2; Length 2709;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGACGGCTCCCAATCTACACGCTGTACCAAGCACTTCGTTAGTGTAGG 50
DB      1108 GGGACGGCTCCCAATCTACACGCTGTACCAAGCACTTCGTTAGTGTAGG 1157

RESULT 9
PCT-US94-01624-11
; Sequence 11, Application PC/TUS9401624
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Arora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND KHOURIE AND CREW
; STREET: Stewart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01624
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; FILING DATE: June 25, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2709 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..2709
; OTHER INFORMATION: /Product="PA(1-725)-----Human CD4
; OTHER INFORMATION: residues(1-178)"
; PCT-US94-01624-11

Query Match      100.0%; Score 50; DB 6; Length 2709;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAGGCTCCATCTACACGTTGTTACCAAGCACTTGTTAGTGG 50
Db      1108 GGGAGGCTCCATCTACACGTTGTTACCAAGCACTTGTTAGTGG 1157

RESULT 10
US-08-021-601-3
; Sequence 3, Application US/08021601
; Patent No. 5591631
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Kimpel, Kurt R.
; APPLICANT: Nichols, Peter J.
; APPLICANT: Atora, Naveen
; APPLICANT: Singh, Yogendra
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Needle & Rosenberg, P.C.
; STREET: 133 Carnegie Way, Suite 400
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/021,601
; FILING DATE: 19930212
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Spratt, Gwendolyn D.
; REGISTRATION NUMBER: 36,016
; REFERENCE/DOCKET NUMBER: 1414.057
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 404/688-9880
; TELEFAX: 404/688-9880
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
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; LENGTH: 4235 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
;
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1891..4095
; US-08-021-601-3

Query Match      100.0%; Score 50; DB 2; Length 4235;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 GGGAGGCTCCATCTACACGTTGTTACCAAGCACTTGTTAGTGG 50
Db      2998 GGGAGGCTCCATCTACACGTTGTTACCAAGCACTTGTTAGTGG 3047

RESULT 11
US-08-082-849B-3
; Sequence 3, Application US/08082849B
; Patent No. 5677274
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Kimpel, Kurt R.
; APPLICANT: Atora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,849B
; FILING DATE: 25-JUN-1993
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,601
; FILING DATE: 12-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-161-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEtical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
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; LOCATION: 1891..4095
; OTHER INFORMATION: /product= "Protective Antigen"
US-08-082-849B-3
Query Match 100.0%; Score 50; DB 2; Length 4235;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGACGGCTTCAATCTACACGTTTACCAACGACTTGGTTAGTGG 50
DB 2998 GGGACGGCTTCAATCTACACGTTTACCAACGACTTGGTTAGTGG 3047

RESULT 12
PCT-US94-01624-3
; Sequence 3, Application PC/TUS9401624
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Klimpel, Kurt R.
; APPLICANT: Atora, Naveen
; APPLICANT: Singh, Yogendra
; APPLICANT: Nichols, Peter J.
; TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
; TITLE OF INVENTION: RELATED METHODS
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
; STREET: Stewart Street Tower, 20th Floor, One Market
; STREET: Plaza
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/01624
; FILING DATE: June 25, 1993
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Kenneth A.
; REGISTRATION NUMBER: 31,677
; REFERENCE/DOCKET NUMBER: 15280-115
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4235 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1891..4095
; OTHER INFORMATION: /product= "Protective Antigen"
PCT-US94-01624-3

Query Match 100.0%; Score 50; DB 6; Length 4235;
Best Local Similarity 100.0%; Pred. No. 1e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 GGGACGGCTTCAATCTACACGTTTACCAACGACTTGGTTAGTGG 50
DB 2998 GGGACGGCTTCAATCTACACGTTTACCAACGACTTGGTTAGTGG 3047
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```
RESULT 13
US-09-328-352-687/c
; Sequence 687, Application US/09328352
; Patent No. 6562358
; GENERAL INFORMATION:
; APPLICANT: Gary L. Bretton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; FILE REFERENCE: GTC99-03PA
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 8252
; SEQ ID NO 687
; LENGTH: 414
; TYPE: DNA
; ORGANISM: Acinetobacter baumannii
US-09-328-352-687

Query Match 32.0%; Score 16; DB 3; Length 414;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 GACTTCGTTAGTGTGA 48
DB 96 GACTTCGTTAGTGTGA 81

RESULT 14
US-08-393-889-14
; Sequence 14, Application US/08393889
; Patent No. 6420152
; GENERAL INFORMATION:
; APPLICANT: Adams, Craig W.
; APPLICANT: Pang, Patsy P.-Y.
; APPLICANT: Bellet, Marina
; TITLE OF INVENTION: Recombinant DNase B Derived from
; TITLE OF INVENTION: Streptococcus pyogenes
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Mak
; STREET: 225 South Lake Avenue, Ninth Floor
; CITY: Pasadena
; STATE: California
; COUNTRY: USA
; ZIP: 91001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/393,889
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/082,845
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Farber, Michael B.
; REGISTRATION NUMBER: 32,612
; REFERENCE/DOCKET NUMBER: 9521
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (818) 795-6321
; TELEFAX: (818) 795-4000
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 937 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
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HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..819  
US-08-393-889-14

Query Match 32.0%; Score 16; DB 3; Length 937;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTCCATCTACACG 22  
Db 667 GCTCCATCTACACG 682

RESULT 15  
US-09-119-900-14  
Sequence 14, Application US/09119900  
Patent No. 6632614  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belei, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/119,900  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 937 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..819  
US-09-119-900-14

Query Match 32.0%; Score 16; DB 3; Length 937;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 7 GCTCCATCTACACG 22  
Db 667 GCTCCATCTACACG 682

RESULT 16  
US-08-472-630-14  
Sequence 14, Application US/08472630  
Patent No. 6770277  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belei, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,630  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 937 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..819  
SEQUENCE DESCRIPTION: SEQ ID NO: 14:  
US-08-472-630-14

Query Match 32.0%; Score 16; DB 3; Length 937;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 17  
PCT-US94-09450-14  
Sequence 14, Application PC/TUS9409450



GENERAL INFORMATION:  
APPLICANT: Beckman Instruments, Inc.  
APPLICANT: 2500 Harbor Boulevard 92634  
APPLICANT: Fullerton, California  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09450  
FILING DATE: 18-AUG-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,845  
FILING DATE: 23-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: May, William H.  
REGISTRATION NUMBER: 26,769  
REFERENCE/DOCKET NUMBER: 39D-1357 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 937 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..819  
PCT-US94-09450-14

Query Match 32.0%; Score 16; DB 6; Length 937;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCATCTACACG 22  
|||||  
DB 667 GCTCCATCTACACG 682

RESULT 18  
US-08-393-889-11  
Sequence 11, Application US/08393889  
Patent No. 6420152  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belei, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena

STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/393,889  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes

US-08-393-889-11

Query Match 32.0%; Score 16; DB 3; Length 940;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCATCTACACG 22  
|||||  
DB 670 GCTCCATCTACACG 685

RESULT 19  
US-09-119-900-11  
Sequence 11, Application US/09119900  
Patent No. 6632614  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belei, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESS: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/119,900  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845



FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
US-09-119-900-11

Query Match 32.0%; Score 16; DB 3; Length 940;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTCCAACTTACAAG 22  
|||||  
Db 670 GCTCCAACTTACAAG 685

RESULT 20  
US-08-472-630-11  
Sequence 11, Application US/08472630  
Patent No. 6770277  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
Pang, Patty P.-Y.  
Belei, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
Streptococcus pyogenes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,630  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-08-472-630-11

Query Match 32.0%; Score 16; DB 3; Length 940;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTCCAACTTACAAG 22  
|||||  
Db 670 GCTCCAACTTACAAG 685

RESULT 21  
PCT-US94-09450-11  
Sequence 11, Application PC/TUS9409450  
GENERAL INFORMATION:  
APPLICANT: Beckman Instruments, Inc.  
APPLICANT: 2500 Harbor Boulevard  
Fullerton, California 92634  
TITLE OF INVENTION: Recombinant DNase B Derived from  
Streptococcus pyogenes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09450  
FILING DATE: 18-AUG-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,845  
FILING DATE: 23-JUN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: May, William H.  
REGISTRATION NUMBER: 26,769  
REFERENCE/DOCKET NUMBER: 39D-1357 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
PCT-US94-09450-11

Query Match 32.0%; Score 16; DB 6; Length 940;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 GCTCCAACTTACAAG 22  
|||||  
Db 670 GCTCCAACTTACAAG 685



RESULT 22  
US-08-393-889-7  
; Sequence 7, Application US/08393889  
; Patent No. 6420152  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Craig W.  
; APPLICANT: Pang, Patty P.-Y.  
; APPLICANT: Belei, Martina  
; TITLE OF INVENTION: Recombinant DNase B Derived from  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/393,889  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,845  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fairber, Michael B.  
; REGISTRATION NUMBER: 32,612  
; REFERENCE/DOCKET NUMBER: 9521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1083 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..944  
; US-08-393-889-7  
; Query Match 32.0%; Score 16; DB 3; Length 1083;  
; Best Local Similarity 100.0%; Pred. No. 11;  
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

; TITLE OF INVENTION: Streptococcus pyogenes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/119,900  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,845  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Fairber, Michael B.  
; REGISTRATION NUMBER: 32,612  
; REFERENCE/DOCKET NUMBER: 9521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1083 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHEICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 129..944  
; US-09-119-900-7  
; Query Match 32.0%; Score 16; DB 3; Length 1083;  
; Best Local Similarity 100.0%; Pred. No. 11;  
; Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 24  
US-08-472-630-7  
; Sequence 7, Application US/08472630  
; Patent No. 6770277  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Craig W.  
; APPLICANT: Pang, Patty P.-Y.  
; APPLICANT: Belei, Martina  
; TITLE OF INVENTION: Recombinant DNase B Derived from  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk



COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,630  
FILING DATE: 07-Jun-1995  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..944  
US-08-472-630-7  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Query Match 32.0%; Score 16; DB 3; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GCTCCATCTTCAACG 22  
|||||  
Db 792 GCTCCATCTTCAACG 807

RESULT 25  
PCT-US94-09450-7  
Sequence 7, Application PC/TUS9409450  
GENERAL INFORMATION:  
APPLICANT: Beckman Instruments, Inc.  
APPLICANT: 2500 Harbor Boulevard  
APPLICANT: Fullerton, California 92634  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Beckman Instruments, Inc.  
STREET: 2500 Harbor Boulevard  
CITY: Fullerton  
STATE: California  
COUNTRY: USA  
ZIP: 92634  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/09450  
FILING DATE: 18-AUG-1994  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/082,845  
FILING DATE: 23-JUN-1993  
ATTORNEY/AGENT INFORMATION:

NAME: May, William H.  
REGISTRATION NUMBER: 26,769  
REFERENCE/DOCKET NUMBER: 39D-1357 PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..944  
PCT-US94-09450-7

Query Match 32.0%; Score 16; DB 6; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 GCTCCATCTTCAACG 22  
|||||  
Db 792 GCTCCATCTTCAACG 807

RESULT 26  
US-09-949-016-12442/c  
Sequence 12442, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: C1001307  
CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 12442  
LENGTH: 27491  
TYPE: DNA  
ORGANISM: Human  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (1)..(27491)  
OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12442

Query Match 32.0%; Score 16; DB 3; Length 27491;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 TACAACGTGTACCA 31  
|||||  
Db 8587 TACAACGTGTACCA 8572

RESULT 27  
US-09-952-060-31  
Sequence 31, Application US/09952060  
Patent No. 6733993



```
; GENERAL INFORMATION:
; APPLICANT: Emini, Emilio A.
; APPLICANT: Youll, Rima
; APPLICANT: Bett, Andrew J.
; APPLICANT: Chen, Ling
; APPLICANT: Kaslow, David C.
; APPLICANT: Shiver, John W.
; APPLICANT: Toner, Timothy J.
; APPLICANT: Casimiro, Danilo R.
; TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
; TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
; FILE REFERENCE: 20747Y
; CURRENT APPLICATION NUMBER: US/09/952,060
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/US01/28861
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/317,814
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/279,056
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/233,180
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 36620
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 nef,
; OTHER INFORMATION: noncoding
US-09-952-060-31
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```
Query Match          32.0%; Score 16; DB 3; Length 36620;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 TCTACACGTGTACC 29
      |||
DB      33118 TCTACACGTGTACC 33133
```

```
RESULT 28
US-09-952-060-26
; Sequence 26, Application US/09952060
; Patent No. 6733993
; GENERAL INFORMATION:
; APPLICANT: Emini, Emilio A.
; APPLICANT: Youll, Rima
; APPLICANT: Bett, Andrew J.
; APPLICANT: Chen, Ling
; APPLICANT: Kaslow, David C.
; APPLICANT: Shiver, John W.
; APPLICANT: Toner, Timothy J.
; APPLICANT: Casimiro, Danilo R.
; TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
; TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
; FILE REFERENCE: 20747Y
; CURRENT APPLICATION NUMBER: US/09/952,060
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/US01/28861
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/317,814
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/279,056
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/233,180
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
```

```
; LENGTH: 37474
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: DNA encoding pMRKAD5 HIV-1 gag, noncoding
US-09-952-060-26
```

```
Query Match          32.0%; Score 16; DB 3; Length 37474;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 TCTACACGTGTACC 29
      |||
DB      33983 TCTACACGTGTACC 33998
```

```
RESULT 29
US-09-952-060-29
; Sequence 29, Application US/09952060
; Patent No. 6733993
; GENERAL INFORMATION:
; APPLICANT: Emini, Emilio A.
; APPLICANT: Youll, Rima
; APPLICANT: Bett, Andrew J.
; APPLICANT: Chen, Ling
; APPLICANT: Kaslow, David C.
; APPLICANT: Shiver, John W.
; APPLICANT: Toner, Timothy J.
; APPLICANT: Casimiro, Danilo R.
; TITLE OF INVENTION: ENHANCED FIRST GENERATION ADENOVIRUS
; TITLE OF INVENTION: VACCINES EXPRESSING CODON OPTIMIZED HIV1-GAG, POL, NEF AND
; FILE REFERENCE: 20747Y
; CURRENT APPLICATION NUMBER: US/09/952,060
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: PCT/US01/28861
; PRIOR FILING DATE: 2001-09-14
; PRIOR APPLICATION NUMBER: 60/317,814
; PRIOR FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: 60/279,056
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 60/233,180
; PRIOR FILING DATE: 2000-09-15
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 29
; LENGTH: 38519
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Codon optimized DNA encoding pMRKADSHIV-1 pol,
; OTHER INFORMATION: noncoding
US-09-952-060-29
```

```
Query Match          32.0%; Score 16; DB 3; Length 38519;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      14 TCTACACGTGTACC 29
      |||
DB      35017 TCTACACGTGTACC 35032
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RESULT 30
US-08-682-218-16/c
; Sequence 16, Application US/08682218
; Patent No. 5747259
; GENERAL INFORMATION:
; APPLICANT: You, Qimin
; TITLE OF INVENTION: MATERIALS AND METHODS FOR
; TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII
; TITLE OF INVENTION: NUCLEIC ACIDS
; NUMBER OF SEQUENCES: 40
```



```

CORRESPONDENCE ADDRESS:
ADDRESS: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,218
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3630
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 602 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: T18492
US-08-682-218-16

Query Match      30.0%; Score 15; DB 2; Length 602;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  CGGCTCCAATCTACA 19
Db      396 CGGCTCCAATCTACA 382

RESULT 31
US-08-682-218-11/c
Sequence 11, Application US/08682218
Patent No. 5747259
GENERAL INFORMATION:
APPLICANT: You, Qimin
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,218
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3630
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 base pairs
```

```

TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: LCDCT711
US-08-682-218-11

Query Match      30.0%; Score 15; DB 2; Length 605;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  CGGCTCCAATCTACA 19
Db      395 CGGCTCCAATCTACA 381

RESULT 32
US-08-682-218-12/c
Sequence 12, Application US/08682218
Patent No. 5747259
GENERAL INFORMATION:
APPLICANT: You, Qimin
TITLE OF INVENTION: MATERIALS AND METHODS FOR
TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII
TITLE OF INVENTION: NUCLEIC ACIDS
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESS: R. J. Rodrick, Becton Dickinson and Company
STREET: 1 Becton Drive
CITY: Franklin Lakes
STATE: NJ
COUNTRY: US
ZIP: 07417
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/682,218
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Fugit, Donna R.
REGISTRATION NUMBER: 32,135
REFERENCE/DOCKET NUMBER: P-3630
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 605 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
STRAIN: LCDCT714
US-08-682-218-12

Query Match      30.0%; Score 15; DB 2; Length 605;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      5  CGGCTCCAATCTACA 19
Db      396 CGGCTCCAATCTACA 382

RESULT 33
US-08-682-218-13/c
Sequence 13, Application US/08682218
Patent No. 5747259
GENERAL INFORMATION:
APPLICANT: You, Qimin
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;; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
;; TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII  
;; TITLE OF INVENTION: NUCLEIC ACIDS  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: R. J. Rodrick, Becton Dickinson and Company  
;; STREET: 1 Becton Drive  
;; CITY: Franklin Lakes  
;; STATE: NJ  
;; COUNTRY: US  
;; ZIP: 07417  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/682,218  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Fugit, Donna R.  
;; REGISTRATION NUMBER: 32,135  
;; REFERENCE/DOCKET NUMBER: P-3630  
;; INFORMATION FOR SEQ ID NO: 13:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 606 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; ORIGINAL SOURCE:  
;; STRAIN: T1492  
;;  
US-08-682-218-13

Query Match 30.0%; Score 15; DB 2; Length 606;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGCTCCATCTACA 19  
DB 396 CGGCTCCATCTACA 382

RESULT 34  
US-08-682-218-4/c  
;; Sequence 4, Application US/08682218  
;; Patent No. 5747259  
;; GENERAL INFORMATION:  
;; APPLICANT: You, Qimin  
;; TITLE OF INVENTION: MATERIALS AND METHODS FOR  
;; TITLE OF INVENTION: SPECIES-SPECIFIC DETECTION OF MYCOBACTERIUM KANSASII  
;; NUMBER OF SEQUENCES: 40  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: R. J. Rodrick, Becton Dickinson and Company  
;; STREET: 1 Becton Drive  
;; CITY: Franklin Lakes  
;; STATE: NJ  
;; COUNTRY: US  
;; ZIP: 07417  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/682,218  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Fugit, Donna R.  
;; REGISTRATION NUMBER: 32,135

;; REFERENCE/DOCKET NUMBER: P-3630  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 655 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: double  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: DNA (genomic)  
;; ORIGINAL SOURCE:  
;; STRAIN: TMC1201  
;;  
US-08-682-218-4

Query Match 30.0%; Score 15; DB 2; Length 655;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGCTCCATCTACA 19  
DB 405 CGGCTCCATCTACA 391

RESULT 35  
US-08-822-774-18/c  
;; Sequence 18, Application US/08822774  
;; Patent No. 6183997  
;; GENERAL INFORMATION:  
;; APPLICANT: HOGREFE, Holly  
;; TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)  
;; TITLE OF INVENTION: Extracts, PEF Protein Complexes, Isolated PEF Proteins,  
;; and Methods for Purifying and Identifying Same  
;; NUMBER OF SEQUENCES: 61  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESS: David J. Kulik, Evenson, McKeown, Edwards &  
;; ADDRESS: Lenahan, P.L.L.C.  
;; STREET: 1200 G Street, N.W. Suite 700  
;; CITY: Washington  
;; STATE: D.C.  
;; ZIP: 20005  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; OPERATING SYSTEM: IBM PC compatible  
;; SOFTWARE: Patentin Release #1.0, Version #1.25  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/822,774  
;; FILING DATE: 21-MAR-1997  
;; CLASSIFICATION: 436  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: KULIK, David J.  
;; REGISTRATION NUMBER: 36,576  
;; REFERENCE/DOCKET NUMBER: 1486/43163  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (202) 628-8800  
;; TELEFAX: (202) 628-8844  
;;  
;; INFORMATION FOR SEQ ID NO: 18:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 1209 base pairs  
;; TYPE: nucleic acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: unknown  
;; MOLECULE TYPE: DNA (genomic)  
;; HYPOTHETICAL: NO  
;; ANTI-SENSE: NO  
;;  
US-08-822-774-18

Query Match 30.0%; Score 15; DB 3; Length 1209;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GTGTTACCAAGACT 36  
DB 1079 GTGTTACCAAGACT 1065



RESULT 36  
US-09-632-711-18/C  
Sequence 18, Application US/09632711  
Patent No. 6333165  
GENERAL INFORMATION:  
APPLICANT: HOGREFE, Holly  
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)  
Extracts, PEF Protein Complexes, Isolated PEF Proteins,  
and Methods for Purifying and Identifying Same  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &  
Lenahan, P.L.L.C.  
STREET: 1200 G Street, N.W. Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/632,711  
FILING DATE: 04-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/822,774  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Kulik, David J.  
REGISTRATION NUMBER: 36,576  
REFERENCE/DOCKET NUMBER: 1486/43163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 628-8800  
TELEFAX: (202) 628-8844  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1209 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-632-711-18  
Query Match 30.0%; Score 15; DB 3; Length 1209;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 22 GTGTACCAAGACT 36  
DB 1079 GTGTACCAAGACT 1065  
RESULT 37  
US-09-632-703B-18/C  
Sequence 18, Application US/09632703B  
Patent No. 6379553  
GENERAL INFORMATION:  
APPLICANT: HOGREFE, Holly  
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF) Extracts, PEF  
Protein Complexes, Isolated PEF Proteins, and Methods for F  
Identifying Same  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Finegan, Henderson, Farabow, Garrett, & Dunner, L.L.P.  
STREET: 1300 I Street, N.W.  
CITY: Washington  
STATE: D.C.

ZIP: 20005-3315  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: <Unknown>  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/632,703B  
FILING DATE: 24-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/822,774  
FILING DATE: 21-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BARKER, M. Paul  
REGISTRATION NUMBER: 32,013  
REFERENCE/DOCKET NUMBER: 4121.0116-04  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (650) 849-6613  
TELEFAX: (650) 849-6666  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1209 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: unknown  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-632-703B-18

Query Match 30.0%; Score 15; DB 3; Length 1209;  
Best Local Similarity 100.0%; Pred. No. 41;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 22 GTGTACCAAGACT 36  
DB 1079 GTGTACCAAGACT 1065  
RESULT 38  
US-09-632-702-18/C  
Sequence 18, Application US/09632702  
Patent No. 644428  
GENERAL INFORMATION:  
APPLICANT: HOGREFE, Holly  
TITLE OF INVENTION: Polymerase Enhancing Factor (PEF)  
Extracts, PEF Protein Complexes, Isolated PEF Proteins,  
and Methods for Purifying and Identifying Same  
NUMBER OF SEQUENCES: 61  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: David J. Kulik, Evenson, McKeown, Edwards &  
Lenahan, P.L.L.C.  
STREET: 1200 G Street, N.W. Suite 700  
CITY: Washington  
STATE: D.C.  
ZIP: 20005  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC Compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/632,702  
FILING DATE: 04-Aug-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/822,774  
FILING DATE: 21-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Kulik, David J.  
REGISTRATION NUMBER: 36,576



```

; REFERENCE/DOCKET NUMBER: 1486/43163
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 1209 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: unknown
;   MOLECULE TYPE: DNA (genomic)
;   HYPOTHETICAL: NO
;   ANTI-SENSE: NO
;   SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-632-702-18

Query Match      30.0%; Score 15; DB 3; Length 1209;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 GTGTTACCAAGCACT 36
DB      1079 GTGTTACCAAGCACT 1065

RESULT 39
US-09-399-003-18/c
; Sequence 18, Application US/09399003
; Patent No. 6734293
; GENERAL INFORMATION:
; APPLICANT: Hogrefe, Holly
; APPLICANT: Hansen, Connie J
; TITLE OF INVENTION: Polymerase Enhancing Factor (PEF) Extracts, PEF Protein Complexes
; FILE REFERENCE: 4121.0116-02
; CURRENT APPLICATION NUMBER: US/09/399,003
; PRIOR FILING DATE: 1999-09-20
; PRIOR APPLICATION NUMBER: PCT/ US98/05497
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: US 08/957,709
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: US 08/822,774
; PRIOR FILING DATE: 1997-03-21
; NUMBER OF SEQ ID NOS: 89
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 18
; LENGTH: 1209
; TYPE: DNA
; ORGANISM: Pyrococcus furiosus
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1209)
; OTHER INFORMATION: "n" is a, t, g, or c
US-09-399-003-18

Query Match      30.0%; Score 15; DB 3; Length 1209;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 GTGTTACCAAGCACT 36
DB      1079 GTGTTACCAAGCACT 1065

RESULT 40
US-09-487-558B-165
; Sequence 165, Application US/09487558B
; Patent No. 6949356
; GENERAL INFORMATION:
; APPLICANT: Busby, Robert
; APPLICANT: Cali, Brian
; APPLICANT: Hecht, Peter
; APPLICANT: Holtzman, Doug
```

```

; APPLICANT: Madden, Kevin
; APPLICANT: Maxon, Mary
; APPLICANT: Milne, Todd
; APPLICANT: No. 6949356man, Thea
; APPLICANT: Royer, John
; APPLICANT: Salama, Sofie
; APPLICANT: Sherman, Amir
; APPLICANT: Silva, Jeff
; APPLICANT: Summers, Eric
; TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
; FILE REFERENCE: 109272.130
; CURRENT APPLICATION NUMBER: US/09/487,558B
; PRIOR FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: US 60/487,558
; PRIOR FILING DATE: 1999-10-20
; NUMBER OF SEQ ID NOS: 446
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 165
; LENGTH: 1986
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-487-558B-165

Query Match      30.0%; Score 15; DB 3; Length 1986;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 ACAACGTGTTACCAA 31
DB      1071 ACAACGTGTTACCAA 1085
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Search completed: April 11, 2006, 21:48:37  
Job time : 54.2944 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 307.15 Seconds  
(without alignment)

9253.359 Million cell updates/sec

Title: US-10-712-654-23

Perfect score: 50  
Sequence: 1 gggacggctccaactacaa.....acgacttcgttaggttagg 50

Scoring table: OLIGO\_NUC  
Gapex 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :

GenEmbl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_px:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	50	100.0	954	6	AX353777
3	50	100.0	1278	6	AX353779
4	50	100.0	1281	6	CS135645
5	50	100.0	1461	6	AX353775
6	50	100.0	1694	1	AY921578
7	50	100.0	1707	6	CS135643
8	50	100.0	1710	6	AR570597
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10	50	100.0	2160	6	169387
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13	50	100.0	2211	6	CS061689
14	50	100.0	2211	6	AR570595
15	50	100.0	2225	1	BAN413937
16	50	100.0	2227	1	AY700758
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18	50	100.0	2292	6	AR570596

19	50	100.0	2295	1	AY997299	AY997299 Bacillus
20	50	100.0	2295	6	CS135651	CS135651 Sequence
21	50	100.0	2295	6	AR570594	AR570594 Sequence
22	50	100.0	2369	1	AF306778	AF306778 Bacillus
23	50	100.0	2369	1	AF306779	AF306779 Bacillus
24	50	100.0	2369	1	AF306780	AF306780 Bacillus
25	50	100.0	2369	1	AF306781	AF306781 Bacillus
26	50	100.0	2369	1	AF306782	AF306782 Bacillus
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28	50	100.0	2549	1	AF268967	AF268967 Bacillus
29	50	100.0	2605	6	AX933603	AX933603 Sequence
30	50	100.0	2709	6	133400	133400 Sequence
31	50	100.0	2709	6	169378	169378 Sequence
32	50	100.0	4235	1	BACPRG	BACPRG
33	50	100.0	4235	6	133396	133396 Sequence
34	50	100.0	4235	6	169374	169374 Sequence
35	50	100.0	181654	1	AF065404	AF065404 Bacillus
36	50	100.0	181677	1	AE011190	AE011190 Bacillus
37	50	100.0	181677	1	AE017336	AE017336 Bacillus
38	19	38.0	1409	15	AK118301	AK118301 Arabidops
39	19	38.0	82890	15	AP000420	AP000420 Arabidops
40	19	38.0	103039	15	AC139525	AC139525 Medicago
41	19	38.0	116349	15	AC146788	AC146788 Medicago
42	18	36.0	110000	9	AE014178	AE014178 Mus muscu
43	18	36.0	110000	15	AP008215	AP008215_128
44	18	36.0	149431	8	AC147066	AC147066 Pan trogl
45	18	36.0	153477	8	AC006332	AC006332 Homo sapi
46	18	36.0	156372	9	AC129299	AC129299 Mus muscu
47	18	36.0	174834	9	AC125270	AC125270 Mus muscu
48	18	36.0	178648	8	AC146512	AC146512 Pan trogl
49	18	36.0	184759	15	AP005702	AP005702 Oryza sat
50	18	36.0	207254	9	AC151910	AC151910 Mus muscu
51	17	34.0	739	1	AJ580865	AJ580865 Vibrio di
52	17	34.0	739	1	AJ842407	AJ842407 Vibrio di
53	17	34.0	1701	1	BT020843	BT020843 Bos tauru
54	17	34.0	110000	15	CR362128	CR362128_21
55	17	34.0	161206	14	AC141737	AC141737 Apis mel
56	17	34.0	200102	5	AC145955	AC145955 Gallus ga
57	17	34.0	202285	9	AC129024	AC129024 Bos muscu
58	17	34.0	205631	14	AC124163	AC124163 Bos tauru
59	16	32.0	414	6	AR318137	AR318137 Sequence
60	16	32.0	693	1	AB180942	AB180942 Streptoco
61	16	32.0	693	1	AB180944	AB180944 Streptoco
62	16	32.0	693	1	AB180946	AB180946 Streptoco
63	16	32.0	693	1	AB180947	AB180947 Streptoco
64	16	32.0	693	1	AB180948	AB180948 Streptoco
65	16	32.0	693	1	AB180950	AB180950 Streptoco
66	16	32.0	693	1	AB180951	AB180951 Streptoco
67	16	32.0	803	10	BV601894	BV601894 S215P6060
68	16	32.0	816	1	SPY295272	SPY295272 Streptoco
69	16	32.0	937	6	A49208	A49208 Sequence 14
70	16	32.0	937	6	AR219229	AR219229 Sequence
71	16	32.0	937	6	AR408521	AR408521 Sequence
72	16	32.0	937	6	AR569535	AR569535 Sequence
73	16	32.0	940	6	A49205	A49205 Sequence 11
74	16	32.0	940	6	AR219226	AR219226 Sequence
75	16	32.0	940	6	AR408518	AR408518 Sequence
76	16	32.0	940	6	AR569532	AR569532 Sequence
77	16	32.0	944	6	CO767310	CO767310 Sequence
78	16	32.0	1021	6	E08254	E08254 DNA encodin
79	16	32.0	1083	6	A49201	A49201 Sequence 7
80	16	32.0	1083	6	CO767306	CO767306 Sequence
81	16	32.0	1083	6	AR219224	AR219224 Sequence
82	16	32.0	1083	6	AR408516	AR408516 Sequence
83	16	32.0	1083	6	AR569530	AR569530 Sequence
84	16	32.0	2099	1	STRMP	STRMP
85	16	32.0	3257	6	CO594401	CO594401 Sequence
86	16	32.0	4334	1	AB030578	AB030578 Streptoco
87	16	32.0	5414	2	DR0DEC	DR0DEC
88	16	32.0	5414	6	CO579411	CO579411 Sequence
89	16	32.0	6430	14	AC023627	AC023627 Mus muscu
90	16	32.0	8558	6	CO579410	CO579410 Sequence
91	16	32.0	10424	1	AE010113	AE010113 Streptoco



C 92	16	32.0	34372	2	U58727	C 165	15	30.0	3930	6	CQ614619	CQ614619 Sequence
C 93	16	32.0	36620	6	AR534338	C 166	15	30.0	4219	5	AB052837	AB052837 Oncorhynch
C 94	16	32.0	37474	6	AR534333	C 167	15	30.0	6420	6	AX702592	AX702592 Sequence
C 95	16	32.0	38519	6	AR534336	C 168	15	30.0	6988	2	ACU82064	U82064 Angiostrong
C 96	16	32.0	44887	14	AC018207	C 169	15	30.0	7058	6	CQ614618	CQ614618 Sequence
C 97	16	32.0	45276	8	AL512654	C 170	15	30.0	8451	15	AY495664	AY495664 Cochliobd
C 98	16	32.0	53291	1	AE014170	C 171	15	30.0	9171	1	AE007469	AE007469 Streptoco
C 99	16	32.0	55208	14	AC087394	C 172	15	30.0	10286	1	AE004493	AE004493 Halobacte
C 100	16	32.0	80268	6	CO870264	C 173	15	30.0	10940	15	SLY224356	AE0224356 Solanum
C 101	16	32.0	84490	14	AE007429	C 174	15	30.0	11049	1	AE010247	AE010247 Pyrococcu
C 102	16	32.0	89791	2	AC005268	C 175	15	30.0	11180	1	AE013811	AE013811 Yersinia
C 103	16	32.0	103417	14	AC141159	C 176	15	30.0	11495	1	AF019747	AF019747 Escherich
C 104	16	32.0	104163	15	AC010155	C 177	15	30.0	11803	1	AF019746	AF019746 Escherich
C 105	16	32.0	110000	1	BA000034_17	C 178	15	30.0	11821	1	EC042604	EC042604 Escherich
C 106	16	32.0	110000	1	CP000056_17	C 179	15	30.0	16915	1	SS065001	U65001 Sporangomn
C 107	16	32.0	110000	1	CP000056_17	C 180	15	30.0	20168	13	AY641576	AE008774 Salmonell
C 108	16	32.0	110000	14	AC120578_0	C 181	15	30.0	27434	1	AY514485	AY514485 Avian inf
C 109	16	32.0	125685	8	AC073310	C 182	15	30.0	27693	13	AY514485	AY514485 Avian inf
C 110	16	32.0	125690	8	AC004827	C 183	15	30.0	32768	6	CQ788980	CQ788980 Sequence
C 111	16	32.0	137334	9	AC121952	C 184	15	30.0	32768	6	BD003751	BD003751 Polynucle
C 112	16	32.0	137987	14	CR456630	C 185	15	30.0	32768	6	BD003751	BD003751 Polynucle
C 113	16	32.0	148125	8	AC079873	C 186	15	30.0	33172	5	BX855595	BX855595 Zebrafish
C 114	16	32.0	156963	8	AL162451	C 187	15	30.0	35330	2	CEM05582	CEM05582 ScvCM582
C 115	16	32.0	157921	8	AL365254	C 188	15	30.0	37672	15	SCVCM582	SCVCM582 ScvCM582
C 116	16	32.0	158990	14	AL591702	C 189	15	30.0	40556	8	AC000007	AC000007 Homo sapi
C 117	16	32.0	160927	14	AL591702	C 190	15	30.0	41351	15	CNS08C7U	CNS08C7U Homo sapi
C 118	16	32.0	163573	8	AL359854	C 191	15	30.0	42441	14	AC109339	AC109339 Homo sapi
C 119	16	32.0	172393	2	AC099007	C 192	15	30.0	42460	15	SPCC1020	SPCC1020 Mus muscu
C 120	16	32.0	177457	14	AC022866	C 193	15	30.0	59928	14	AC101489	AC101489 Mus muscu
C 121	16	32.0	180645	9	AL732468	C 194	15	30.0	69142	15	AB012239	AB012239 Arabidops
C 122	16	32.0	191286	9	AC112793	C 195	15	30.0	71336	14	AC024264	AC024264 Homo sapi
C 123	16	32.0	192296	8	AC009654	C 196	15	30.0	73334	6	AX347027	AX347027 Sequence
C 124	16	32.0	192713	9	AC118211	C 197	15	30.0	73334	8	AX356494	AX356494 Sequence
C 125	16	32.0	193861	9	AC122226	C 198	15	30.0	73401	6	AC004467	AC004467 Homo sapi
C 126	16	32.0	197470	14	AC163621	C 199	15	30.0	73907	14	AC018257	AC018257 Drosophil
C 127	16	32.0	197786	8	AL450326	C 200	15	30.0	85934	14	AC165825	AC165825 Bos tauru
C 128	16	32.0	202768	8	AL450326	C 201	15	30.0	87835	2	AC005428	AC005428 Drosophil
C 129	16	32.0	224784	14	CR450685	C 202	15	30.0	92756	14	AF322454	AF322454 Homo sapi
C 130	16	32.0	232993	14	AC166063	C 203	15	30.0	96540	15	ATAC012328	ATAC012328 Arabidops
C 131	16	32.0	240262	14	AC137467	C 204	15	30.0	100559	15	ATAC018363	ATAC018363 Arabidops
C 132	16	32.0	242558	14	AC098938	C 205	15	30.0	101363	14	AP008186	AP008186 Lotus cor
C 133	16	32.0	269093	14	AC120719	C 206	15	30.0	110000	1	CR543861_09	CR543861_09 Continuation (11 o
C 134	16	32.0	279337	14	AC111720	C 207	15	30.0	110000	1	AE017220_17	AE017220_17 Continuation (18 o
C 135	16	32.0	302101	1	AB016784	C 208	15	30.0	110000	1	AE017355_40	AE017355_40 Continuation (41 o
C 136	16	32.0	303438	2	AE003452	C 209	15	30.0	110000	1	BA000031_03	BA000031_03 Continuation (4 o f
C 137	15	30.0	535	15	AY346932	C 210	15	30.0	110000	1	BX936398_25	BX936398_25 Continuation (26 o
C 138	15	30.0	602	6	AR004614	C 211	15	30.0	110000	1	CP000001_41	CP000001_41 Continuation (42 o
C 139	15	30.0	605	6	AR004609	C 212	15	30.0	110000	1	CP000026_12	CP000026_12 Continuation (33 o
C 140	15	30.0	605	6	AR004610	C 213	15	30.0	110000	1	CP000058_32	CP000058_32 Continuation (3 o f
C 141	15	30.0	606	6	AR004611	C 214	15	30.0	110000	2	AC125735_2	AC125735_2 Continuation (3 o f
C 142	15	30.0	655	6	AR004602	C 215	15	30.0	110000	15	AP008215_006	AP008215_006 Continuation (7 o f
C 143	15	30.0	797	1	AJ842431	C 216	15	30.0	110000	15	AP008216_199	AP008216_199 Continuation (200
C 144	15	30.0	834	6	AX653362	C 217	15	30.0	110000	15	AE008218_202	AE008218_202 Continuation (5 o f
C 145	15	30.0	874	6	AX571731	C 218	15	30.0	110000	15	CR382130_04	CR382130_04 Continuation (5 o f
C 146	15	30.0	1089	5	XIHB0X12	C 219	15	30.0	110000	15	AC145127_06	AC145127_06 Continuation (7 o f
C 147	15	30.0	1209	1	AY066006	C 220	15	30.0	110000	15	AE017343_05	AE017343_05 Continuation (6 o f
C 148	15	30.0	1209	6	BD133209	C 221	15	30.0	110000	15	AP008207_023	AP008207_023 Continuation (24 o
C 149	15	30.0	1209	6	AR180946	C 222	15	30.0	110000	15	AP008207_329	AP008207_329 Continuation (330
C 150	15	30.0	1209	6	AR207501	C 223	15	30.0	110000	15	AP008207_330	AP008207_330 Continuation (131
C 151	15	30.0	1209	6	AR225624	C 224	15	30.0	110000	15	AP008210_121	AP008210_121 Continuation (172
C 152	15	30.0	1209	6	AR535041	C 225	15	30.0	110000	15	AP008211_171	AP008211_171 Continuation (172
C 153	15	30.0	1209	6	AR535041	C 226	15	30.0	116932	15	AC074232	AC074232 Oryza sat
C 154	15	30.0	1333	1	AY540749	C 227	15	30.0	120268	14	AC146557	AC146557 Medicago
C 155	15	30.0	1606	6	CO720967	C 228	15	30.0	120791	14	AP007706	AP007706 Lotus cor
C 156	15	30.0	1608	8	S82986	C 229	15	30.0	124281	14	AC160925	AC160925 Medicago
C 157	15	30.0	1672	6	CS130819	C 230	15	30.0	126113	14	AC150230	AC150230 Carolinia
C 158	15	30.0	1691	6	MMHXP2	C 231	15	30.0	127311	14	AX004821	AX004821 Zebrafish
C 159	15	30.0	1737	6	CQ498407	C 232	15	30.0	127474	15	AX004821	AX004821 Zebrafish
C 160	15	30.0	1800	5	AB047032	C 233	15	30.0	133335	9	AC125164	AC125164 Mus muscu
C 161	15	30.0	1821	5	AF232215	C 234	15	30.0	135169	15	OSJ000180	OSJ000180 Oryza sat
C 162	15	30.0	2279	9	S74185	C 235	15	30.0	135171	14	AC120056	AC120056 Homo sapi
C 163	15	30.0	2372	15	SCYOR275C	C 236	15	30.0	137547	14	AC154915	AC154915 Bos tauru
C 164	15	30.0	2854	15	AB008372	C 237	15	30.0	138350	9	AC157809	AC157809 Mus muscu
			3182	13	BBU65985							



238	15	30.0	139388	14	AC137962	AC137962 Homo sapi	311	15	30.0	238562	14	AC096104	AC096104 Rattus no
C 239	15	30.0	140126	8	AC141424	AC141424 Homo sapi	312	15	30.0	240411	14	AC105428	AC105428 Mus muscu
C 240	15	30.0	143021	8	CR376784	CR376784 Dario rer	C 313	15	30.0	245523	14	AC094840	AC094840 Rattus no
C 241	15	30.0	145625	14	AC131010	AC131010 Homo sapi	C 314	15	30.0	249408	14	AC127448	AC127448 Rattus no
C 242	15	30.0	146296	14	AC129973	AC129973 Felis cat	C 315	15	30.0	255008	9	AC117574	AC117574 Mus muscu
C 243	15	30.0	148373	15	AC134348	AC134348 Oryza sat	C 316	15	30.0	255124	14	AC109417	AC109417 Rattus no
C 244	15	30.0	148456	9	AC132299	AC132299 Mus muscu	C 317	15	30.0	261733	14	AC098757	AC098757 Rattus no
C 245	15	30.0	149622	13	AY864330	AY864330 Chrysodei	C 318	15	30.0	265861	14	AC157223	AC157223 Bos tauru
C 246	15	30.0	150800	14	AC089997	AC089997 Homo sapi	C 319	15	30.0	266050	1	AL627270	AL627270 Salmoell
C 247	15	30.0	151694	9	AC119238	AC119238 Mus muscu	C 320	15	30.0	270080	14	AC113644	AC113644 Rattus no
C 248	15	30.0	152740	8	AF490843	AF490843 Homo sapi	C 321	15	30.0	273388	14	AC126969	AC126969 Rattus no
C 249	15	30.0	154604	14	AC135159	AC135159 Oryza sat	C 322	15	30.0	280977	14	AC129751	AC129751 Rattus no
C 250	15	30.0	154970	14	AC106808	AC106808 Homo sapi	C 323	15	30.0	284312	14	CR555293	CR555293 Dario rer
C 251	15	30.0	155263	15	AP003224	AP003224 Oryza sat	C 324	15	30.0	288814	1	AE017378	AE017378 Bacillus
C 252	15	30.0	155560	14	AC138154	AC138154 Dario rer	C 325	15	30.0	290029	1	AE017134	AE017134 Yersinia
C 253	15	30.0	155780	8	HS336012	HS336012 Homo sapi	C 326	15	30.0	290053	14	AC106953	AC106953 Rattus no
C 254	15	30.0	156328	14	AC148280	AC148280 Sorex ara	C 327	15	30.0	290667	2	AE003663	AE003663 Drosoephil
C 255	15	30.0	157766	12	AC099017	AC099017 Drosoephil	C 328	15	30.0	299744	14	AC095105	AC095105 Rattus no
C 256	15	30.0	158998	8	AC091516	AC091516 Homo sapi	C 329	15	30.0	300029	1	AE016839	AE016839 Salmoell
C 257	15	30.0	159200	9	AL731554	AL731554 Mouse DNA	C 330	15	30.0	300029	15	AE017714	AE017714 Oryza sat
C 258	15	30.0	161822	8	AC013246	AC013246 Homo sapi	C 331	15	30.0	300511	1	AE016775	AE016775 Pseudomon
C 259	15	30.0	163494	5	EX088649	EX088649 Zebrafish	C 332	15	30.0	301566	1	AE016769	AE016769 Bacterich
C 260	15	30.0	163812	5	EX088572	EX088572 Zebrafish	C 333	15	30.0	301731	1	AE016934	AE016934 Baceteroid
C 261	15	30.0	164064	15	AC135929	AC135929 Oryza sat	C 334	15	30.0	302422	1	AE017011	AE017011 Bacillus
C 262	15	30.0	165658	9	AC116663	AC116663 Rattus no	C 335	15	30.0	304564	15	AE017049	AE017049 Oryza sat
C 263	15	30.0	167229	14	CR352259	CR352259 Dario rer	C 336	15	30.0	308160	14	AC120326	AC120326 Rattus no
C 264	15	30.0	167405	15	AP002483	AP002483 Oryza sat	C 337	15	30.0	312773	14	AC117017	AC117017 Rattus no
C 265	15	30.0	169047	8	AL357935	AL357935 Human DNA	C 338	15	30.0	331409	14	AC155865	AC155865 Bos tauru
C 266	15	30.0	171949	8	AC012531	AC012531 Homo sapi	C 339	15	30.0	334050	1	AJ414151	AJ414151 Yersinia
C 267	15	30.0	173537	14	CR855297	CR855297 Dario rer	C 340	15	30.0	349980	6	AX571765	AX571765 Sequence
C 268	15	30.0	173767	8	AC002449	AC002449 Human PAC	C 341	14	28.0	64	15	U64682	U64682 Cladonia be
C 269	15	30.0	175565	15	AP003311	AP003311 Oryza sat	C 342	14	28.0	168	15	AP295795	AP295795 Pennerope
C 270	15	30.0	176695	14	AL606844	AL606844 Homo sapi	C 343	14	28.0	173	15	BOL29340	BOL29340 Braselica
C 271	15	30.0	178631	8	AL512635	AL512635 Human DNA	C 344	14	28.0	191	2	AME509460	AME509460 Apis mell
C 272	15	30.0	179115	5	EX323449	EX323449 Zebrafish	C 345	14	28.0	214	10	BX572714	BX572714 Arabidops
C 273	15	30.0	180689	14	AC145073	AC145073 Sus scrofa	C 346	14	28.0	238	6	CO444703	CO444703 Sequence
C 274	15	30.0	181927	8	AC114980	AC114980 Homo sapi	C 347	14	28.0	267	15	AJ837755	AJ837755 Arabidops
C 275	15	30.0	184532	9	AC124345	AC124345 Mus muscu	C 348	14	28.0	285	6	AR321225	AR321225 Sequence
C 276	15	30.0	186271	14	AC116473	AC116473 Mus muscu	C 349	14	28.0	300	6	AB31122	AB31122 Sequence 1
C 277	15	30.0	188171	9	AC117695	AC117695 Mus muscu	C 350	14	28.0	300	6	BD062081	BD062081 Dna encod
C 278	15	30.0	188523	9	AC099641	AC099641 Mus muscu	C 351	14	28.0	322	3	AY576915	AY576915 Unculture
C 279	15	30.0	189283	14	AC150623	AC150623 Carolinia	C 352	14	28.0	322	3	AY576919	AY576919 Unculture
C 280	15	30.0	189349	15	AC068654	AC068654 Genomic S	C 353	14	28.0	325	6	AX309740	AX309740 Sequence
C 281	15	30.0	191152	14	CT025580	CT025580 Dario rer	C 354	14	28.0	382	10	BV155439	BV155439 Ntlim1-13
C 282	15	30.0	192592	9	AC101663	AC101663 Mus muscu	C 355	14	28.0	401	15	ATH55689	ATH55689 Arabidops
C 283	15	30.0	192640	9	AC135354	AC135354 Mus muscu	C 356	14	28.0	411	13	AF271839	AF271839 Hepatilis
C 284	15	30.0	194157	14	AC145788	AC145788 Xenopus t	C 357	14	28.0	439	15	AFH53149	AFH53149 Arabidops
C 285	15	30.0	194754	14	AC141132	AC141132 Rattus no	C 358	14	28.0	450	10	BV165438	BV165438 Ntlim1-12
C 286	15	30.0	194760	14	CR788313	CR788313 Dario rer	C 359	14	28.0	459	15	AY831969	AY831969 Philodend
C 287	15	30.0	198721	9	AC123844	AC123844 Mus muscu	C 360	14	28.0	474	2	AF354524	AF354524 Giardia i
C 288	15	30.0	199102	8	AC129507	AC129507 Homo sapi	C 361	14	28.0	486	6	AR153089	AR153089 Sequence
C 289	15	30.0	201768	5	EX323591	EX323591 Zebrafish	C 362	14	28.0	486	6	AR176975	AR176975 Sequence
C 290	15	30.0	203106	9	AC021667	AC021667 Mus muscu	C 363	14	28.0	486	6	AR533066	AR533066 Sequence
C 291	15	30.0	204959	9	AC107865	AC107865 Mus muscu	C 364	14	28.0	486	6	AX077089	AX077089 Sequence
C 292	15	30.0	206868	9	AC151294	AC151294 Mus muscu	C 365	14	28.0	486	6	AX077104	AX077104 Sequence
C 293	15	30.0	206973	14	AC130594	AC130594 Rattus no	C 366	14	28.0	501	6	AX077082	AX077082 Sequence
C 294	15	30.0	207571	9	AL670951	AL670951 Mouse DNA	C 367	14	28.0	511	6	AX077103	AX077103 Sequence
C 295	15	30.0	208059	8	AC114192	AC114192 Rattus no	C 368	14	28.0	524	15	AY831971	AY831971 Bichhorni
C 296	15	30.0	208592	14	AC117539	AC117539 Papio ham	C 369	14	28.0	544	15	AY361215	AY361215 Sphagnum
C 297	15	30.0	211450	9	AL672090	AL672090 Mouse DNA	C 370	14	28.0	544	15	AY361215	AY361215 Sphagnum
C 298	15	30.0	214685	14	AC159060	AC159060 Bos tauru	C 371	14	28.0	544	15	AY361216	AY361216 Sphagnum
C 299	15	30.0	217013	14	AC106439	AC106439 Rattus no	C 372	14	28.0	544	15	AY361217	AY361217 Sphagnum
C 300	15	30.0	220336	14	AC156208	AC156208 Bos tauru	C 373	14	28.0	544	15	AY361218	AY361218 Sphagnum
C 301	15	30.0	220437	9	AC155824	AC155824 Mus muscu	C 374	14	28.0	544	15	AY361219	AY361219 Sphagnum
C 302	15	30.0	220748	14	AC131125	AC131125 Rattus no	C 375	14	28.0	544	15	AY361220	AY361220 Sphagnum
C 303	15	30.0	225031	9	AC132481	AC132481 Mus muscu	C 376	14	28.0	544	15	AY361221	AY361221 Sphagnum
C 304	15	30.0	225159	9	AC135086	AC135086 Mus muscu	C 377	14	28.0	556	6	AR484036	AR484036 Sequence
C 305	15	30.0	226432	14	AC134654	AC134654 Rattus no	C 378	14	28.0	566	6	AX142187	AX142187 Sequence
C 306	15	30.0	227524	14	AC129956	AC129956 Bos tauru	C 379	14	28.0	566	5	AF520596	AF520596 Bsox luci
C 307	15	30.0	228327	14	CR456625	CR456625 Dario rer	C 380	14	28.0	573	15	RG4808378	RG4808378 Ramaria g
C 308	15	30.0	228603	5	AC145942	AC145942 Gallus ga	C 381	14	28.0	594	6	AR454299	AR454299 Sequence
C 309	15	30.0	230210	14	AC164267	AC164267 Bos tauru	C 382	14	28.0	594	6	AR629504	AR629504 Sequence
C 310	15	30.0	233477	14	AC103427	AC103427 Rattus no	C 383	14	28.0	600	15	CNS01B0R	CNS01B0R Botrytis



384	14	28.0	613	10	G76572	G76572 S208P6047RH	457	14	28.0	3590	1	D85526	D85526 Clostridium
C 385	14	28.0	621	6	AR546995	AR546995 Sequence	C 458	14	28.0	3711	15	AY093202	AY093202 Arabidops
C 386	14	28.0	618	15	AB187518	AB187518 Physcomit	C 459	14	28.0	3778	1	AVIALG6A	AVIALG6A Azotobacter
C 387	14	28.0	626	10	BV395752	BV395752 S243P6119	C 460	14	28.0	3998	4	BTCNG3	BTCNG3 B. tauros CN
C 388	14	28.0	650	15	CNS01CCZ	AL115371 Botrytis	C 461	14	28.0	4159	8	C0603698	C0603698 Sequence
C 389	14	28.0	692	10	BV537261	BV537261 G591P6349	C 462	14	28.0	4601	8	AL627410	AL627410 Human DNA
C 390	14	28.0	693	6	AX505654	AX505654 Sequence	C 463	14	28.0	4967	1	AY591755	AY591755 Sulfolobu
C 391	14	28.0	705	10	BV658227	BV658227 S215P6840	C 464	14	28.0	5058	1	BTU995369	BTU995369 B. tauros
C 392	14	28.0	709	15	ATH552834	ATH552834 Arabidops	C 465	14	28.0	5119	6	C0575141	C0575141 Sequence
C 393	14	28.0	711	15	AY557678	AY557678 Saccharom	C 466	14	28.0	5224	1	AF505958	AF505958 Centibacte
C 394	14	28.0	777	6	AR397353	AR397353 Sequence	C 467	14	28.0	5386	1	AX345435	AX345435 Sequence
C 395	14	28.0	780	10	BV621315	BV621315 S217P6026	C 468	14	28.0	5441	2	AME517411	AME517411 Apis mell
C 396	14	28.0	800	15	AK061592	AK061592 Oryza sat	C 469	14	28.0	5634	6	C0585842	C0585842 Sequence
C 397	14	28.0	807	8	HSU67225	U67225 Human clone	C 470	14	28.0	5673	15	AB114052	AB114052 Arabidops
C 398	14	28.0	810	6	AR236373	AR236373 Sequence	C 471	14	28.0	5735	6	AX348453	AX348453 Sequence
C 399	14	28.0	821	15	AF095709	AF095709 Oryza sat	C 472	14	28.0	5940	15	OLU72727	OLU72727 Oryza longi
C 400	14	28.0	834	10	CNS06F7D	AL396047 T3 end of	C 473	14	28.0	6089	15	AJ622818	AJ622818 Encalypta
C 401	14	28.0	855	2	AS119221	Y19221 Antisakris si	C 474	14	28.0	6110	15	AJ622821	AJ622821 Rhacocarp
C 402	14	28.0	878	8	AF001985	AF001985 Homo sapi	C 475	14	28.0	6113	15	AJ622819	AJ622819 Ulota cri
C 403	14	28.0	883	15	BT009493	BT009493 Trifolium	C 476	14	28.0	6133	2	AY029070	AY029070 Trypanoso
C 404	14	28.0	894	10	CNS06F19	AR395827 T3 end of	C 477	14	28.0	6398	6	AX346002	AX346002 Sequence
C 405	14	28.0	912	6	AR549309	AR549309 Sequence	C 478	14	28.0	6617	13	AJ586803	AJ586803 Tobacco r
C 406	14	28.0	951	6	AR395021	AR395021 Sequence	C 479	14	28.0	6641	6	AX344595	AX344595 Sequence
C 407	14	28.0	1005	15	YSCNBP2	D43693 Yeast NBP2	C 480	14	28.0	6983	15	UFAPJ3067	UFAPJ3067 Uromyces
C 408	14	28.0	1080	6	AR377649	AR377649 Sequence	C 481	14	28.0	6988	15	AY545666	AY545666 Conyza ca
C 409	14	28.0	1086	6	AR628167	AR628167 Sequence	C 482	14	28.0	8592	5	XLHSH3A	XLHSH3A Xanthopus lae
C 410	14	28.0	1092	15	AR506964	AR506964 Oryza sat	C 483	14	28.0	8608	5	XELHX1H3	XELHX1H3 X. laevis hi
C 411	14	28.0	1100	6	AR506690	AR506690 Sequence	C 484	14	28.0	8622	8	D84294	D84294 Homo sapien
C 412	14	28.0	1149	2	AY060681	AY060681 Drosophill	C 485	14	28.0	9767	6	BD193536	BD193536 Enterococ
C 413	14	28.0	1174	5	AK058820	AK058820 Oryza sat	C 486	14	28.0	9973	1	AE004495	AE004495 Vibrio ch
C 414	14	28.0	1197	13	AY434111	AY434111 Hepatitlis	C 487	14	28.0	10029	1	AE007905	AE007905 Agrobacte
C 415	14	28.0	1253	6	AR507825	AR507825 Sequence	C 488	14	28.0	10122	4	AB042982	AB042982 Sus scrofa
C 416	14	28.0	1327	13	AB198422	AB198422 Heterosig	C 489	14	28.0	10202	6	C0573339	C0573339 Sequence
C 417	14	28.0	1487	15	BT022147	BT022147 Drosophill	C 490	14	28.0	10485	5	AB020734	AB020734 Oryzias l
C 418	14	28.0	1506	15	AY144995	AY144995 Saccharom	C 491	14	28.0	10571	2	DROZRH2	DROZRH2 Drosophilla
C 419	14	28.0	1509	8	AK026407	AK026407 Homo sapi	C 492	14	28.0	10633	1	AE008958	AE008958 Agrobacte
C 420	14	28.0	1568	2	AY060910	AY060910 Drosophill	C 493	14	28.0	11011	6	AX411375	AX411375 Sequence
C 421	14	28.0	1608	6	C0603699	C0603699 Sequence	C 494	14	28.0	11317	8	AF33285752	AF33285752 Homo sapi
C 422	14	28.0	1634	15	SCYGR230W	Z73015 S. cerevisia	C 495	14	28.0	11317	8	AE004044	AE004044 Xylella f
C 423	14	28.0	1682	15	AK109629	AK109629 Oryza sat	C 496	14	28.0	12958	1	AE010206	AE010206 Pyrococcu
C 424	14	28.0	1701	9	AB045313	AB045313 Mus muscu	C 497	14	28.0	13068	1	AE000994	AE000994 Archaeogl
C 425	14	28.0	1703	8	AB049472	AB049472 Hylobates	C 498	14	28.0	13737	1	AE011469	AE011469 Leprosplr
C 426	14	28.0	1708	9	AF312208	AF312208 Mus muscu	C 499	14	28.0	13905	13	MHVORF	X73559 MHV-A59 gen
C 427	14	28.0	1733	9	BC003215	BC003215 Mus muscu	C 500	14	28.0	14823	6	AR619692	AR619692 Sequence
C 428	14	28.0	1750	6	C0739288	C0739288 Sequence	C 501	14	28.0	15759	1	AVIALGEB	L33096 Azotobacter
C 429	14	28.0	1773	15	SCYUR115W	Z49615 S. cerevisia	C 502	14	28.0	16410	4	AP006470	AP006470 Balanopt
C 430	14	28.0	1886	15	LECHLO	XY7898 Arabidopsis	C 503	14	28.0	17577	1	AE001202	AE001202 Treponema
C 431	14	28.0	1910	8	AK130868	AK130868 Homo sapi	C 504	14	28.0	18231	15	AP000384	AP000384 Arabidops
C 432	14	28.0	2185	6	AX416592	AX416592 Sequence	C 505	14	28.0	19229	15	CR626932	CR626932 Trifolium
C 433	14	28.0	2199	8	AB056371	AB056371 Macaca fa	C 506	14	28.0	19274	15	CR626930	CR626930 Trifolium
C 434	14	28.0	2302	2	AK116655	AK116655 Clona int	C 507	14	28.0	19603	6	C0573338	C0573338 Sequence
C 435	14	28.0	2306	15	SCYUR113C	Z49615 S. cerevisia	C 508	14	28.0	20072	6	BD193495	BD193495 Enterococ
C 436	14	28.0	2311	15	AK073664	AK073664 Oryza sat	C 509	14	28.0	20225	14	AC014863	AC014863 Drosophill
C 437	14	28.0	2692	2	AK116462	AK116462 Clona int	C 510	14	28.0	22624	8	AC112708	AC112708 Homo sapi
C 438	14	28.0	2699	6	C0580697	C0580697 Sequence	C 511	14	28.0	25663	8	AF053936	AF053936 Homo sapi
C 439	14	28.0	2896	15	SCYGR228W	Z73015 S. cerevisia	C 512	14	28.0	27475	13	AY851295	AY851295 Avian inf
C 440	14	28.0	2943	6	C0585843	C0585843 Sequence	C 513	14	28.0	28645	2	U97000	U97000 Caenorhabdi
C 441	14	28.0	2965	1	AF099799	AF099799 Azotobact	C 514	14	28.0	29585	15	AC158193	AC158193 Selaginell
C 442	14	28.0	2967	1	AF269424	AF269424 Staphyloc	C 515	14	28.0	29653	15	SPAC50D11	Z67961 S. pombe chr
C 443	14	28.0	2967	6	AX4485380	AX4485380 Sequence	C 516	14	28.0	29774	1	AF193754	AF193754 Zymomonas
C 444	14	28.0	2967	6	AX144744	AX144744 Sequence	C 517	14	28.0	29912	6	CQ363719	CQ363719 Sequence
C 445	14	28.0	2997	2	AY118573	AY118573 Drosophill	C 518	14	28.0	30601	2	U39744	U39744 Caenorhabdi
C 446	14	28.0	3003	1	AF111424	AF111424 Mycoplasma	C 519	14	28.0	30841	8	AC109817	AC109817 Homo sapi
C 447	14	28.0	3090	15	BT010593	BT010593 Arabidops	C 520	14	28.0	31233	13	AF208067	AF208067 Murine he
C 448	14	28.0	3127	8	AB009298	AB009298 Homo sapi	C 521	14	28.0	31335	13	AY700211	AY700211 Murine he
C 449	14	28.0	3128	8	BC036233	BC036233 Homo sapi	C 522	14	28.0	31357	13	AF029248	AF029248 Mouse hep
C 450	14	28.0	3153	8	DO091293	DO091293 Homo sapi	C 523	14	28.0	31409	11	AY910861	AY910861 Synthetic
C 451	14	28.0	3217	6	C0582518	C0582518 Sequence	C 524	14	28.0	31934	2	U64859	U64859 Caenorhabdi
C 452	14	28.0	3285	15	YXSKPML	L337875 Kluyveromyc	C 525	14	28.0	31934	2	U64859	U64859 Caenorhabdi
C 453	14	28.0	3386	15	PYPR10GN	X96999 P. vulgaris	C 526	14	28.0	33444	14	AC014246	AC014246 Drosophill
C 454	14	28.0	3580	6	BD160173	BD160173 Primer fo	C 527	14	28.0	33479	15	AB022221	AB022221 Arabidops
C 455	14	28.0	3580	6	AX883181	AX883181 Sequence	C 528	14	28.0	34101	2	CEM110	Z49968 Caenorhabdi
C 456	14	28.0	3580	8	AK023747	AK023747 Homo sapi	C 529	14	28.0	34548	6	AX349035	AX349035 Sequence



C 530	14	28.0	34923	2	U40945	U40945 Caenorhabdi	603	14	28.0	91979	15	AC002510	AC002510 Arabidops
C 531	14	28.0	35358	14	AC015115	AC015115 Drosophi1	C 604	14	28.0	92921	14	AP003823	AP003823 Oryza sat
C 532	14	28.0	36699	6	AR643126	AR643126 Sequence	C 605	14	28.0	97323	14	AC161645	AC161645 Bos tauru
C 533	14	28.0	37064	5	BX27350	BX27350 Zebrafish	C 606	14	28.0	98770	8	HS36411	HS36411 Human DNA
C 534	14	28.0	37221	14	AC013974	AC013974 Drosophi1	C 607	14	28.0	100294	15	AP003840	AP003840 Oryza sat
C 535	14	28.0	37716	6	CQ363765	CQ363765 Sequence	C 608	14	28.0	101568	14	AC154036	AC154036 Medicago
C 536	14	28.0	39461	15	AC152115	AC152115 Pichia st	C 609	14	28.0	102151	14	AP007814	AP007814 Lotus cor
C 537	14	28.0	39649	2	U41541	U41541 Caenorhabdi	C 610	14	28.0	102495	8	AC010100	AC010100 Homo sapi
C 538	14	28.0	39920	14	AC020334	AC020334 Drosophi1	C 611	14	28.0	102517	14	AP002876	AP002876 Homo sapi
C 539	14	28.0	40679	8	AC002052	AC002052 Homo sapi	C 612	14	28.0	102824	15	AP003864	AP003864 Oryza sat
C 540	14	28.0	40970	2	LMFLJUNK03	LMFLJUNK03 Leishmani	C 613	14	28.0	103229	14	AC166127	AC166127 Bos tauru
C 541	14	28.0	43118	15	SCDNAGENS	SCDNAGENS X87994 S. cerevisia	C 614	14	28.0	103550	14	AP004003	AP004003 Oryza sat
C 542	14	28.0	43468	15	SC8358	SC8358 S. cerevisia	C 615	14	28.0	103679	2	AL137005	AL137005 Human DNA
C 543	14	28.0	45410	2	U61947	U61947 Caenorhabdi	C 616	14	28.0	103809	8	AC018478	AC018478 Drosophi1
C 544	14	28.0	49961	14	AP008171	AP008171 Lotus cor	C 617	14	28.0	104071	14	AP007994	AP007994 Lotus cor
C 545	14	28.0	51059	8	AL139417	AL139417 Human DNA	C 618	14	28.0	104170	14	AC091510	AC091510 Leishmani
C 546	14	28.0	51962	8	AL1355492	AL1355492 Human DNA	C 619	14	28.0	104485	8	AC069439	AC069439 Homo sapi
C 547	14	28.0	53198	5	AC149152	AC149152 Xenopus t	C 620	14	28.0	106494	14	BX537124_3	BX537124_3
C 548	14	28.0	55038	14	AC015270	AC015270 Drosophi1	C 621	14	28.0	107403	14	AC144395	AC144395 Rattus no
C 549	14	28.0	59113	14	AC136784	AC136784 Homo sapi	C 622	14	28.0	107408	14	AP007617	AP007617 Lotus cor
C 550	14	28.0	60066	15	T1F15	AC004393 Arabidops	C 623	14	28.0	108623	8	AC012380	AC012380 Genomic S
C 551	14	28.0	60190	14	AC127498	AC127498 Homo sapi	C 624	14	28.0	108976	5	AC008604	AC008604 Homo sapi
C 552	14	28.0	60391	2	AC024796	AC024796 Caenorhab	C 625	14	28.0	108982	5	CR376728	CR376728 Zebrafish
C 553	14	28.0	61985	3	AY744396	AY744396 Unculture	C 626	14	28.0	109375	15	AC003672	AC003672 Arabidops
C 554	14	28.0	62357	14	AC158001	AC158001 Bos tauru	C 627	14	28.0	110000	1	AE005674_44	AE005674_44
C 555	14	28.0	62442	5	AC092089	AC092089 Dario rer	C 628	14	28.0	110000	1	CR848038_03	CR848038_03
C 556	14	28.0	63659	14	AP008149	AP008149 Lotus cor	C 629	14	28.0	110000	1	AE008692_09	AE008692_09
C 557	14	28.0	64365	14	AC009089	AC009089 Homo sapi	C 630	14	28.0	110000	1	AE016853_00	AE016853_00
C 558	14	28.0	65143	14	AL672261_3	Continuation (4 of	C 631	14	28.0	110000	1	AE016853_54	AE016853_54
C 559	14	28.0	65426	14	AC121449_3	Continuation (4 of	C 632	14	28.0	110000	1	AE017283_10	AE017283_10
C 560	14	28.0	65982	14	CT009603	Continuation (4 of	C 633	14	28.0	110000	1	AE017283_17	AE017283_17
C 561	14	28.0	66265	2	AC129948	AC129948 Branchios	C 634	14	28.0	110000	1	AP006878_11	AP006878_11
C 562	14	28.0	66993	15	AP008218_275	Continuation (276	C 635	14	28.0	110000	1	BA000012_50	BA000012_50
C 563	14	28.0	67270	8	AC083822	AC083822 Homo sapi	C 636	14	28.0	110000	1	BA000012_51	BA000012_51
C 564	14	28.0	68430	8	AC087215	AC087215 Papio ano	C 637	14	28.0	110000	1	BA000013_1	BA000013_1
C 565	14	28.0	71090	14	AC105097	AC105097 Homo sapi	C 638	14	28.0	110000	1	BA000013_2	BA000013_2
C 566	14	28.0	71201	14	BX321914	BX321914 Dario rer	C 639	14	28.0	110000	1	BA000013_25	BA000013_25
C 567	14	28.0	71462	2	AC087231	AC087231 Caenorhab	C 640	14	28.0	110000	1	BA000031_30	BA000031_30
C 568	14	28.0	73180	1	CP000083_53	Continuation (54 o	C 641	14	28.0	110000	1	BA000040_25	BA000040_25
C 569	14	28.0	73874	1	BHR56197	Continuation (54 o	C 642	14	28.0	110000	1	CP000029_00	CP000029_00
C 570	14	28.0	75815	6	CS086068	CS086068 Sequence	C 643	14	28.0	110000	1	CP000058_02	CP000058_02
C 571	14	28.0	76513	15	AE016820_14	Continuation (15 o	C 644	14	28.0	110000	1	CP000058_50	CP000058_50
C 572	14	28.0	76860	14	AC091631	Continuation (15 o	C 645	14	28.0	110000	1	CP000058_53	CP000058_53
C 573	14	28.0	77872	6	CS086076	CS086076 Sequence	C 646	14	28.0	110000	1	CP000075_51	CP000075_51
C 574	14	28.0	78611	15	CNS09SC0	BX664710 Oryza sat	C 647	14	28.0	110000	1	CP000075_55	CP000075_55
C 575	14	28.0	79459	15	AB022217	AB022217 Arabidops	C 648	14	28.0	110000	1	CP000076_61	CP000076_61
C 576	14	28.0	79490	14	AC165642	AC165642 Bos tauru	C 649	14	28.0	110000	1	CP000076_62	CP000076_62
C 577	14	28.0	81806	15	AB062087	AB062087 Arabidops	C 650	14	28.0	110000	1	CP000082_00	CP000082_00
C 578	14	28.0	83270	8	AL1354879	AL1354879 Human DNA	C 651	14	28.0	110000	1	CP000082_01	CP000082_01
C 579	14	28.0	83751	14	CR954209_6	Continuation (7 of	C 652	14	28.0	110000	1	CP000083_25	CP000083_25
C 580	14	28.0	83857	15	AP004012	AP004012 Oryza sat	C 653	14	28.0	110000	2	CP000084_43	CP000084_43
C 581	14	28.0	83865	15	AB006700	AB006700 Arabidops	C 654	14	28.0	110000	1	CP000081_11	CP000081_11
C 582	14	28.0	84034	9	AC006943	AC006943 Mus muscu	C 655	14	28.0	110000	14	AC096079_3	AC096079_3
C 583	14	28.0	84478	8	AL133462	AL133462 Human DNA	C 656	14	28.0	110000	14	AC102394_0	AC102394_0
C 584	14	28.0	86057	14	AC136464	AC136464 Rattus no	C 657	14	28.0	110000	14	AC111335_1	AC111335_1
C 585	14	28.0	86065	15	AB005243	AB005243 Arabidops	C 658	14	28.0	110000	14	AC111624_0	AC111624_0
C 586	14	28.0	86446	5	CR354371	CR354371 Zebrafish	C 659	14	28.0	110000	14	AC123241_2	AC123241_2
C 587	14	28.0	86498	14	AP007955	AP007955 Lotus cor	C 660	14	28.0	110000	14	AC156265_12	AC156265_12
C 588	14	28.0	86699	15	AB009050	AB009050 Arabidops	C 661	14	28.0	110000	14	AP006484_0	AP006484_0
C 589	14	28.0	87325	8	AC108933	AC108933 Homo sapi	C 662	14	28.0	110000	14	AP006495_4	AP006495_4
C 590	14	28.0	87470	14	AP007857	AP007857 Lotus cor	C 663	14	28.0	110000	14	BX537124_0	BX537124_0
C 591	14	28.0	88655	8	AC079135	AC079135 Homo sapi	C 664	14	28.0	110000	14	BX901880_1	BX901880_1
C 592	14	28.0	88838	8	DO144993	DO144993 Homo sapi	C 665	14	28.0	110000	14	CR954199_00	CR954199_00
C 593	14	28.0	89758	15	AC149805	AC149805 Medicago	C 666	14	28.0	110000	14	CT005253_2	CT005253_2
C 594	14	28.0	89767	5	BX908721	BX908721 Zebrafish	C 667	14	28.0	110000	14	CT005253_3	CT005253_3
C 595	14	28.0	90082	5	BX294102	BX294102 Zebrafish	C 668	14	28.0	110000	14	CT005270_09	CT005270_09
C 596	14	28.0	90113	8	AY682080	AY682080 Homo sapi	C 669	14	28.0	110000	14	CT005271_04	CT005271_04
C 597	14	28.0	90802	5	BX510955	BX510955 Zebrafish	C 670	14	28.0	110000	14	CT005271_13	CT005271_13
C 598	14	28.0	90802	1	AE016752	AE016752 Staphyloc	C 671	14	28.0	110000	14	LMFLCHR16_00	LMFLCHR16_00
C 599	14	28.0	91001	15	AC013453	AC013453 Arabidops	C 672	14	28.0	110000	14	LMFLCHR32_17	LMFLCHR32_17
C 600	14	28.0	91151	14	AP007835	AP007835 Lotus cor	C 673	14	28.0	110000	14	LMFLCHR32_21	LMFLCHR32_21
C 601	14	28.0	91356	9	AL732462	AL732462 Mouse DNA	C 674	14	28.0	110000	14	LMFLCHR32_22	LMFLCHR32_22
C 602	14	28.0	91529	15	AC011020	AC011020 Arabidops	C 675	14	28.0	110000	14	Continuation (23 o	Continuation (23 o



C 676	14	28.0	110000	14	TANN1.19	Continuation (20 o	C 749	14	28.0	112830	14	AC151678	AC151678 Gallus ga
C 677	14	28.0	110000	15	AP008214_049	Continuation (50 o	750	14	28.0	113187	15	AP005721	AP005721 Oryza sat
C 678	14	28.0	110000	15	AP008214_150	Continuation (151	751	14	28.0	113325	15	AP003999	AP003999 Oryza sat
C 679	14	28.0	110000	15	AP008214_154	Continuation (155	C 752	14	28.0	114534	14	AP008116	AP008116 Lotus cor
C 680	14	28.0	110000	15	AP008214_160	Continuation (161	753	14	28.0	114549	14	AP007642	AP007642 Lotus cor
C 681	14	28.0	110000	15	AP008214_174	Continuation (175	754	14	28.0	114577	14	AP005318	AP005318 Oryza sat
C 682	14	28.0	110000	15	AP008215_002	Continuation (3 o f	C 755	14	28.0	115136	8	AL390994	AL390994 Human DNA
C 683	14	28.0	110000	15	AP008215_062	Continuation (63 o	C 756	14	28.0	117176	14	AP008103	AP008103 Oryza sat
C 684	14	28.0	110000	15	AP008215_173	Continuation (174	C 757	14	28.0	117443	15	OSJN00211	OSJN00211 Oryza sat
C 685	14	28.0	110000	15	AP008215_184	Continuation (185	758	14	28.0	117676	14	AP006427	AP006427 Lotus cor
C 686	14	28.0	110000	15	AP008215_205	Continuation (206	759	14	28.0	119151	14	CR936399	CR936399 Danio rer
C 687	14	28.0	110000	15	AP008216_003	Continuation (4 o f	760	14	28.0	121056	15	OSJN00204	OSJN00204 Oryza sat
C 688	14	28.0	110000	15	AP008216_004	Continuation (5 o f	C 761	14	28.0	121590	8	HS314N7	HS314N7 Oryza sat
C 689	14	28.0	110000	15	AP008216_017	Continuation (18 o	762	14	28.0	122313	14	AC091688	AC091688 Oryza sat
C 690	14	28.0	110000	15	AP008216_052	Continuation (53 o	763	14	28.0	122916	5	CR388065	CR388065 zebrafish
C 691	14	28.0	110000	15	AP008216_187	Continuation (188	C 764	14	28.0	123078	15	AP004902	AP004902 Lotus cor
C 692	14	28.0	110000	15	AP008217_126	Continuation (127	C 765	14	28.0	123109	14	AC007149	AC007149 Drosophila
C 693	14	28.0	110000	15	AP008217_172	Continuation (173	C 766	14	28.0	124028	15	AP005567	AP005567 Oryza sat
C 694	14	28.0	110000	15	AP008217_199	Continuation (200	767	14	28.0	124374	14	CR974440	CR974440 Danio rer
C 695	14	28.0	110000	15	AP008217_244	Continuation (245	C 768	14	28.0	125331	8	DQ015703	DQ015703 Homo sapi
C 696	14	28.0	110000	15	AP008218_120	Continuation (121	C 769	14	28.0	125350	14	AC020768	AC020768 Homo sapi
C 697	14	28.0	110000	15	AP008218_241	Continuation (242	770	14	28.0	125844	14	AC143699	AC143699 Macaca mu
C 698	14	28.0	110000	15	CR380955_02	Continuation (3 o f	771	14	28.0	126546	14	AC153334	AC153334 Loxodonta
C 699	14	28.0	110000	15	CR380955_08	Continuation (9 o f	772	14	28.0	127068	15	AC091238	AC091238 Oryza sat
C 700	14	28.0	110000	15	CR380958_07	Continuation (8 o f	773	14	28.0	127089	15	AP004165	AP004165 Oryza sat
C 701	14	28.0	110000	15	CR380959_11	Continuation (12 o	774	14	28.0	128493	15	AC135918	AC135918 Homo sapi
C 702	14	28.0	110000	15	CR380959_12	Continuation (13 o	775	14	28.0	128817	8	AC010731	AC010731 Homo sapi
C 703	14	28.0	110000	15	CR382121_07	Continuation (8 o f	C 776	14	28.0	128950	8	AP006271	AP006271 Pan trogl
C 704	14	28.0	110000	15	CR382128_09	Continuation (10 o	C 777	14	28.0	129950	15	AC078840	AC078840 Oryza sat
C 705	14	28.0	110000	15	CR382128_13	Continuation (14 o	C 778	14	28.0	130058	15	AC134347	AC134347 Oryza sat
C 706	14	28.0	110000	15	CR382130_21	Continuation (22 o	779	14	28.0	130735	8	AC093505	AC093505 Homo sapi
C 707	14	28.0	110000	15	CR382132_16	Continuation (17 o	780	14	28.0	131489	14	AC091689	AC091689 Oryza sat
C 708	14	28.0	110000	15	AC145127_03	Continuation (4 o f	781	14	28.0	131519	5	BY927112	BY927112 zebrafish
C 709	14	28.0	110000	15	AC145127_04	Continuation (5 o f	782	14	28.0	131708	15	AC134232	AC134232 Oryza sat
C 710	14	28.0	110000	15	AC145127_17	Continuation (18 o	783	14	28.0	131883	15	AC134232	AC134232 Oryza sat
C 711	14	28.0	110000	15	AE016817_02	Continuation (3 o f	C 784	14	28.0	131972	15	AP004742	AP004742 Oryza sat
C 712	14	28.0	110000	15	AE017343_03	Continuation (4 o f	785	14	28.0	132337	8	AC006917	AC006917 Homo sapi
C 713	14	28.0	110000	15	AE017344_07	Continuation (8 o f	C 786	14	28.0	132699	15	AC006917	AC006917 Homo sapi
C 714	14	28.0	110000	15	AP008207_194	Continuation (195	C 787	14	28.0	132718	8	AC107908	AC107908 Homo sapi
C 715	14	28.0	110000	15	AP008207_240	Continuation (241	788	14	28.0	132733	15	CNS08C44	CNS08C44 Oryza sat
C 716	14	28.0	110000	15	AP008208_022	Continuation (23 o	C 789	14	28.0	132894	15	AC141323	AC141323 Oryza sat
C 717	14	28.0	110000	15	AP008208_107	Continuation (108	790	14	28.0	132933	14	AC152154	AC152154 Oryza sat
C 718	14	28.0	110000	15	AP008208_156	Continuation (157	791	14	28.0	132987	15	AC090874	AC090874 Oryza sat
C 719	14	28.0	110000	15	AP008208_223	Continuation (224	C 792	14	28.0	133121	15	AC092553	AC092553 Oryza sat
C 720	14	28.0	110000	15	AP008208_295	Continuation (296	793	14	28.0	133127	14	CR392338	CR392338 Danio rer
C 721	14	28.0	110000	15	AP008208_304	Continuation (305	794	14	28.0	133381	9	AC109308	AC109308 Mus muscu
C 722	14	28.0	110000	15	AP008209_084	Continuation (85 o	C 795	14	28.0	133765	8	H657E13	H657E13 Human DNA
C 723	14	28.0	110000	15	AP008209_097	Continuation (98 o	796	14	28.0	133968	5	BS11174	BS11174 zebrafish
C 724	14	28.0	110000	15	AP008209_101	Continuation (102	797	14	28.0	134540	14	AC090898	AC090898 Homo sapi
C 725	14	28.0	110000	15	AP008209_102	Continuation (103	C 798	14	28.0	134556	15	AC151526	AC151526 Medicago
C 726	14	28.0	110000	15	AP008209_104	Continuation (105	799	14	28.0	134804	15	AP004888	AP004888 Oryza sat
C 727	14	28.0	110000	15	AP008209_221	Continuation (222	C 800	14	28.0	134844	14	AC142020	AC142020 Rattus no
C 728	14	28.0	110000	15	AP008209_350	Continuation (351	C 801	14	28.0	135011	14	CR381579	CR381579 Danio rer
C 729	14	28.0	110000	15	AP008210_114	Continuation (115	C 802	14	28.0	135425	15	AC104846	AC104846 Oryza sat
C 730	14	28.0	110000	15	AP008210_186	Continuation (187	C 803	14	28.0	137071	14	CNS08CE3	CNS08CE3 Oryza sat
C 731	14	28.0	110000	15	AP008210_245	Continuation (246	C 804	14	28.0	137956	14	AC010918	AC010918 Drosophila
C 732	14	28.0	110000	15	AP008210_261	Continuation (262	C 805	14	28.0	138005	14	AC113908	AC113908 Rattus no
C 733	14	28.0	110000	15	AP008210_266	Continuation (267	806	14	28.0	138048	14	AC113575	AC113575 Tetradon
C 734	14	28.0	110000	15	AP008211_064	Continuation (65 o	807	14	28.0	138607	8	AL161650	AL161650 Human DNA
C 735	14	28.0	110000	15	AP008212_060	Continuation (61 o	C 808	14	28.0	139076	14	AC004147	AC004147 Homo sapi
C 736	14	28.0	110000	15	AP008212_090	Continuation (91 o	C 809	14	28.0	139201	8	CR788316	CR788316 Danio rer
C 737	14	28.0	110000	15	AP008212_104	Continuation (105	C 810	14	28.0	139357	15	AC010907	AC010907 Homo sapi
C 738	14	28.0	110000	15	AP008212_162	Continuation (163	C 811	14	28.0	139693	8	AP004465	AP004465 Oryza sat
C 739	14	28.0	110000	15	AP008212_163	Continuation (164	C 812	14	28.0	139714	15	AC137931	AC137931 Oryza sat
C 740	14	28.0	110000	15	AP008213_152	Continuation (164	C 813	14	28.0	139814	14	AP003964	AP003964 Oryza sat
C 741	14	28.0	110000	15	AP008213_184	Continuation (185	C 814	14	28.0	139922	14	BX901877	BX901877 Danio rer
C 742	14	28.0	110000	15	AP008213_240	Continuation (241	C 815	14	28.0	139961	15	AP004668	AP004668 Oryza sat
C 743	14	28.0	110000	15	AP008213_244	Continuation (245	816	14	28.0	140063	14	CR812464	CR812464 Danio rer
C 744	14	28.0	110275	9	AL6653028	Continuation (245	C 817	14	28.0	140063	15	AP005314	AP005314 Oryza sat
C 745	14	28.0	110603	8	HSJ421D16	Continuation (245	C 818	14	28.0	140106	14	AC156771	AC156771 Rhinolph
C 746	14	28.0	110758	15	AC147774	Continuation (245	C 819	14	28.0	140200	15	AP005562	AP005562 Oryza sat
C 747	14	28.0	111202	15	AP003750	Continuation (245	C 820	14	28.0	140513	15	AP007253	AP007253 Oryza sat
C 748	14	28.0	111517	15	ATP11C18	Continuation (245	C 821	14	28.0	140774	5	CR381657	CR381657 zebrafish



C 822	14	28.0	140863	15	AP004375	AP004375 Oryza sat	C 895	14	28.0	154082	14	AC108756	AC108756 Oryza sat
C 823	14	28.0	140962	14	CR387991	Danio rer	C 896	14	28.0	154104	14	AC129073	AC129073 Felis cat
C 824	14	28.0	140992	15	AP005891	Oryza sat	C 897	14	28.0	154291	2	AC159450	AC159450 Trypanoso
C 825	14	28.0	141017	15	AC037197	Oryza sat	C 898	14	28.0	154478	15	AP000423	AP000423 Arabidops
C 826	14	28.0	141034	9	AC140379	Mus muscu	C 899	14	28.0	154682	8	AL159158	AL159158 Human DNA
C 827	14	28.0	141041	14	AC026135	AC026135 Homo sapi	C 900	14	28.0	155288	5	CR749167	CR749167 Zebrafish
C 828	14	28.0	141466	9	AC144817	Mus muscu	C 901	14	28.0	155879	14	AC147926	AC147926 Rattus no
C 829	14	28.0	141497	8	AC005410	Homo sapi	C 902	14	28.0	156023	15	AC092173	AC092173 Oryza sat
C 830	14	28.0	141741	8	AC090329	Homo sapi	C 903	14	28.0	156180	8	AC007428	AC007428 Homo sapi
C 831	14	28.0	141984	15	P9L1	AC079591 Arabidops	C 904	14	28.0	156265	8	AC079140	AC079140 Homo sapi
C 832	14	28.0	142203	14	AC079521	Mus muscu	C 905	14	28.0	156408	14	AL772286	AL772286 Homo sapi
C 833	14	28.0	142289	14	AC135222	AC135222 Felis cat	C 906	14	28.0	156592	5	AL935181	AL935181 Zebrafish
C 834	14	28.0	142574	14	CR848838	CR848838 Danio rer	C 907	14	28.0	156989	15	AP006161	AP006161 Oryza sat
C 835	14	28.0	142805	8	AL592525	Human DNA	C 908	14	28.0	157081	8	AL139186	AL139186 Human DNA
C 836	14	28.0	142874	14	AC129075	AC129075 Felis cat	C 909	14	28.0	157289	5	AL9321912	AL9321912 Zebrafish
C 837	14	28.0	143049	14	CR536606	CR536606 Homo sapi	C 910	14	28.0	157546	8	AL953854	AL953854 Human DNA
C 838	14	28.0	143993	14	AC162879	AC162879 Mus muscu	C 911	14	28.0	157962	15	AC150202	AC150202 Oryza sat
C 839	14	28.0	144557	14	AP004631	AP004631 Oryza sat	C 912	14	28.0	157662	8	AL139035	AL139035 Human DNA
C 840	14	28.0	144954	15	AP005425	AP005425 Oryza sat	C 913	14	28.0	157691	5	AL935143	AL935143 Zebrafish
C 841	14	28.0	145055	2	AC007453	AC007453 Drosophil	C 914	14	28.0	157807	8	AC073573	AC073573 Homo sapi
C 842	14	28.0	145104	15	AC125495	AC125495 Oryza sat	C 915	14	28.0	157823	14	CR450770	CR450770 Danio rer
C 843	14	28.0	1451722	14	AC152483	AC152483 Daerypus n	C 916	14	28.0	157966	14	AC141732	AC141732 Apis mell
C 844	14	28.0	146010	8	AC009289	AC009289 Homo sapi	C 917	14	28.0	157991	9	RM187K23	RM187K23 Rattus no
C 845	14	28.0	146110	14	AC148742	AC148742 Macropus	C 918	14	28.0	158040	14	AC127476	AC127476 Felis cat
C 846	14	28.0	146313	15	OSJN00261	AL731617 Oryza sat	C 919	14	28.0	158118	15	AP005440	AP005440 Oryza sat
C 847	14	28.0	146539	15	AC136009	AC136009 Oryza sat	C 920	14	28.0	158641	14	AC159604	AC159604 Rhinoloph
C 848	14	28.0	146551	15	AP004621	AP004621 Oryza sat	C 921	14	28.0	158660	14	AC068425	AC068425 Mus muscu
C 849	14	28.0	146936	14	AP005010	AP005010 Oryza sat	C 922	14	28.0	158925	14	CT009606	CT009606 Danio rer
C 850	14	28.0	147207	14	AC078890	AC078890 Oryza sat	C 923	14	28.0	159413	14	AC155128	AC155128 Bos tauru
C 851	14	28.0	147826	8	AP001328	AP001328 Homo sapi	C 924	14	28.0	159448	14	AC025141	AC025141 Homo sapi
C 852	14	28.0	147869	5	BX649329	BX649329 Chicken D	C 925	14	28.0	159656	5	AL929243	AL929243 Zebrafish
C 853	14	28.0	147890	15	AP004395	AP004395 Oryza sat	C 926	14	28.0	159901	14	AP004226	AP004226 Oryza sat
C 854	14	28.0	148041	14	AC021320	AC021320 Homo sapi	C 927	14	28.0	160038	14	CR790381	CR790381 Danio rer
C 855	14	28.0	148065	8	AC026414	AC026414 Homo sapi	C 928	14	28.0	160095	8	AC087798	AC087798 Homo sapi
C 856	14	28.0	148111	14	CR762412	CR762412 Danio rer	C 929	14	28.0	160456	15	OSJN00176	AL662977 Oryza sat
C 857	14	28.0	148115	14	AC125498	AC125498 Danio rer	C 930	14	28.0	160521	14	AC127728	AC127728 Rattus no
C 858	14	28.0	148130	8	AC092925	AC092925 Homo sapi	C 931	14	28.0	160541	15	AP005751	AP005751 Oryza sat
C 859	14	28.0	148191	15	OSJN00067	AL606602 Oryza sat	C 932	14	28.0	160736	5	BX530031	BX530031 Zebrafish
C 860	14	28.0	148464	2	AC159435	AC159435 Trypanoso	C 933	14	28.0	160850	8	AC130184	AC130184 Macaca mu
C 861	14	28.0	148508	15	AP004645	AP004645 Oryza sat	C 934	14	28.0	160920	15	AC137072	AC137072 Genomic s
C 862	14	28.0	148654	15	AC146938	AC146938 Oryza sat	C 935	14	28.0	161272	14	AC119528	AC119528 Rattus no
C 863	14	28.0	148678	5	AL929281	AL929281 Zebrafish	C 936	14	28.0	161252	14	AC127992	AC127992 Rattus no
C 864	14	28.0	148781	8	AC007114	AC007114 Homo sapi	C 937	14	28.0	162471	14	CR936281	CR936281 Danio rer
C 865	14	28.0	148811	14	AC025567	AC025567 Homo sapi	C 938	14	28.0	162561	9	AC155945	AC155945 Mus muscu
C 866	14	28.0	148845	8	AP001067	AP001067 Homo sapi	C 939	14	28.0	162685	14	AC022943	AC022943 Homo sapi
C 867	14	28.0	148864	14	CR788286	CR788286 Danio rer	C 940	14	28.0	162784	15	AP006860	AP006860 Oryza sat
C 868	14	28.0	149011	15	AP004646	AP004646 Oryza sat	C 941	14	28.0	162785	5	AL845295	AL845295 Zebrafish
C 869	14	28.0	149085	14	AC123364	AC123364 Rattus no	C 942	14	28.0	162977	14	CR385071	CR385071 Danio rer
C 870	14	28.0	149319	5	AL929010	AL929010 Zebrafish	C 943	14	28.0	163109	5	BX901980	BX901980 Zebrafish
C 871	14	28.0	149986	8	AC069256	AC069256 Homo sapi	C 944	14	28.0	163419	5	BX323847	BX323847 Zebrafish
C 872	14	28.0	150109	9	AC132334	AC132334 Mus muscu	C 945	14	28.0	163672	9	AC084256	AC084256 Homo sapi
C 873	14	28.0	150375	9	AC124404	AC124404 Mus muscu	C 946	14	28.0	163719	14	AC116693	AC116693 Mus muscu
C 874	14	28.0	150601	2	AC159454	AC159454 Trypanoso	C 947	14	28.0	164026	8	CR788268	CR788268 Human DNA
C 875	14	28.0	150662	14	AC138550	AC138550 Danio rer	C 948	14	28.0	164159	14	AC100853	AC100853 Homo sapi
C 876	14	28.0	150902	14	AC018391	AC018391 Homo sapi	C 949	14	28.0	164179	8	AC116901	AC116901 Homo sapi
C 877	14	28.0	151071	15	AP003449	AP003449 Oryza sat	C 950	14	28.0	164435	14	AC153073	AC153073 Cercopitl
C 878	14	28.0	151133	8	AC013355	AC013355 Homo sapi	C 951	14	28.0	164654	14	AC009545	AC009545 Homo sapi
C 879	14	28.0	151359	15	AC025098	AC025098 Oryza sat	C 952	14	28.0	164711	14	CT010455	CT010455 Mus muscu
C 880	14	28.0	151685	15	AP005818	AP005818 Oryza sat	C 953	14	28.0	164839	15	AP002844	AP002844 Oryza sat
C 881	14	28.0	152081	5	AL929131	AL929131 Zebrafish	C 954	14	28.0	164928	8	AC087752	AC087752 Homo sapi
C 882	14	28.0	152130	8	AC104574	AC104574 Homo sapi	C 955	14	28.0	164974	14	AC019082	AC019082 Homo sapi
C 883	14	28.0	152185	2	AC159448	AC159448 Trypanoso	C 956	14	28.0	165129	8	AP003552	AP003552 Homo sapi
C 884	14	28.0	152593	14	AC156750	AC156750 Otlemur	C 957	14	28.0	165655	8	AL136962	AL136962 Human DNA
C 885	14	28.0	152734	14	CR762429	CR762429 Danio rer	C 958	14	28.0	165766	15	AP004706	AP004706 Oryza sat
C 886	14	28.0	152824	8	AC107072	AC107072 Homo sapi	C 959	14	28.0	165774	5	AL845507	AL845507 Homo sapi
C 887	14	28.0	153308	15	AC118668	AC118668 Genomic s	C 960	14	28.0	166074	8	AL935106	AL935106 Callithri
C 888	14	28.0	153351	15	AC108761	AC108761 Oryza sat	C 961	14	28.0	166118	14	AC151016	AC151016 Zebrafish
C 889	14	28.0	153361	14	AC148606	AC148606 Galectost	C 962	14	28.0	166320	5	BX005069	BX005069 Zebrafish
C 890	14	28.0	153426	9	AC121949	AC121949 Mus muscu	C 963	14	28.0	166417	9	AC134792	AC134792 Mus muscu
C 891	14	28.0	153897	5	AL928656	AL928656 Zebrafish	C 964	14	28.0	166486	9	AC131115	AC131115 Mus muscu
C 892	14	28.0	153929	15	AP004266	AP004266 Oryza sat	C 965	14	28.0	167258	14	AP004766	AP004766 Oryza sat
C 893	14	28.0	154028	8	AL136529	AL136529 Human DNA	C 966	14	28.0	167403	14	AC015686	AC015686 Homo sapi
C 894	14	28.0	154037	8	AP000782	AP000782 Homo sapi	C 967	14	28.0	167534	9	AC155725	AC155725 Mus muscu



968	14	28.0	167582	5	BX294387	BX294387 Zebrafish
969	14	28.0	167757	14	CR792425	CR792425 Dario rer
C 970	14	28.0	168030	14	AC110663	AC110663 Bos taurus
C 971	14	28.0	168098	5	BX323583	BX323583 Zebrafish
C 972	14	28.0	168177	8	AC092597	AC092597 Homo sapi
C 973	14	28.0	168302	8	AP005639	AP005639 Homo sapi
C 974	14	28.0	168396	14	AC162603	AC162603 Bos taurus
C 975	14	28.0	168638	14	CR548631	CR548631 Dario rer
C 976	14	28.0	169092	14	AC027572	AC027572 Homo sapi
C 977	14	28.0	169147	8	AC007238	AC007238 Homo sapi
C 978	14	28.0	169378	15	AP004001	AP004001 Oryza sat
C 979	14	28.0	169465	8	HSU96409	HSU96409 Human Xp22
C 980	14	28.0	169573	9	AC099637	AC099637 Mus muscu
C 981	14	28.0	169823	15	AP006061	AP006061 Oryza sat
C 982	14	28.0	169841	15	BX511216	BX511216 Zebrafish
C 983	14	28.0	170099	14	AC092459	AC092459 Homo sapi
C 984	14	28.0	170535	9	HS158K17	HS158K17 Homo sapi
C 985	14	28.0	170708	9	AL607125	AL607125 Mouse DNA
C 986	14	28.0	170908	14	CR848844	CR848844 Dario rer
C 987	14	28.0	170961	14	AC112202	AC112202 Homo sapi
C 988	14	28.0	171084	14	CR847866	CR847866 Dario rer
C 989	14	28.0	171110	14	AC119699	AC119699 Rattus no
C 990	14	28.0	171286	2	AC008226	AC008226 Drosophila
C 991	14	28.0	171376	15	AC104487	AC104487 Oryza sat
C 992	14	28.0	171438	5	BX901918	BX901918 Zebrafish
C 993	14	28.0	171572	14	CR847514	CR847514 Dario rer
C 994	14	28.0	171647	14	BX927406	BX927406 Mus muscu
C 995	14	28.0	171728	9	AC103620	AC103620 Mus muscu
C 996	14	28.0	171751	2	AC023697	AC023697 Drosophila
C 997	14	28.0	172190	2	AC010668	AC010668 Drosophila
C 998	14	28.0	172587	5	BX005125	BX005125 Zebrafish
C 999	14	28.0	172954	5	AL929152	AL929152 Zebrafish
C 1000	14	28.0	173058	14	AC159957	AC159957 Rhinophora

ALIGNMENTS

RESULT 1  
LOCUS AB125961 721 bp DNA linear BCT 02-APR-2004  
DEFINITION Bacillus anthracis plasmid pXOI pagA gene, partial cde.  
ACCESSION AB125961  
VERSION AB125961.1 GI:46093482  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
REFERENCE 1 Inoue, S., Noguchi, A., Tanabayashi, K. and Yamada, A.  
AUTHORS Inoue, S., and Noguchi, A.  
TITLE Preparation of a positive control DNA for molecular diagnosis of  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 721)  
AUTHORS Inoue, S., and Noguchi, A.  
TITLE Direct Submission  
JOURNAL Submitted (06-NOV-2003) Satochi Inoue, National Institute of  
Infectious Diseases, Laboratory of Transmission Control of  
Zoonosis, Department of Veterinary Science, 1-23-1 Toyama,  
Shinjuku-ku, Tokyo 162-8640, Japan (E-mail: sinoue@nih.go.jp,  
Tel:81-3-5285-1111 (ex.2620), Fax:81-3-5285-1179)  
FEATURES  
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/db\_xref="taxon:1392"  
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extension PCR"  
complement(1..721)

gene

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/db\_xref="gi:46093483"  
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IHEKKGLTKYSSPEKSTADPSDEPKYGRIDKNVSPARPIVAAYIVADIE  
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VLGNQTLATIKAKENQLSQTL"

Query Match 100.0%; Score 50; DB 1; Length 721;  
Beet Local Similarity 100.0%; Pred. No. 1.7e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 2  
LOCUS AX353777 954 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 8 from Patent WO0204646.  
ACCESSION AX353777  
VERSION AX353777.1 GI:18618828  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Williamson, E.D., Miller, J., Walker, N.J., Ballile, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 8 17-JAN-2002;  
The Secretary of State for Defense (GB)  
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source  
1..954  
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ORIGIN  
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Beet Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCGGCTCCATCTACACGCTTTACCAAGCACTTGTTAGTTAGG 50  
DB 601 GGAGCGGCTCCATCTACACGCTTTACCAAGCACTTGTTAGTTAGG 650  
RESULT 3  
LOCUS AX353779 1278 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 10 from Patent WO0204646.  
ACCESSION AX353779  
VERSION AX353779.1 GI:18618829  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Williamson, E.D., Miller, J., Walker, N.J., Ballile, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifent, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 10 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
Location/Qualifiers  
1  
synthetic construct  
synthetic construct  
other sequences; artificial sequences.



source 1..1278  
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ORIGIN

Query Match 100.0%; Score 50; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 50  
601 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 650

RESULT 4  
LOCUS CS135645 1281 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 10 from Patent WO2005068493.  
ACCESSION CS135645  
VERSION CS135645.1 GI:72056311  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 10 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
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/organism="Bacillus anthracis"  
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/db\_xref="taxon:1392"

ORIGIN

Query Match 100.0%; Score 50; DB 6; Length 1281;  
Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 50  
607 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 656

RESULT 5  
LOCUS AX353775 1461 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 6 from Patent WO0204646.  
ACCESSION AX353775  
VERSION AX353775.1 GI:18618827  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Williamson, E.D., Miller, J., Walker, N.J., Baillie, L.W., Holden, P.T.,  
Plick-Smith, H.C., Bullifent, H.L., Titchall, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 6 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source 1..1461  
/organism="synthetic construct"  
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/note="DNA sequence used to encode SEQ ID NO: 5"

ORIGIN

Query Match 100.0%; Score 50; DB 6; Length 1461;

Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 50  
1108 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 1157

RESULT 6  
LOCUS AY921578 1694 bp DNA linear BCT 16-APR-2005  
DEFINITION Bacillus anthracis isolate 34f2 plasmid pXOI protective antigen  
ACCESSION (pa) gene, partial cds.  
AY921578  
VERSION AY921578.1 GI:62467684  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 1694)  
AUTHORS Vahedi, F., Moazeni Jula, G. and Mahmoudi, M.  
TITLE Humoral immunity in mice induced by vaccination with a plasmid  
JOURNAL encoding anthrax protective antigen  
REFERENCE 2 (bases 1 to 1694)  
AUTHORS Vahedi, F., Moazeni Jula, G. and Mahmoudi, M.  
TITLE Direct Submmission  
JOURNAL Submitted (06-FEB-2005) Immunology Research Center, BuAli Research  
Institute, Mashhad University of Medical Sciences, BuAli Sq.,  
Mashhad, Iran  
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/protein\_id="AA084029.1"  
/db\_xref="GI:62467685"  
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TIKAKENQLSQILAPNNVYPSKNIAPIALNAQDDFSSPTIMNNOFLBETKQQLRL  
DTPDVGYNATVYENGVRVDTGSNMSVLPQIQETIARIIFNGKDLVERRIAAV  
NPSDPLETTRKPDMLKEALKAPFENGNGLOVQGDITFEDNFDOOTSONIKNOI  
AEANATNIVTLVDKIKINAKKNILIRDKRPHVDNNNTAMGSDSVYKRAHREVINNST  
EGLINIDKDIRKLISGYIYEIETBEKKEVINRDMNINSSLRQDKRTIDPFKKN  
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ORIGIN

Query Match 100.0%; Score 50; DB 1; Length 1694;  
Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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587 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTGG 636

RESULT 7  
LOCUS CS135643 1707 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 8 from Patent WO2005068493.  
ACCESSION CS135643



VERSION CS135643.1 GI:72056309  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
REFERENCE  
1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 8 28-JUL-2005; (GB)  
Royal Holloway and Bedford New College  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 607 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 656  
RESULT 8  
AR570597 1710 bp DNA linear PAT 14-DEC-2004  
LOCUS AR570597  
DEFINITION Sequence 4 from patent US 6770479.  
ACCESSION AR570597  
VERSION AR570597.1 GI:56571410  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 1710)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 4 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOX;  
FEATURES  
source Location/Qualifiers  
1. .1710  
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/mol\_type="genomic DNA"  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 50  
Db 610 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 659  
RESULT 9  
AX353781 1785 bp DNA linear PAT 06-FEB-2002  
LOCUS AX353781  
DEFINITION Sequence 12 from Patent WO0204646.  
ACCESSION AX353781  
VERSION AX353781.1 GI:18618830  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE other sequences; artificial sequences.  
1  
AUTHORS Williamson, B.D., Miller, J., Walker, N.J., Ballie, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullivant, H.L., Tibball, R.W. and Topping, A.W.  
TITLE Expression system

JOURNAL Patent: WO 0204646-A 12 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source Location/Qualifiers  
1. .1785  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 50  
Db 1108 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 1157  
RESULT 10  
169387 2160 bp DNA linear PAT 04-FEB-1998  
LOCUS 169387  
DEFINITION Sequence 30 from patent US 5677274.  
ACCESSION 169387  
VERSION 169387.1 GI:2831509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2160)  
AUTHORS Leppla, S.H., Klumpel, K.R., Arora, N., Singh, Y. and Nicholas, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 30 14-OCT-1997;  
Location/Qualifiers  
1. .2160  
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/mol\_type="unassigned DNA"  
ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 50  
Db 1120 GGGACGGCTCCATCTACACGCTTACCAAGCACTTCGTTAGTGTAGG 1169  
RESULT 11  
CS135652 2208 bp DNA linear PAT 09-AUG-2005  
LOCUS CS135652  
DEFINITION Sequence 17 from Patent WO2005068493.  
ACCESSION CS135652  
VERSION CS135652.1 GI:72056316  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
REFERENCE  
1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 17 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
source Location/Qualifiers  
1. .2208  
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/mol\_type="unassigned DNA"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;



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Qy 1 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 50
Db 1108 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 1157

RESULT 12
AX353783
LOCUS AX353783 2208 bp DNA linear PAT 06-FEB-2002
DEFINITION Sequence 14 from Patent WO204646.
ACCESSION AX353783
VERSION AX353783.1 GI:18618831
KEYWORDS
SOURCE
ORGANISM
synthetic construct
synthetic construct
other sequences; artificial sequences.
REFERENCE
1
AUTHORS
Williams, B.D., Miller, J., Walker, N.J., Baillie, L.W., Holden, P.T.,
Flick-Smith, H.C., Bullifent, H.L., Titchall, R.W. and Topping, A.W.
TITLE
Expression system
JOURNAL
Patent: WO 0204646-A 14 17-JAN-2002;
The Secretary of State for Defense (GB)
FEATURES
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location/Qualifiers
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ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 50
Db 1108 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 1157

RESULT 13
CS061689
LOCUS CS061689 2211 bp DNA linear PAT 13-APR-2005
DEFINITION Sequence 9 from Patent WO2005026203.
ACCESSION CS061689
VERSION CS061689.1 GI:62553664
KEYWORDS
SOURCE
ORGANISM
Bacillus anthracis
Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1
AUTHORS
Kopecko, D.J., Osoerio, M., Bhattacharyya, S., Giri, C.P. and Blake, M.
TITLE
DNA promoters and anthrax vaccines
JOURNAL
Patent: WO 2005026203-A 9 24-MAR-2005;
Department of Health and Human Services (US)
FEATURES
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location/Qualifiers
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/db_xref="taxon:1392"
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 50
Db 1111 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 1160

RESULT 14

AR570595
LOCUS AR570595 2211 bp DNA linear PAT 14-DEC-2004
DEFINITION Sequence 2 from patent US 6770479.
ACCESSION AR570595
VERSION AR570595.1 GI:56571408
KEYWORDS
SOURCE
ORGANISM
unknown.
Unclassified.
REFERENCE
1 (bases 1 to 2211)
AUTHORS
Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.
TITLE
Anthrax vaccine
JOURNAL
Patent: US 6770479-A 2 03-AUG-2004;
The United States of America as represented by the Secretary of the
Army; Washington, DC;
FEATURES
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location/Qualifiers
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/mol_type="genomic DNA"
ORIGIN
Query Match 100.0%; Score 50; DB 6; Length 2211;
Best Local Similarity 100.0%; Pred. No. 1.6e-17;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1111 GGGAGCGCTCCATCTACACAGCTGTGTACCAAGCACTTGCTTAGTGTAGG 1160

RESULT 15
BAN413937
LOCUS BAN413937 2225 bp DNA linear BCT 22-MAY-2002
DEFINITION Bacillus anthracis partial pag gene, isolate IT-Carbi-6241.
ACCESSION AJ413937
VERSION AJ413937.1 GI:16031494
KEYWORDS
SOURCE
ORGANISM
pag gene.
Bacillus anthracis
Bacillus anthracis
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
cereus group.
REFERENCE
1
AUTHORS
Adone, R., Pasquali, P., La Rosa, G., Mariani, C., Muscillo, M.,
Pasanello, A., Francia, M. and Cinchini, F.
TITLE
Sequence analysis of the gene encoding for the major virulence
factors of bacillus anthracis vaccine strain 'Carbosap
JOURNAL
2 (bases 1 to 2225)
APPL. Microbiol. 92, 1-5 (2002)
Muscillo, M.
Direct Submission
Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199,
Italy
FEATURES
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DEFINITION gene, complete cde.  
ACCESSION AY700758  
VERSION AY700758.1 GI:51235129  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2227)  
Aziz, M.A. and Bhatnagar, R.  
Mature protective antigen gene with prokaryotic ribosomal binding  
site  
Unpublished  
2 (bases 1 to 2227)  
Aziz, M.A. and Bhatnagar, R.  
Direct Submission  
Submitted (29-JUL-2004) Centre for Biotechnology, Jawaharlal Nehru  
University, New Mehrauli Road, New Delhi 110067, India  
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ORIGIN

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DEFINITION A0413936  
ACCESSION A0413936.1 GI:16031492  
VERSION A0413936.1 GI:16031492  
KEYWORDS pag gene.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1  
Adone, R., Pasquali, P., La Rosa, G., Marilone, C., Muscillo, M.,  
Fasanella, A., Francia, M. and Ciuchini, F.  
Sequence analysis of the gene encoding for the major virulence  
factor of bacillus anthracis vaccine strain 'Carbosap'  
J. Appl. Microbiol. 92, 1-5 (2002)  
2 (bases 1 to 2231)  
Muscillo, M.  
Direct Submission  
Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene,  
Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199,  
Italy  
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ORIGIN



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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AR570596 2292 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 3 from patent US 6770479.  
ACCESSION AR570596  
VERSION AR570596.1 GI:56571409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.

REFERENCE  
AUTHORS 1 (bases 1 to 2292)  
TITLE Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.  
JOURNAL Anthrax vaccine  
Patent: US 6770479-A 3 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOX;

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1192 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGGTAGTGG 1241

RESULT 19  
LOCUS AY997299 2295 bp DNA linear BCT 26-APR-2005  
DEFINITION Bacillus anthracis strain A16r protective antigen (pag) gene,  
complete cds.  
ACCESSION AY997299  
VERSION AY997299.1 GI:62823103  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE  
AUTHORS 1 (bases 1 to 2295)  
TITLE Xu,J., Dong,D. and Chen,W.  
JOURNAL Protective antigen gene of Bacillus anthracis strain A16r  
UNPUBLISHED 2 (bases 1 to 2295)  
AUTHORS Xu,J., Dong,D. and Chen,W.  
TITLE Direct Submission  
JOURNAL Submitted (03-APR-2005) Department of Molecular Biology, Beijing  
Institute of Microbiology and Epidemiology, 20 Dongdajie, Fengtai,  
Beijing 100071, China  
location/Qualifiers  
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LOCUS CS135651 2295 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 16 from Patent WO2005068493.  
ACCESSION CS135651  
VERSION CS135651.1 GI:72056315  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE  
AUTHORS Cutting,S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 16 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
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DEFINITION Sequence 1 from patent US 6770479.  
ACCESSION AR570594  
VERSION AR570594.1 GI:56571407  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
Unclassified.



REFERENCE 1 (bases 1 to 2295)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 1 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army: Washington, DC;  
MOX;

FEATURES  
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Best Local Similarity 100.0%; Pred. No. 1.6e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1195 GGGACGGCTCCATCTACACGCTGTTACCAAGCACTTCGTTAGTTAGG 1244

RESULT 22  
AF306778 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306778.1 GI:10880942  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCES 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

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REFERENCE 1 (bases 1 to 2295)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 1 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army: Washington, DC;  
MOX;

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ORIGIN  
Query Match 100.0%; Score 50; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCATCTACACGCTGTTACCAAGCACTTCGTTAGTTAGG 50  
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RESULT 23  
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LOCUS Bacillus anthracis isolate 28 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306779.1 GI:10880944  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCES 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

FEATURES  
source location/Qualifiers  
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Db 1243 GGGACGGCTCCATCTACACGCTGTACCAAGCAGCTTGTTAGTTAGG 1292

RESULT 24  
AF306780 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS AF306780  
DEFINITION Bacillus anthracis isolate BA1035 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306780  
VERSION AF306780.1 GI:10880946  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCES 2 (bases 1 to 2369)  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
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SOGILGYFSDLPQAPMVVTSSTGGLSIPSSLEINPSENQYFQSAIWSGFIYVK  
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FKLYWTDQNKKEVYSSDNQLPELKQSSNSRKRSTASGPTVDPDNDGIPLSLEY  
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NABVHAFPDIGGSVSAFNSNSSTVAIDHSLSLAGERTWAEFTMGNTADTARLAN  
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NAQDDFSTPIITMNNQFLELEKTKQLDLDQYGNATYFENGRVRYVTSWSE  
VLPQIOETTAIIFNGKDLNVERLIAVNSDPLETTKPMPTLKEALKIIFGNEPN  
GNLYOGKIDTEFPNDQTSQNIKNQLELANNTIYTLVDKIKLANKNAILLRDKR  
PHYDRNNIANGADSEVKEAREVINSSTGGLNLTIDKIKLISGYIVLEIDTEGLK  
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Query Match 100.0%; Score 50; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCTCCATCTACACGCTGTACCAAGCAGCTTGTTAGTTAGG 50  
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Db 1243 GGGACGGCTCCATCTACACGCTGTACCAAGCAGCTTGTTAGTTAGG 1292

RESULT 25  
AF306781 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS AF306781  
DEFINITION Bacillus anthracis isolate 33 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306781

VERSION AF306781.1 GI:10880948  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCES 2 (bases 1 to 2369)  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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GNLYOGKIDTEFPNDQTSQNIKNQLELANNTIYTLVDKIKLANKNAILLRDKR  
PHYDRNNIANGADSEVKEAREVINSSTGGLNLTIDKIKLISGYIVLEIDTEGLK  
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ENGDSTNGIKILIFSKGYEIG"

Query Match 100.0%; Score 50; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCTCCATCTACACGCTGTACCAAGCAGCTTGTTAGTTAGG 50  
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Db 1243 GGGACGGCTCCATCTACACGCTGTACCAAGCAGCTTGTTAGTTAGG 1292

RESULT 26  
AF306782 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS AF306782  
DEFINITION Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306782  
VERSION AF306782.1 GI:10880950  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE  
AUTHORS Price,L.B., Hugh-Jones,M., Jackson,P.J. and Keim,P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus



JOURNAL anthracis  
PUBMED J. Bacteriol. 181 (8), 2358-2362 (1999)  
REFERENCE 10197996  
AUTHORS 2 (bases 1 to 2369)  
TITLE Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
JOURNAL Direct Submission  
Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
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49..2343  
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/translation="MKRRKVLPIPMALSTIVSGTNLEVIQAEVKQENRLNSESSE  
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ORIGIN

Query Match 100.0%; Score 50; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAGTTAG 50  
1243 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAG 1292

Db 1243 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAG 1292

RESULT 27  
AF306783 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate BAI024 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306783  
VERSION AF306783.1 GI:10880952  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCES 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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Location/Qualifiers

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FYHRRNNAVAGADESVVKAAREVINSSTEGILLNIDKIRKILSGYIVLEDTGK  
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ORIGIN

Query Match 100.0%; Score 50; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 1 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAGTTAG 50  
1243 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAG 1292

Db 1243 GGAGCGCTCCATCTACACGCTTACCAAGACTTGGTTAG 1292

RESULT 28  
AF268967 2549 bp DNA linear BCT 31-JUL-2000  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (paga) gene,  
DEFINITION complete cds.  
ACCESSION AF268967  
VERSION AF268967.1 GI:92280532  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2549)  
AUTHORS Cohen, S., Mendelson, I., Altboun, Z., Koblier, D., Elhanany, B.,  
Bino, T., Leitner, M., Indar, I., Rosenbery, H., Gozes, Y., Barak, R.,  
Fisher, M., Kronman, C., Velan, B. and Shaffer, A.  
TITLE Attenuated nontoxicogenic and nonencapsulated recombinant Bacillus  
anthracis spore vaccines protect against anthrax  
JOURNAL Infect. Immun. 68 (8), 4549-4558 (2000)  
PUBMED 10899854  
REFERENCES 2 (bases 1 to 2549)  
AUTHORS Cohen, S., Mendelson, I. and Shaffer, A.  
TITLE Direct Submission  
JOURNAL Submitted (18-MAY-2000) Department of Biochemistry, Israel  
Institute for Biological Research, P.O. Box 19, Nees Ziona 74100,  
Israel  
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EGYTVDNKRRTFLSPMISNIHEKGLTKYKSSPEKMSADPSDFEKVGRIDKNV  
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GNLYOGKDIIEFDENFDQOTSQNIKNGLAEIANTINIYTVLDKILANMNLIDKRR  
PHYDRNNIYAVGADSEVKEAREVINSSTEGILNIDIDIRKILSGYVETEDTEGLK  
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ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 50; DB 1; Length 2549;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCCAATCTACACGCTGTACCAAGACTTGGTAGTGAAG 50  
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Db 1346 GGGACGGCTCCCAATCTACACGCTGTACCAAGACTTGGTAGTGAAG 1395

RESULT 29  
AX933603 2605 bp DNA linear PAT 22-DEC-2003  
LOCUS Sequence 3 from Patent WO03087378.  
DEFINITION AX933603  
ACCESSION AX933603.1 GI:40312826  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE  
1 Schmaljohn, C.U. and Fuller, J.  
Nucleic acid immunization  
Patent: WO 03087378-A 3 23-OCT-2003;  
PowderJect Research Limited (GB)  
FEATURES  
Location/Qualifiers  
1..2605  
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ORIGIN

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Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1368 GGGACGGCTCCCAATCTACACGCTGTACCAAGACTTGGTAGTGAAG 1417

RESULT 30  
I33400 133400 2709 bp DNA linear PAT 06-FEB-1997  
LOCUS Sequence 11 from patent US 5591631.  
DEFINITION I33400  
ACCESSION I33400  
VERSION I33400.1 GI:1824191  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 2709)  
AUTHORS Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholls, P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 11 07-JAN-1997;  
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Location/Qualifiers  
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ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 50; DB 6; Length 2709;  
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Db 1108 GGGACGGCTCCCAATCTACACGCTGTACCAAGACTTGGTAGTGAAG 1157

RESULT 31  
I69378 169378 2709 bp DNA linear PAT 04-FEB-1998  
LOCUS Sequence 11 from patent US 5677274.  
DEFINITION I69378  
ACCESSION I69378  
VERSION I69378.1 GI:2831500  
KEYWORDS  
SOURCE  
ORGANISM  
Unknown.  
Unclassified.

REFERENCE  
1 (bases 1 to 2709)  
AUTHORS Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nichols, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 11 14-OCT-1997;  
FEATURES  
Location/Qualifiers  
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ORIGIN

Query Match  
Best Local Similarity 100.0%; Score 50; DB 6; Length 2709;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 1 GGGACGGCTCCAACTTACACGTTTACCAAGACTTGGTTAGT 50  
DB 1108 GGGACGGCTCCAACTTACACGTTTACCAAGACTTGGTTAGT 1157

RESULT 32  
BACPAGE 4235 bp DNA linear BCT 02-AUG-1999  
LOCUS Bacillus anthracis cryptic protein and protective antigen precursor  
(paga) genes, complete cds.  
ACCESSION M22589  
VERSION M22589.1 GI:143280  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 4235)  
Melkos, S.L., Lowe, J.R., Eden-McCutchan, F., Vodkin, M., Leppla, S.H.  
and Schmidt, J.J.  
Sequence and analysis of the DNA encoding protective antigen of  
Bacillus anthracis  
JOURNAL 3148491  
PUBMED Gene 69 (2), 287-300 (1988)  
REFERENCE 2 (bases 1 to 4235)  
Melkos, S.  
Direct Submission  
Submitted (15-JUN-1989) Bacteriology, USAMRIID, Ft. Detrick,  
Frederick, MD 21702, USA  
JOURNAL  
FEATURES  
source Location/Qualifiers  
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ENMRSLVDPGDVYVAATKEDFNAAVTRDENGNIAKNTLVLSGKIKEINIKITNI  
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Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
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QY 1 GGGACGGCTCCAACTTACACGTTTACCAAGACTTGGTTAGT 50  
DB 2998 GGGACGGCTCCAACTTACACGTTTACCAAGACTTGGTTAGT 3047

RESULT 33  
LOCUS 133396 4235 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5591631.  
ACCESSION 133396  
VERSION 133396.1 GI:1824187  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4235)  
Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholas, P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 3 07-JAN-1997;  
FEATURES  
source Location/Qualifiers  
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ORIGIN  
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DB 2998 GGGACGGCTCCAACTTACACGTTTACCAAGACTTGGTTAGT 3047

RESULT 34  
LOCUS 169374 4235 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 3 from patent US 5677274.  
ACCESSION 169374  
VERSION 169374.1 GI:2831496  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 4235)  
Leppla, S.H., Klimpel, K.R., Arora, N., Singh, Y. and Nicholas, P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 3 14-OCT-1997;  
FEATURES  
source Location/Qualifiers  
1. 4235  
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Best Local Similarity 100.0%; Pred. No. 1.5e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 35  
AF065404/c



LOCUS AF065404 181654 bp DNA circular BCT 01-OCT-2003  
DEFINITION Bacillus anthracis virulence plasmid pX01, complete sequence.  
ACCESSION AF065404  
VERSION AF065404.1 GI:4894216  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.  
REFERENCE 1 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A.R., Hill,K.K., Keim,P., Koehler,T.M., Lanke,G., Kumano,S., Mahillon,J., Menter,D., Martinez,Y., Ricke,D., Svensson,R. and Jackson,P.J.  
TITLE Sequence and organization of pX01, the large Bacillus anthracis plasmid harboring the anthrax toxin genes  
JOURNAL J. Bacteriol. 181 (20), 6509-6515 (1999)  
PUBMED 10515943  
REFERENCE 2 (bases 1 to 181654)  
AUTHORS Okinaka,R.T., Cloud,K., Hampton,O., Hoffmaster,A., Hill,K., Keim,P., Koehler,T., Kumano,S., Lanke,G., Menter,D., Martinez,Y., Ricke,D.O., Svensson,R. and Jackson,P.  
TITLE Direct Submission  
JOURNAL Submitted (14-May-1998) Life Sciences Division, Los Alamos National Laboratory, T443, LS-6, HR-1, MS M888, Los Alamos, NM 87545, USA  
FEATURES  
SOURCE Location/Qualifiers  
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CDS complement(5720..6220)  
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REFERENCE	TITLE	JOURNAL	PUBMED	AUTHORS
1 (bases 1 to 181677)	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.			
2 (bases 1 to 181677)	Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Unayam, L., Jiang, L., Holtzapfel, E., Bush, J.D., Smith, K.L., Schupp, J.M., Solomon, D., Keim, P. and Fraser, C.M.			
Comparative genome sequencing for discovery of novel polymorphisms in <i>Bacillus anthracis</i>				
Science 296 (5575), 2028-2033 (2002)				
12004073				
2 (bases 1 to 181677)	Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Unayam, L., Jiang, L., Holtzapfel, E., Bush, J.D., Smith, K.L., Schupp, J.M., Solomon, D., Keim, P. and Fraser, C.M.			
Direct Submission				
Submitted (09-MAY-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA				
Location/Qualifiers				
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Best Local Similarity 100.0%; Pred. No. 1,2e-17;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGACGGGCTCAATCTACCAAGTGTACCAAGCACTTGTTAGTGTAGG 50  
DB 144973 GGGACGGCTCAATCTACCAAGTGTGTACCAAGCACTTGTTAGG 145022  
RESULT 37  
AE017336  
LOCUS  
DEFINITION 181677 bp DNA circular BCT 09-JUL-2004  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
Bacillus anthracis str. 'Ames Ancestor'  
Bacillus anthracis str. 'Ames Ancestor'  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
Cereus group.  
1 (bases 1 to 181677)  
Ravel,J., Raeko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,  
Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,  
Salzberg,S. and Fraser,C.M.



TITLE	JOURNAL	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
Bacillus anthracis comparative genomics	Unpublished	2 (bases 1 to 181677)	Ravel, J., Raebko, D.A., Shumway, M.F., Jiang, L., Cer, R.Z., Federova, N.B., Salzberg, S. and Fraser, C.M.	Submitted (17-MAY-2004)	The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA	On May 23, 2004 this sequence version replaced gi:47499967. This sequence is to be utilized as the reference strain for Bacillus anthracis research - all other sequences should be compared to this sequence.	Location/Qualifiers 1. 181677 /organism="Bacillus anthracis str. 'Ames Ancestor'" /mol_type="genomic DNA" /strain="Ames Ancestor; A2084" /db_xref="taxon:261594" /plasmid="pXOI" /note="MLVA types GT62 and A3.b" 462. .554 /locus_tag="GBAA_pXOI_0001" 462. .554 /locus_tag="GBAA_pXOI_0001" 462. .554 /locus_tag="GBAA_pXOI_0001" /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=1 /product="hypothetical protein" /protein_id="AAT28742.2" /db_xref="GI:47552138" /translation="MVARIHILIKRVVVKSKRHSNECLFLWTK" complement(966. .1109) /locus_tag="GBAA_pXOI_0002" complement(966. .1109) /locus_tag="GBAA_pXOI_0002" /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=1 /product="hypothetical protein" /protein_id="AAT28743.2" /db_xref="GI:47552139" /translation="MLVYIGELVLSIYAIKLMKYYLKKKKDFFVKKKG" complement(1127. .1765) /locus_tag="GBAA_pXOI_0003" complement(1127. .1765) /locus_tag="GBAA_pXOI_0003" /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=1 /product="hypothetical protein, (pXOI-01)" /protein_id="AAT28744.2" /db_xref="GI:47552140" /translation="MEVILIFELILIAVLIPLVSVKKHVPKKGAKGKLVKMLSTLDPKSYVLANTVYTBEGDITQIDHIVYIAEGVAVETKATYEGHIVTSSKCAARTQGI FRKSSFPQNDPHYQKIKALEMIIEQQLPCTISAAHPKSLKRVAVSKERGVLY NDLKCSIBSYDVLITNDVQLEHILHTILIRANIMDKDIEKGVYLIANKPAQ" complement(1782. .2165) /locus_tag="GBAA_pXOI_0004" complement(1782. .2165) /locus_tag="GBAA_pXOI_0004" complement(1782. .2165) /locus_tag="GBAA_pXOI_0004" /note="Identified by Glimmer2; putative" /codon_start=1 /transl_table=1 /product="hypothetical protein" /protein_id="AAT28745.2" /db_xref="GI:47552141" /translation="MNRNRITYALRNSISIGMLTCTIVTGISYFSSVYLLIGCFIL SLKQIGMTGVNVEKRLPTFANFGVIEKPVAVRATRPFGQGLVSLAIGFVEMVIK GLCTSYFGLGELTVFLMRNRAN" 2291. .2875 /locus_tag="GBAA_pXOI_0005" 2291. .2875 /locus_tag="GBAA_pXOI_0005" /locus_tag="GBAA_pXOI_0005"

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VERSION	AK118301.1	GI:26451643		
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SOURCE	Arabidopsis thaliana			
ORGANISM	Arabidopsis thaliana			
	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eustroids II; Brassicales; Brassicaceae; Arabidopsis.			
REFERENCE				
AUTHORS	Seki, M., Iida, K., Satou, M., Sekurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Natsusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.			
TITLE	Arabidopsis thaliana full-length cDNA			
JOURNAL	Published Only in Database (2002)			
REFERENCE				
AUTHORS	Seki, M., Iida, K., Satou, M., Sekurai, T., Akiyama, K., Ishida, J., Nakajima, M., Enju, A., Kamiya, A., Natsusaka, M., Carninci, P., Kawai, J., Hayashizaki, Y. and Shinozaki, K.			

**TITLE** Direct Submission  
**JOURNAL** Submitted (25-NOV-2002) Motoaki Seki, RIKEN Genomic Sciences Center; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: msek@gscc.riken.go.jp, URL: <http://pifweb.gsc.riken.go.jp>, Tel: 81-45-503-9625, Fax: 81-45-503-9586)  
**COMMENT** An Arabidopsis full-length cDNA library was constructed essentially as reported previously (Seki et al. (1998) Plant J. 15:707-720; Seki et al. (2002) Science 296:141-145). cDNA cleaved with BamHI and XhoI was ligated to modified lambda PUC-1-E vector (Garnini et al. (2001) Genome 77:79-90) digested with BamHI and SalI. This clone is in a modified pBluescript vector. Please visit our web site (<http://pifweb.gsc.riken.go.jp/>) for further details.  
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**Db** 1213 ATCTACAACGTTACCA 1195  
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VERSION AP000420.1 GI:5832741  
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**ORGANISM** Arabidopsis thaliana  
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**REFERENCE** 1  
**AUTHORS** Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.  
**TITLE** Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty P1 and TAC clones  
**JOURNAL** DNA Res. 7 (2), 131-135 (2000)  
**REFERENCE** 2 (bases 1 to 82890)  
**PUBMED** Sato,S., Nakamura,Y., Kaneko,T., Katoh,T., Asamizu,E. and Tabata,S.  
**AUTHORS** Direct Submission  
**TITLE** Submitted (03-SEP-1999) Yasukazu Nakamura, Kazusa DNA Research Institute, Department of Plant Gene Research, 1532-3, Yana,







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ORGANISM Medicago truncatula  
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
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Medicago.  
1 (bases 1 to 103039)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
Medicago truncatula BAC Clone mth2-26o22  
Unpublished  
2 (bases 1 to 103039)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
Direct Submission  
Submitted (05-FEB-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
3 (bases 1 to 103039)  
Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
Direct Submission  
Submitted (06-FEB-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,

OK 73019, USA  
REFERENCE 4 (bases 1 to 103039)  
AUTHORS Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
TITLE Direct Submission  
JOURNAL Submitted (22-FEB-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
REFERENCE 5 (bases 1 to 103039)  
AUTHORS Shauli,S., Lin,S., Dixon,R., May,G., Sumner,L., Gonzales,B.,  
Cook,D., Kim,D. and Roe,B.A.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-2003) Department Of Chemistry And Biochemistry,  
The University Of Oklahoma, 620 Parrington Oval, Room 208, Norman,  
OK 73019, USA  
COMMENT On Feb 22, 2003 this sequence version replaced gi:28261517.  
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Center: Department Of Chemistry And Biochemistry  
The University Of Oklahoma  
Center code:UOKNOR  
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Db 40918 TTACCAAGCACTTGCTTAG 40900

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using ew model

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Scoring table: OLIGO\_MUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 9993364

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Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

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- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003s:\*
- 7: Geneseq2004s:\*
- 8: Geneseq2005s:\*
- 9: Geneseq2006s:\*
- 10: Geneseq2007s:\*
- 11: Geneseq2008s:\*
- 12: Geneseq2009s:\*
- 13: Geneseq2010s:\*
- 14: Geneseq2011s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	50	100.0	1272	12 ADL16358	Adl16358 pBp113 ve
5	50	100.0	1278	6 AAD29119	Aad29119 Bacillus
6	50	100.0	1281	14 AEB63722	Aeb63722 DNA encod
7	50	100.0	1461	6 AAD29117	Aad29117 Bacillus
8	50	100.0	1704	14 AAD51325	Adt51325 Nucleotid
9	50	100.0	1707	13 AEB63720	Aeb63720 DNA encod
10	50	100.0	1710	3 AAZ56877	Aaz56877 B. anthra
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15	50	100.0	2208	6 AAD29121	Aad29121 Bacillus
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17	50	100.0	2208	12 ADL16343	Adl16343 Bacillus
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19	50	100.0	2208	14 ADM05484	Adm05484 B. anthra

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21	50	100.0	2211	3 AAZ56875	Aaz56875 B. anthra
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24	50	100.0	2235	13 ADR40459	Adr40459 Bacillus
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26	50	100.0	2295	3 AAZ56874	Aaz56874 B. anthra
27	50	100.0	2295	4 AAC86016	Aac86016 Wild type
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34	50	100.0	4235	10 ACF58207	Acf58207 B. anthrac
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36	50	100.0	8198	12 ADL16342	Adl16342 pBp103 ex
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38	25	50.0	25	13 ADR48507	Adr48507 paga prob
39	25	50.0	25	13 ADR48508	Adr48508 paga prob
40	19	38.0	20	10 ADC51669	Adc51669 Bacillus
41	17	34.0	101	14 ADZ51287	Adz51287 Nucleotid
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43	17	34.0	4365	14 ADZ51333	Adz51333 Nucleotid
44	17	34.0	4365	14 ADZ51335	Adz51335 Nucleotid
45	16	32.0	103	14 ADZ51288	Adz51288 Nucleotid
46	16	32.0	944	9 ADA29400	Ada29400 DNA encod
47	16	32.0	944	2 AAO85037	Aao85037 DNA-ase-B
48	16	32.0	944	2 AAT12780	Aat12780 DNase B m
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50	16	32.0	1083	2 AAT12774	Aat12774 S. pyogen
51	16	32.0	3257	4 ABL16612	Ab116612 Drosophill
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53	16	32.0	8558	4 AB106618	Ab106618 Drosophill
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69	15	30.0	874	10 ABX08185	Abx08185 S. pneumo
70	15	30.0	1209	2 AAV63859	Aav63859 Polymexas
71	15	30.0	1594	12 ADQ6473	Adq6473 Human tum
72	15	30.0	1608	12 ADN04266	Adn04266 Antiporri
73	15	30.0	1608	13 ADR25189	Adr25189 Breast ca
74	15	30.0	1672	14 AEB22810	Aeb22810 Human col
75	15	30.0	1736	5 ADQ22478	Adq22478 Human sof
76	15	30.0	1737	2 ABB30256	Abb30256 Human pro
77	15	30.0	2145	8 ACA43761	Acc43761 Prokaryot
78	15	30.0	3930	4 ABL33091	Ab133091 Drosophill
79	15	30.0	6420	6 ABB79011	Abb79011 E. coli C
80	15	30.0	6420	10 ADH80578	Adh80578 Escherich
81	15	30.0	7058	4 ABL33090	Ab133090 Drosophill
82	15	30.0	32768	2 AAV52204	Aav52204 Streptoco
83	15	30.0	73334	6 ABL34125	Ab134125 Human imm
84	15	30.0	73334	6 ABL92319	Ab192319 Chemical
85	15	30.0	110000	10 ABB56454_15	Continuation (16 o
86	14	28.0	28	14 ADW40088	Adw40088 Arbidops
87	14	28.0	34	12 ADQ36618	Adq36618 Bacillus
88	14	28.0	34	12 ADQ36630	Adq36630 Bacillus
89	14	28.0	57	6 ACN24439	Acc24439 WNV Amber
90	14	28.0	234	8 ACA20912	Acc20912 Prokaryot
91	14	28.0	237	6 ABB92319	Abb92319 Staphyloc
92	14	28.0	238	6 ABB20993	Abb20993 Human ORF



C 93	14	28.0	276	14	ACL60395	Ac160395 Human col	C 166	14	28.0	11101	6	ABN83947	Abn83947 Human tra
C 94	14	28.0	285	9	ADA32488	Ada32488 DNA encod	C 167	14	28.0	12588	3	AAO63293	AAO63293 Sequence
C 95	14	28.0	300	2	ADA02171	Ada02171 D. melano	C 168	14	28.0	14823	14	ACT64624	Act64624 M. xanthu
C 96	14	28.0	326	6	ABN76416	Abn76416 Human rib	C 169	14	28.0	19603	4	ABL02570	Ab102570 Drosophill
C 97	14	28.0	486	3	AAA66880	Aaa66880 NDPK nucl	C 170	14	28.0	20072	2	ABL13026	Aab13026 Enterococ
C 98	14	28.0	486	3	AAAF5991	Aaf5991 Pyrococcu	C 171	14	28.0	20072	6	ABN98821	Abn98821 Enterococ
C 99	14	28.0	486	4	AAAF5978	Aaf5978 P. furios	C 172	14	28.0	29912	4	AAAF59507	Aaf59507 Pyrobionb
C 100	14	28.0	486	4	AAAD23064	Aad23064 Pyrococcu	C 173	14	28.0	29912	8	ACF64436	Acf64436 Pyrobionb
C 101	14	28.0	501	4	AAAF59974	Aaf59974 Pyrococcu	C 174	14	28.0	31233	14	ADV96543	Adv96543 Pyrobionb
C 102	14	28.0	501	4	AAAF59990	Aaf59990 Pyrococcu	C 175	14	28.0	31357	14	ADV96541	Adv96541 Coronavir
C 103	14	28.0	511	4	AAAF59989	Aaf59989 Pyrococcu	C 176	14	28.0	31357	14	ADV96542	Adv96542 Coronavir
C 104	14	28.0	540	6	ABO53519	Abq53519 Oligonuc1	C 177	14	28.0	34548	6	ABL70603	Ab170603 Chemocall
C 105	14	28.0	540	6	ABO53518	Abq53518 Oligonuc1	C 178	14	28.0	37116	4	ACF64482	Acf64482 Pyrobionb
C 106	14	28.0	556	13	AAAF52758	Aaf52758 S. epider	C 179	14	28.0	37116	8	ADBF16928	Adbf16928 Human dyx
C 107	14	28.0	556	13	ADAF52737	Adaf52737 Novel can	C 180	14	28.0	49939	9	ADBF16928	Adbf16928 Human imm
C 108	14	28.0	570	6	ABQ21270	Abq21270 Oligonuc1	C 181	14	28.0	56743	4	AAK68202	Aak68202 Human imm
C 109	14	28.0	570	6	ABQ21271	Abq21271 Oligonuc1	C 182	14	28.0	56743	4	AAK81760	Aak81760 Human imm
C 110	14	28.0	570	6	ABO52804	Abq52804 Oligonuc1	C 183	14	28.0	68295	14	ABE76936	Abe76936 Chicken o
C 111	14	28.0	590	6	ABO52805	Abq52805 Oligonuc1	C 184	14	28.0	75815	14	ADW44335	Adw44335 Chicken o
C 112	14	28.0	603	6	ABO19173	Abq19173 Oligonuc1	C 185	14	28.0	75815	14	AEA00969	Aea00969 DNA innee
C 113	14	28.0	603	6	ABO19172	Abq19172 Oligonuc1	C 186	14	28.0	75815	14	ABE76922	Abe76922 Chicken o
C 114	14	28.0	681	6	ABO38196	Abq38196 Oligonuc1	C 187	14	28.0	77872	14	ADW44343	Adw44343 Ovomucoid
C 115	14	28.0	681	6	ABO38197	Abq38197 Oligonuc1	C 188	14	28.0	77872	14	AEA00977	Aea00977 Ovomucoid
C 116	14	28.0	689	6	ABO35766	Abq35766 Oligonuc1	C 189	14	28.0	77872	14	ABE76930	Abe76930 Chicken o
C 117	14	28.0	689	6	ABO35767	Abq35767 Oligonuc1	C 190	14	28.0	81684	13	ABD33502	Abd33502 Murine ca
C 118	14	28.0	693	6	ABZ13454	Abz13454 Arabidops	C 191	14	28.0	90435	12	ADQ59524	Adq59524 Human can
C 119	14	28.0	693	7	ADZ75131	Adz75131 Arabidops	C 192	14	28.0	90537	12	ADZ13905	Adz13905 Human can
C 120	14	28.0	732	6	ABQ21665	Abq21665 Oligonuc1	C 193	14	28.0	110000	12	ADN46845_11	Adn46845_11
C 121	14	28.0	732	6	ABQ21664	Abq21664 Oligonuc1	C 194	14	28.0	110000	12	ADN47591_09	Adn47591_09
C 122	14	28.0	777	10	ADH85483	Adh85483 Enterococ	C 195	14	28.0	110000	12	ADN46123_11	Adn46123_11
C 123	14	28.0	816	6	ABN92317	Abn92317 Staphyloc	C 196	14	28.0	110000	12	ADN47209_09	Adn47209_09
C 124	14	28.0	816	6	ADSO9361	Adt18514 Plant CDN	C 197	14	28.0	110000	12	ADN46464_11	Adn46464_11
C 125	14	28.0	824	6	ABO24999	Abq24999 Oligonuc1	C 198	14	28.0	110000	12	ADN47960_09	Adn47960_09
C 126	14	28.0	824	6	ABO24998	Abq24998 Oligonuc1	C 199	14	28.0	110000	12	ADQ97138_1	Adq97138_1
C 127	14	28.0	824	6	ABO24998	Abq24998 Oligonuc1	C 200	14	28.0	110000	12	ADQ97138_2	Adq97138_2
C 128	14	28.0	850	13	ADX54535	Adx54535 Plant ful	C 201	14	28.0	185548	13	ADV34986	Adv34986 Murine cd
C 129	14	28.0	857	13	ADOB82161	Adob82161 Plant ful	C 202	14	28.0	25	9	ACT36832	Act36832 Human mic
C 130	14	28.0	951	10	ADH83151	Adh83151 Enterococ	C 203	14	28.0	25	9	ACT15350	Act15350 Human mic
C 131	14	28.0	1014	4	AAAD06246	Aaad06246 Domestic	C 204	14	28.0	25	9	ACT109648	Act109648 Human mic
C 132	14	28.0	1017	5	AAAF78325	Aaaf78325 DNA encod	C 205	14	28.0	25	9	ACT100250	Act100250 Human mic
C 133	14	28.0	1080	10	ADP02370	Adp02370 Bacterial	C 206	14	28.0	25	9	ACT18578	Act18578 Human mic
C 134	14	28.0	1086	14	ADCF73105	Adcf73105 M. xanthu	C 207	14	28.0	25	9	ACT16467	Act16467 Human mic
C 135	14	28.0	1161	2	AAOC63295	Aaoc63295 Consensus	C 208	14	28.0	25	9	ACT148588	Act148588 Human mic
C 136	14	28.0	1174	4	AEBA65571	Aeba65571 Rice geno	C 209	14	28.0	25	9	ACK08185	Ack08185 Human mic
C 137	14	28.0	1608	4	AB122811	Ab122811 Drosophill	C 210	14	28.0	25	9	ACT10284	Act10284 Human mic
C 138	14	28.0	1804	13	ADX34769	Adx34769 Plant ful	C 211	14	28.0	25	9	ACK08406	Ack08406 Human mic
C 139	14	28.0	2185	6	ABQ70770	Abq70770 Listeria	C 212	14	28.0	27	10	ADD28488	Add28488 Bacterich
C 140	14	28.0	2469	11	ADOB07623	Adob07623 Novel cod	C 213	14	28.0	27	10	ADD28489	Add28489 Bacterich
C 141	14	28.0	2568	11	ACL30644	Ac130644 Rice abio	C 214	14	28.0	31	6	ACN22301	Acn22301 WNVDNAZy
C 142	14	28.0	2673	11	ACT28134	Act28134 Rice abio	C 215	14	28.0	46	14	ADZ51126	Adz51126 PCR prime
C 143	14	28.0	2699	4	AB107476	Ab107476 Drosophill	C 216	14	28.0	46	14	ADZ51125	Adz51125 PCR prime
C 144	14	28.0	2943	4	AB110907	Ab110907 Drosophill	C 217	14	28.0	57	6	ABK60436	Abk60436 Human CTC
C 145	14	28.0	2967	4	AAH54102	Aah54102 S. epider	C 218	14	28.0	57	6	ACN24484	Acn24484 WNVDNAZy
C 146	14	28.0	3217	4	AB108690	Ab108690 Drosophill	C 219	14	28.0	95	13	ADM69774	Adm69774 Refractor
C 147	14	28.0	3580	4	AAH18181	Aah18181 Human CDN	C 220	14	28.0	152	2	AAT25144	Aat25144 Human gen
C 148	14	28.0	3939	12	ADMG9323	Admg9323 C heteros	C 221	14	28.0	166	8	ABX91206	Abx91206 Murine ge
C 149	14	28.0	4159	4	AB122810	Ab122810 Drosophill	C 222	14	28.0	190	7	ADG31292	Adg31292 Human gen
C 150	14	28.0	5119	4	AB103772	Ab103772 Drosophill	C 223	14	28.0	190	7	ADY36680	Ady36680 HIRA geno
C 151	14	28.0	5151	4	AAU36207	Aau36207 Human mus	C 224	14	28.0	207	11	ABD10265	Abd10265 Pseudomon
C 152	14	28.0	5151	8	ABX59195	Abx59195 cDNA enco	C 225	14	28.0	226	5	ABY60275	AbY60275 Human pro
C 153	14	28.0	5151	12	ADJ29945	Adj29945 Human mus	C 226	14	28.0	230	7	ADG31291	Adg31291 Human gen
C 154	14	28.0	5386	4	AB132533	Ab132533 Human imm	C 227	14	28.0	230	7	ADY36679	Ady36679 HIRA geno
C 155	14	28.0	5673	4	AB140906	Ab140906 Drosophill	C 228	14	28.0	259	7	ADG67783	Adg67783 Corn seed
C 156	14	28.0	5735	14	ADM40020	Adm40020 Arabidops	C 229	14	28.0	259	10	ADD28652	Add28652 Bacterich
C 157	14	28.0	5735	14	ABK40066	Abk40066 Human che	C 230	14	28.0	259	10	ADD28653	Add28653 Bacterich
C 158	14	28.0	5940	2	AAAX3526	Aax3526 O. longis	C 231	14	28.0	276	6	ABN75643	Abn75643 Human hel
C 159	14	28.0	6398	6	ABN13100	Abn13100 Human imm	C 232	14	28.0	277	10	ADD28654	Add28654 Bacterich
C 160	14	28.0	6641	6	ABN80003	Abn80003 Human che	C 233	14	28.0	277	10	ADD28655	Add28655 Bacterich
C 161	14	28.0	7593	6	ABO18252	Abq18252 Oligonuc1	C 234	14	28.0	279	5	ABV61405	Abv61405 Human pro
C 162	14	28.0	7593	6	ABO18253	Abq18253 Oligonuc1	C 235	14	28.0	280	13	ADT90394	Adt90394 Human gen
C 163	14	28.0	9767	2	AAAX1367	Aax13067 Enterococ	C 236	14	28.0	281	6	AB168999	Ab168999 Kidney ca
C 164	14	28.0	9767	6	ABN98862	Abn98862 Enterococ	C 237	14	28.0	292	10	ABX82069	Abx82069 Corn ear-
C 165	14	28.0	10202	4	AB102571	Ab102571 Drosophill	C 238	14	28.0	322	6	ABN76355	Abn76355 Human ORF



C 239	13	26.0	331	5	ABAI1057	Abai1057 Human ner	312	13	26.0	590	10	ADK57307	Adk57307 Plant DNA
C 240	13	26.0	362	12	ABD55682	Abd55682 Toxicity-	C 313	13	26.0	591	11	ADT94638	Adt94638 Colon can
C 241	13	26.0	370	5	ABV59149	Abv59149 Human pro	C 314	13	26.0	591	11	ADK41120	Adk41120 Human CDN
C 242	13	26.0	380	10	ABX61440	Abx61440 Arabidops	C 315	13	26.0	594	6	ABN66753	Abn66753 Streptoco
C 243	13	26.0	380	10	ADK54057	Adk54057 Plant DNA	C 316	13	26.0	596	12	ACH76817	Ach76817 Human gen
C 244	13	26.0	393	10	ADD16558	Add16558 DNA (Seqi	C 317	13	26.0	597	6	ABO24336	Abp24336 Oligonuc1
C 245	13	26.0	393	10	ADK58167	Adk58167 Plant DNA	C 318	13	26.0	597	6	ABO24337	Abp24337 Oligonuc1
C 246	13	26.0	399	4	AAK58149	Aak58149 Human 1mm	C 319	13	26.0	603	5	ABV56335	Abv56335 Human pro
C 247	13	26.0	401	13	ADR60283	Adr60283 Cotton cd	C 320	13	26.0	603	8	ACA33885	Act33885 Prokaryot
C 248	13	26.0	407	6	ABL87225	Ab187225 Human ova	C 321	13	26.0	607	2	AAT36876	Aat36876 Plascicoll1
C 249	13	26.0	432	8	ACA39726	Act39726 Prokaryot	C 322	13	26.0	607	13	ACN47709	Actn47709 Cotton pr
C 250	13	26.0	433	12	ACH49977	Ach49977 Human leu	C 323	13	26.0	607	13	ADK53459	Adk53459 Plant ful
C 251	13	26.0	432	9	ADP93539	Adp93539 Cotton ex	C 324	13	26.0	607	13	ADK36103	Adk36103 Plant ful
C 252	13	26.0	434	3	AAC17634	Aac17634 Human sec	C 325	13	26.0	612	11	ABD11261	Abd11261 Pseudomon
C 253	13	26.0	444	8	ABZ73248	Abz73248 Rice leaf	C 326	13	26.0	612	11	ADK53835	Adk53835 Plant ful
C 254	13	26.0	450	9	ACH35813	Ach35813 Human end	C 327	13	26.0	613	13	ADK53768	Adk53768 Plant ful
C 255	13	26.0	453	6	ABZ31895	Abz31895 Candida a	C 328	13	26.0	615	13	ADK53935	Adk53935 Plant ful
C 256	13	26.0	454	13	ADK11957	Adk11957 Plant ful	C 329	13	26.0	615	13	ADK49963	Adk49963 Plant ful
C 257	13	26.0	459	12	ADP95249	Adp95249 Cotton ex	C 330	13	26.0	615	13	ADK53561	Adk53561 Plant ful
C 258	13	26.0	459	13	ADK34144	Adk34144 Plant ful	C 331	13	26.0	620	13	ADK53391	Adk53391 Plant ful
C 259	13	26.0	462	4	AAK88834	Aak88834 Human dig	C 332	13	26.0	621	13	ADK53376	Adk53376 Plant ful
C 260	13	26.0	463	8	ABZ56819	Abz56819 Aspergill1	C 333	13	26.0	623	13	ADK53533	Adk53533 Plant ful
C 261	13	26.0	465	11	ABD11525	Abd11525 Pseudomon	C 334	13	26.0	623	13	ADK53533	Adk53533 Plant ful
C 262	13	26.0	477	9	ACH21751	Ach21751 Human adu	C 335	13	26.0	626	3	AAK49540	Aak49540 Arabidops
C 263	13	26.0	478	8	ACA05095	Act05095 Rice leaf	C 336	13	26.0	627	3	AAK50183	Aak50183 Arabidops
C 264	13	26.0	480	11	ABD00994	Abd00994 Klebsiell	C 337	13	26.0	627	13	ADK53369	Adk53369 Plant ful
C 265	13	26.0	486	3	AAC67118	Aac67118 Zea maye	C 338	13	26.0	627	13	ADK53464	Adk53464 Plant ful
C 266	13	26.0	488	13	ADK34580	Adk34580 Plant ful	C 339	13	26.0	628	6	ABQ18850	Abq18850 Oligonuc1
C 267	13	26.0	490	4	AA111145	AA111145 Probe #10	C 340	13	26.0	628	6	ABQ18851	Abq18851 Oligonuc1
C 268	13	26.0	490	4	ABA52804	Ab52804 Human foe	C 341	13	26.0	628	6	ABQ18851	Abq18851 Oligonuc1
C 269	13	26.0	490	4	AA132410	AA132410 Probe #10	C 342	13	26.0	636	3	AAK38488	Aak38488 Arabidops
C 270	13	26.0	490	4	ABA432410	Ab432410 Probe #10	C 343	13	26.0	637	3	AAK50823	Aak50823 Arabidops
C 271	13	26.0	490	4	ABR22589	Ab22589 Probe #10	C 344	13	26.0	639	13	ADK55643	Adk55643 Bacterial
C 272	13	26.0	490	4	AAK26515	Aak26515 Human bon	C 345	13	26.0	644	13	ADK48145	Adk48145 Plant ful
C 273	13	26.0	490	4	AAK01058	Aak01058 Human bra	C 346	13	26.0	645	6	ABQ20832	Abq20832 Oligonuc1
C 274	13	26.0	490	4	ABS26108	Ab26108 Human liv	C 347	13	26.0	648	2	AAT71748	Aat71748 Fibrobact
C 275	13	26.0	490	5	AA101063	AA101063 Probe #10	C 348	13	26.0	649	13	ADK53362	Adk53362 Plant ful
C 276	13	26.0	490	6	ABS01106	Ab01106 Human gen	C 349	13	26.0	653	13	ADK53352	Adk53352 Plant ful
C 277	13	26.0	501	6	ABQ42770	Abq42770 Oligonuc1	C 350	13	26.0	654	13	ADK50127	Adk50127 Bacterial
C 278	13	26.0	501	6	ABQ49912	Abq49912 Oligonuc1	C 351	13	26.0	657	13	ADK54253	Adk54253 Plant ful
C 279	13	26.0	501	6	ABQ49913	Abq49913 Oligonuc1	C 352	13	26.0	658	4	AA122913	AA122913 Human bre
C 280	13	26.0	501	6	ABQ42771	Abq42771 Oligonuc1	C 353	13	26.0	660	6	ABQ25756	Abq25756 Oligonuc1
C 281	13	26.0	510	6	ABQ25113	Abq25113 Oligonuc1	C 354	13	26.0	660	6	ABQ25757	Abq25757 Oligonuc1
C 282	13	26.0	510	6	ABQ25112	Abq25112 Oligonuc1	C 355	13	26.0	664	6	ABQ21118	Abq21118 Oligonuc1
C 283	13	26.0	516	6	ABQ49529	Abq49529 Oligonuc1	C 356	13	26.0	664	6	ABQ21119	Abq21119 Oligonuc1
C 284	13	26.0	516	6	ABQ49528	Abq49528 Oligonuc1	C 357	13	26.0	678	3	AAK34709	Aak34709 Arabidops
C 285	13	26.0	519	10	ADK59395	Adk59395 Plant DNA	C 358	13	26.0	692	3	AAK12051	Aak12051 Aspergill1
C 286	13	26.0	526	4	AA114051	AA114051 Human bre	C 359	13	26.0	692	13	ADK56092	Adk56092 Aspergill1
C 287	13	26.0	528	3	AAF08327	Aaf08327 Fusarium	C 360	13	26.0	692	14	ADK294095	Adk294095 Arabidops
C 288	13	26.0	528	13	ADU53368	Adu53368 Fusarium	C 361	13	26.0	699	6	ABQ30520	Abq30520 Oligonuc1
C 289	13	26.0	528	14	ADZ90371	Adz90371 Fusarium	C 362	13	26.0	705	6	ABQ30521	Abq30521 Oligonuc1
C 290	13	26.0	536	13	ADU12052	Adu12052 Solid tum	C 363	13	26.0	709	8	ACA29840	Act29840 Prokaryot
C 291	13	26.0	544	6	ABQ27103	Abq27103 Oligonuc1	C 364	13	26.0	713	6	ABQ65616	Abq65616 Arabidops
C 292	13	26.0	544	6	ABQ27102	Abq27102 Oligonuc1	C 365	13	26.0	714	6	ABQ28510	Abq28510 Oligonuc1
C 293	13	26.0	555	6	ABO20404	Abq20404 Oligonuc1	C 366	13	26.0	714	6	ABQ28511	Abq28511 Oligonuc1
C 294	13	26.0	555	6	ABQ20405	Abq20405 Oligonuc1	C 367	13	26.0	714	11	ACN84108	Actn84108 Breast ca
C 295	13	26.0	556	12	ADP71715	Adp71715 Renal tox	C 368	13	26.0	723	3	AAK34859	Aak34859 Arabidops
C 296	13	26.0	557	5	ABV49822	Abv49822 Human pro	C 369	13	26.0	731	4	AA196260	AA196260 Human neu
C 297	13	26.0	562	6	ABN60757	Abn60757 Human can	C 370	13	26.0	736	6	ABO48972	Abq48972 Oligonuc1
C 298	13	26.0	562	14	ACL57748	Act157748 Human col	C 371	13	26.0	736	6	ABO48973	Abq48973 Oligonuc1
C 299	13	26.0	564	13	ADK12605	Adk12605 Plant ful	C 372	13	26.0	764	3	AAK39414	Aak39414 Arabidops
C 300	13	26.0	566	10	ADB50616	Adb50616 Primary t	C 373	13	26.0	765	10	ACF96887	Actf96887 Phototrab
C 301	13	26.0	572	13	ACN47763	Actn47763 Cotton pr	C 374	13	26.0	766	4	AAH71252	Aah71252 Human cer
C 302	13	26.0	573	5	AAH87650	Aah87650 Peppermih	C 375	13	26.0	767	6	ABQ35947	Abq35947 Oligonuc1
C 303	13	26.0	578	13	ABAI14660	Abai14660 Human ner	C 376	13	26.0	777	6	ABO68897	Abq68897 Oligonuc1
C 304	13	26.0	579	13	ACN60641	Actn60641 Cotton gy	C 377	13	26.0	777	6	ABO68897	Abq68897 Oligonuc1
C 305	13	26.0	581	3	AAF08864	Aaf08864 Fusarium	C 378	13	26.0	777	6	ABQ70328	Abq70328 Listeria
C 306	13	26.0	581	6	ABO46609	Abq46609 Oligonuc1	C 379	13	26.0	789	5	ABV20064	Abv20064 Human pro
C 307	13	26.0	581	6	ABQ46608	Abq46608 Oligonuc1	C 380	13	26.0	790	13	ADK53103	Adk53103 Plant ful
C 308	13	26.0	581	13	ADU52905	Adu52905 Fusarium	C 381	13	26.0	795	11	ABD10153	Abd10153 Pseudomon
C 309	13	26.0	581	13	ADZ90908	Adz90908 Arabidops	C 382	13	26.0	801	6	ABN99043	Abn99043 Arabidops
C 310	13	26.0	584	12	ACH66908	Ach66908 Human gen	C 383	13	26.0	807	2	AAT71749	Aat71749 Fibrobact
C 311	13	26.0	590	10	ADK56782	Adk56782 Plant DNA	C 384	13	26.0	816	4	AA196114	AA196114 Human neu



C 385	13	26.0	818	3	AAC50818	Aac50818	Arabidops	458	13	1338	14	ACT69731	Act69731 M. xanthu
C 386	13	26.0	822	3	AAC33622	Aac33622	Arabidops	C 459	13	1340	14	ACT63857	Act63857 M. xanthu
C 387	13	26.0	825	13	ADX64265	Adx64265	Plant ful	C 460	13	1341	14	ACT71692	Act71692 M. xanthu
C 388	13	26.0	834	14	ACL72229	Act72229	M. xanthu	C 461	13	1345	13	ADV04908	Adv04908 Nicotiana
C 389	13	26.0	835	4	AAH04103	Aah04103	Human cDN	C 462	13	1356	8	ACA47963	Act47963 Prokaryot
C 390	13	26.0	845	3	AAC36937	Aac36937	Arabidops	C 463	13	1360	9	ACD98379	Acc98379 A. thalia
C 391	13	26.0	853	3	AAC34182	Aac34182	Arabidops	C 464	13	1360	10	ADD55751	Add55751 Thalecres
C 392	13	26.0	864	4	AB113167	Ab113167	Drosophill	C 465	13	1360	12	ADI43562	Adi43562 Plant tra
C 393	13	26.0	882	6	ABQ29808	Abq29808	Oligonuc	C 466	13	1360	12	ADI61324	Adi61324 cDNA enco
C 394	13	26.0	882	6	ABQ29809	Abq29809	Oligonuc	C 467	13	1360	12	ADO01940	Ado01940 Thalecres
C 395	13	26.0	912	6	ACF70695	Act70695	Photornab	C 468	13	1360	12	ADO03374	Ado03374 Thalecres
C 396	13	26.0	922	13	ADX13916	Adx13916	Plant DNA	C 469	13	1360	14	AEA27088	Aea27088 Streps to
C 397	13	26.0	935	10	ADX65781	Adx65781	Plant ful	C 470	13	1374	6	ABN70973	Abn70973 Streptoco
C 398	13	26.0	958	6	AA562742	Aae62742	cDNA sequ	C 471	13	1377	13	ADV84332	Adv84332 Streptoco
C 399	13	26.0	959	6	ABQ29637	Abq29637	Oligonuc	C 472	13	1380	3	AAA53603	Aaa53603 M. tuberc
C 400	13	26.0	959	6	ABQ29636	Abq29636	Oligonuc	C 473	13	1401	4	ABL27523	Ab127523 Drosophill
C 401	13	26.0	981	6	ABL53115	Ab153115	Micro-org	C 474	13	1401	6	ABN68725	Abn68725 Streptoco
C 402	13	26.0	981	8	ABZ51484	Abz51484	Aspergill	C 475	13	1413	10	ADF01495	Adf01495 Bacteriat
C 403	13	26.0	986	13	ADX11441	Adx11441	Plant ful	C 476	13	1416	10	ADK57306	Adk57306 Plant DNA
C 404	13	26.0	987	8	AA529664	Aad52964	Moraxella	C 477	13	1418	14	ADM93336	Adm93336 C. subver
C 405	13	26.0	991	13	ADX61143	Adx61143	Plant ful	C 478	13	1418	14	ADY52722	Ady52722 Ceritporio
C 406	13	26.0	996	8	ACF73537	Act73537	Streptylot	C 479	13	1434	6	ABL42037	Ab142037 Nucleotid
C 407	13	26.0	1002	8	ACA38071	Act38071	Prokaryot	C 480	13	1435	6	AMS18563	Ams18563 Xylella f
C 408	13	26.0	1005	6	ABK73893	Abk73893	Bacilllus	C 481	13	1460	6	AAH88585	Aah88585 Human GCR
C 409	13	26.0	1005	6	ADS62524	Ad62524	Bacteriat	C 482	13	1470	6	AB214084	Ab214084 Arabidops
C 410	13	26.0	1005	13	ADS59540	Ad59540	Bacteriat	C 483	13	1477	13	ADX09593	Adx09593 Plant ful
C 411	13	26.0	1005	13	ADS62935	Ad62935	Bacteriat	C 484	13	1485	6	ABO52207	Ab052207 Oligonuc
C 412	13	26.0	1008	12	ADL04032	Adl04032	DNA enco	C 485	13	1501	3	AMC36748	Ams36748 Arabidops
C 413	13	26.0	1012	14	ABE26896	Ab26896	Pinus rad	C 486	13	1501	3	AMS53346	Ams53346 Haemophil
C 414	13	26.0	1037	5	ABA18938	Ab18938	Human nar	C 487	13	1512	4	ACA34210	Act34210 Prokaryot
C 415	13	26.0	1052	13	ADX36864	Adx36864	Plant ful	C 488	13	1512	8	ACN34210	Act34210 Prokaryot
C 416	13	26.0	1056	11	ABD00492	Abd00492	Klebsiell	C 489	13	1514	3	AACT9643	Aac79643 Virulence
C 417	13	26.0	1059	3	AAC53269	Aac53269	Arabidops	C 490	13	1514	6	ABO83520	Ab083520 Pasteurel
C 418	13	26.0	1068	13	ADR85502	Adr85502	Aspergill	C 491	13	1542	13	ADT48223	Adt48223 Bacteriat
C 419	13	26.0	1074	13	ADX28886	Adx28886	Plant ful	C 492	13	1547	13	ADS60460	Ad60460 Bacteriat
C 420	13	26.0	1080	14	ADX05047	Adx05047	Horae alt	C 493	13	1551	13	ADS58580	Ad58580 Bacteriat
C 421	13	26.0	1084	6	ABQ18719	Abq18719	Oligonuc	C 494	13	1559	12	ADQ23543	Adq23543 Human sof
C 422	13	26.0	1084	6	ABO18718	Ab018718	Oligonuc	C 495	13	1565	13	ADX31271	Adx31271 Plant ful
C 423	13	26.0	1084	14	ABR27006	Ab27006	Pinus rad	C 496	13	1605	3	AAC49422	Aac49422 Arabidops
C 424	13	26.0	1087	2	AA727350	Aat727350	Meioidogy	C 497	13	1607	3	AAC36102	Aac36102 Arabidops
C 425	13	26.0	1094	6	ABK30611	Abk30611	Plant dwa	C 498	13	1612	1	AMN60392	Ams60392 Sequence
C 426	13	26.0	1094	6	ABL49424	Ab149424	Sequence	C 499	13	1629	4	AAH32797	Aah32797 Human sec
C 427	13	26.0	1094	6	ADY47059	Ady47059	Plant ful	C 500	13	1629	8	ABZ73319	Abz73319 Secreted
C 428	13	26.0	1101	11	ABD10427	Abd10427	Pseudomon	C 501	13	1629	8	ADA97932	Ada97932 Human sec
C 429	13	26.0	1101	2	AA727351	Aat727351	Meioidogy	C 502	13	1629	8	ADA43844	Ad43844 Human sec
C 430	13	26.0	1117	4	AAK72072	Aak72072	Human imm	C 503	13	1629	10	ADFC0092	Adc0092 Human sec
C 431	13	26.0	1117	4	AAK72071	Aak72071	Human imm	C 504	13	1629	10	ADFI0561	Adfi0561 Human sec
C 432	13	26.0	1118	13	ABE27005	Ab27005	Pinus rad	C 505	13	1629	10	ABZ66932	Abz66932 Human sec
C 433	13	26.0	1121	13	ADT15741	Adt15741	Plant cDN	C 506	13	1656	9	ADA48687	Ada48687 Rice gene
C 434	13	26.0	1134	11	ACH99580	Ach99580	Klebsiell	C 507	13	1656	9	ADA48243	Ada48243 Rice gene
C 435	13	26.0	1147	6	ABQ44263	Abq44263	Oligonuc	C 508	13	1664	6	ABL39598	Ab139598 Human can
C 436	13	26.0	1147	6	ABQ44262	Abq44262	Oligonuc	C 509	13	1692	13	ADT45472	Adt45472 Bacteriat
C 437	13	26.0	1155	10	ADC91570	Adc91570	E. faeciu	C 510	13	1701	13	ADO82386	Ado82386 Plant ful
C 438	13	26.0	1166	14	ABE27003	Ab27003	Pinus rad	C 511	13	1715	13	ADX29016	Adx29016 Plant ful
C 439	13	26.0	1179	14	ABE65604	Aeb65604	Rice geno	C 512	13	1719	13	ADX64286	Adx64286 Plant ful
C 440	13	26.0	1194	12	ADJ34593	Adj34593	DNA enco	C 513	13	1728	13	ADX10675	Adx10675 Plant ful
C 441	13	26.0	1197	4	AB129887	Ab129887	Drosophill	C 514	13	1737	8	ACA25297	Aca25297 Prokaryot
C 442	13	26.0	1201	13	ADK48941	Adk48941	Plant ful	C 515	13	1755	8	ACA39688	Act39688 Prokaryot
C 443	13	26.0	1218	6	ADA28936	Ada28936	DNA enco	C 516	13	1764	4	ABL27679	Ab127679 Drosophill
C 444	13	26.0	1236	6	ABQ16826	Abq16826	Oligonuc	C 517	13	1764	4	ADL45904	Adl45904 Human ova
C 445	13	26.0	1269	10	ADT16996	Adt16996	Plant cDN	C 518	13	1776	14	ACT170583	Act170583 M. xanthu
C 446	13	26.0	1287	14	ABE27004	Ab27004	Pinus rad	C 519	13	1797	4	ABL23649	Ab123649 Drosophill
C 447	13	26.0	1293	8	ACA44004	Aca44004	Prokaryot	C 520	13	1803	13	ADX54077	Adx54077 Plant ful
C 448	13	26.0	1305	8	ACA43644	Act43644	Prokaryot	C 521	13	1809	13	ADT45158	Adt45158 Bacteriat
C 449	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 522	13	1812	10	ADA53958	Ada53958 Bacteriat
C 450	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 523	13	1820	13	ADK13584	Adk13584 Plant ful
C 451	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 524	13	1843	10	ADK53717	Adk53717 Human cod
C 452	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 525	13	1848	8	ABX08473	Abx08473 DNA enco
C 453	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 526	13	1857	13	ADU07417	Adu07417 Human cDN
C 454	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 527	13	1857	13	AAH15458	Aah15458 Human cDN
C 455	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 528	13	1916	4	AA531435	Aas31435 Human cDN
C 456	13	26.0	1311	2	AA554290	Aas54290	Pseudomon	C 529	13	1916	6	ABQ66759	Abq66759 Human pol
C 457	13	26.0	1332	4	ABL22381	Ab122381	Drosophill	C 530	13	1916	10	ADCI0781	Adci0781 Human cDN



C 531	13	26.0	1917	3	AAFI6019	Human pro	604	13	26.0	2726	12	AD167047	AD167047 Novel	Lac
C 532	13	26.0	1918	6	AA531327	Human cDN	605	13	26.0	2751	10	ACRF7761	ACRF7761 Photorhab	
C 533	13	26.0	1918	6	AB066551	Human pol	606	13	26.0	2774	4	ABL09942	ABL09942 Drosophill	
C 534	13	26.0	1918	10	ADCI0673	Human cDN	607	13	26.0	2902	4	ABL27678	ABL27678 Drosophill	
C 535	13	26.0	1918	12	ADH51279	Surrogate	608	13	26.0	2903	4	ABL25414	ABL25414 Drosophill	
C 536	13	26.0	1941	3	AAc69622	Human sec	609	13	26.0	3007	12	ADN98944	ADN98944 Drosophill	
C 537	13	26.0	1941	8	ABZ73417	Secreted	610	13	26.0	3090	6	ABK89045	ABK89045 Transposi	
C 538	13	26.0	1941	8	ADA97984	Human sec	611	13	26.0	3132	6	ABK48054	ABK48054 CDNA enco	
C 539	13	26.0	1941	10	ABZ67022	Human sec	612	13	26.0	3141	2	AAV71746	AAV71746 Fibroact	
C 540	13	26.0	2000	6	ABZ17414	Arabidops	613	13	26.0	3163	4	AAI59475	AAI59475 Human pol	
C 541	13	26.0	2000	6	ABZ17281	Arabidops	614	13	26.0	3173	6	ABN59891	ABN59891 Novel hum	
C 542	13	26.0	2000	8	ADA68890	Arabidops	615	13	26.0	3218	12	ADOC63784	ADOC63784 Novel hum	
C 543	13	26.0	2000	10	ACC60993	Gene sequ	616	13	26.0	3231	12	ADOC97827	ADOC97827 Human can	
C 544	13	26.0	2000	10	ADK62375	Disease t	617	13	26.0	3247	4	AAI59476	AAI59476 Human pol	
C 545	13	26.0	2000	11	ACL38304	Rice etre	618	13	26.0	3271	14	ADY37344	ADY37344 Non-codin	
C 546	13	26.0	2000	11	ACL37492	Rice etre	619	13	26.0	3286	14	ADY37346	ADY37346 Non-codin	
C 547	13	26.0	2000	11	ACL36317	Rice etre	620	13	26.0	3332	12	ADQC97829	ADQC97829 Human can	
C 548	13	26.0	2000	11	ACL38005	Rice etre	621	13	26.0	3336	12	ADQC97825	ADQC97825 Human can	
C 549	13	26.0	2000	11	ACL36816	Rice etre	622	13	26.0	3390	12	ADQ30762	ADQ30762 A fumigat	
C 550	13	26.0	2000	11	ACL37303	Rice etre	623	13	26.0	3402	6	ABN70514	ABN70514 Streptoco	
C 551	13	26.0	2005	4	AAFI8105	Human sec	624	13	26.0	3402	12	ADQ10472	ADQ10472 DNA enco	
C 552	13	26.0	2015	13	ADT19899	Plant cDN	625	13	26.0	3402	12	ADZ02906	ADZ02906 Streptoco	
C 553	13	26.0	2049	13	AD557895	Bacterial	626	13	26.0	3453	13	ADU69394	ADU69394 S agalact	
C 554	13	26.0	2070	3	AAFI21689	Human bre	627	13	26.0	3453	13	ADV84265	ADV84265 Streptoco	
C 555	13	26.0	2074	6	ABQ76949	Human ner	628	13	26.0	3543	6	ABN66454	ABN66454 Streptoco	
C 556	13	26.0	2075	2	AAQ46554	C. neofo	629	13	26.0	3546	13	ADR83817	ADR83817 S. pyogen	
C 557	13	26.0	2080	6	ABQ54584	Human ova	630	13	26.0	3553	14	ADX05045	ADX05045 Horae IL4	
C 558	13	26.0	2092	13	ADX30963	Human ova	631	13	26.0	3575	4	ABL13166	ABL13166 Drosophill	
C 559	13	26.0	2092	12	ADN73818	Thale cre	632	13	26.0	3656	4	ABL24634	ABL24634 Drosophill	
C 560	13	26.0	2130	12	ADN73818	Thale cre	633	13	26.0	3703	13	ADRO6569	ADRO6569 Full leng	
C 561	13	26.0	2135	8	ABT42911	Human neu	634	13	26.0	3756	13	ADQ86784	ADQ86784 Human tum	
C 562	13	26.0	2165	13	ADX53477	Plant ful	635	13	26.0	3767	5	ABX71408	ABX71408 Human tes	
C 563	13	26.0	2176	3	AAFC51825	Arabidops	636	13	26.0	3797	4	ABL23648	ABL23648 Drosophill	
C 564	13	26.0	2177	13	ADX46717	Plant ful	637	13	26.0	3813	4	ABL27522	ABL27522 Drosophill	
C 565	13	26.0	2180	2	AAV07121	Altermo	638	13	26.0	3817	4	ABL24634	ABL24634 Drosophill	
C 566	13	26.0	2207	10	ADB61982	Human cDN	639	13	26.0	3933	8	ADA69695	ADA69695 Rice gene	
C 567	13	26.0	2217	3	AAFC51366	Arabidops	640	13	26.0	3968	6	ABQ76374	ABQ76374 S. cerevi	
C 568	13	26.0	2233	12	ADQ25443	Human bof	641	13	26.0	3975	6	ABU02896	ABU02896 Drosophill	
C 569	13	26.0	2261	14	ABZ23946	Human PRO	642	13	26.0	4011	4	ABL30268	ABL30268 Drosophill	
C 570	13	26.0	2358	12	ADQ30791	A fumigat	643	13	26.0	4074	10	ADBS69083	ADBS69083 C. neofo	
C 571	13	26.0	2379	8	ACA30692	Prokaryot	644	13	26.0	4131	2	AAV89290	AAV89290 Dogfish s	
C 572	13	26.0	2382	3	AAA96494	C. neofo	645	13	26.0	4131	6	ABD41631	ABD41631 SKCR DNA	
C 573	13	26.0	2474	13	ADR84612	Aspergill	646	13	26.0	4134	6	ABK14910	ABK14910 DNA enco	
C 574	13	26.0	2497	13	ADT20038	Plant cDN	647	13	26.0	4134	6	ABL59964	ABL59964 Dogfish s	
C 575	13	26.0	2516	4	ABL10045	Drosophill	648	13	26.0	4134	10	ADH10916	ADH10916 Shark pol	
C 576	13	26.0	2530	13	ADSL14604	Pseudomon	649	13	26.0	4134	10	AAD64738	AAD64738 Dogfish s	
C 577	13	26.0	2536	12	ADL90456	Clostridi	650	13	26.0	4134	12	AD119962	AD119962 Dogfish s	
C 578	13	26.0	2586	12	ADL90375	Clostridi	651	13	26.0	4197	8	ACA45555	ACA45555 Prokaryot	
C 579	13	26.0	2592	12	ADL90452	Clostridi	652	13	26.0	4199	4	ABL22380	ABL22380 Drosophill	
C 580	13	26.0	2592	12	ADL90383	Clostridi	653	13	26.0	4233	8	ACRA3760	ACRA3760 Prokaryot	
C 581	13	26.0	2592	12	ADL90454	Clostridi	654	13	26.0	4260	12	ADL90391	ADL90391 Clostridi	
C 582	13	26.0	2595	12	ADL90381	Clostridi	655	13	26.0	4356	4	ABL06508	ABL06508 Drosophill	
C 583	13	26.0	2597	4	ABL25416	Drosophill	656	13	26.0	4371	2	AAV81917	AAV81917 Caenorhab	
C 584	13	26.0	2598	12	ADL90369	Clostridi	657	13	26.0	4518	10	ADP81917	ADP81917 Leukaemia	
C 585	13	26.0	2598	12	ADL90385	Clostridi	658	13	26.0	4523	13	ADQ85404	ADQ85404 Human tum	
C 586	13	26.0	2601	12	ADL90379	Clostridi	659	13	26.0	4523	14	ADX98504	ADX98504 Human BAI	
C 587	13	26.0	2601	12	ADL90379	Clostridi	660	13	26.0	4526	4	AAK81822	AAK81822 Human imm	
C 588	13	26.0	2601	12	ADL90379	Clostridi	661	13	26.0	4532	14	ACL64163	ACL64163 M. xanthu	
C 589	13	26.0	2607	5	AAFI97848	Human neu	662	13	26.0	4668	13	ADR25108	ADR25108 Breast ca	
C 590	13	26.0	2610	12	ADL90373	Clostridi	663	13	26.0	4684	12	ADQ18635	ADQ18635 Human bof	
C 591	13	26.0	2613	12	ADL90371	Clostridi	664	13	26.0	4849	4	ABL08580	ABL08580 Drosophill	
C 592	13	26.0	2613	12	ADL90365	Clostridi	665	13	26.0	4859	5	ABV29317	ABV29317 Human pro	
C 593	13	26.0	2613	12	ADL90367	Clostridi	666	13	26.0	4859	5	ABV23122	ABV23122 Human pro	
C 594	13	26.0	2628	12	ADL90387	Clostridi	667	13	26.0	4859	5	ABV23459	ABV23459 Human pro	
C 595	13	26.0	2628	12	ADL90363	Clostridi	668	13	26.0	4859	5	ABV28963	ABV28963 Human pro	
C 596	13	26.0	2628	12	ADL90389	Clostridi	669	13	26.0	4861	4	ABL29670	ABL29670 Drosophill	
C 597	13	26.0	2634	11	ABD10372	Pseudomon	670	13	26.0	4997	8	ACA47635	ACA47635 Prokaryot	
C 598	13	26.0	2657	4	ABL18896	Drosophill	671	13	26.0	5051	4	ABL29693	ABL29693 Drosophill	
C 599	13	26.0	2664	12	ADL90393	Clostridi	672	13	26.0	5097	14	ACL69092	ACL69092 M. xanthu	
C 600	13	26.0	2669	2	AAQ03738	Mitecanthu	673	13	26.0	5176	4	AAK84365	AAK84365 Human imm	
C 601	13	26.0	2718	3	AAZ46362	Haemorrhha	674	13	26.0	5184	6	ABK31485	ABK31485 Signal tr	
C 602	13	26.0	2720	2	AAK81870	DNA enco	675	13	26.0	5184	6	ABL70454	ABL70454 Chemicall	
C 603	13	26.0	2726	12	AD167035	Novel Lac	676	13	26.0	5184	6	AA561421	AA561421 Human gen	



c 677	13	26.0	5244	8	AB210025	Abz110025 Haematopo	c 750	13	13225	8	ACF64492	Acf64492 Propionib
c 678	13	26.0	5244	8	AB210171	Abz10171 Haematopo	751	13	13375	6	ABO93457	ABO93457 Human cDN
c 679	13	26.0	5252	6	ABK28302	Abk28302 Human trans	752	13	13468	6	ABO93458	ABO93458 Human cDN
c 680	13	26.0	5379	6	ABJ32330	Abj32330 Human imm	753	13	13509	8	ABX76175	Abx76175 Lung canc
c 681	13	26.0	5422	10	ACC45138	Acc45138 Escherich	754	13	13509	10	ADB85658	Ad85658 Farnesyl
c 682	13	26.0	5476	4	AA545500	AA545500 Chemicali	755	13	13509	10	ADF18734	Adf18734 DNA-depen
c 683	13	26.0	5476	6	ABJ34115	Abj34115 Human imm	756	13	13509	14	ADX05477	Adx05477 Cyclin-de
c 684	13	26.0	5476	6	ABJ49382	Abj49382 Human pol	757	13	13511	6	ABL32280	Ab132280 Human imm
c 685	13	26.0	5499	5	ABO66972	Ab066972 Human ang	758	13	14158	14	ACL64606	Ac164606 M. xanthu
c 686	13	26.0	5569	5	AA572560	AA572560 DNA encod	759	13	14335	4	AAF28524	AAF28524 Genomic f
c 687	13	26.0	5816	11	ACN91561	Acn91561 Breast ca	760	13	14361	4	ABL02618	Ab102618 Drosophi
c 688	13	26.0	5917	6	ABK31468	Abk31468 Signal tr	761	13	14449	4	ABL11710	Ab111710 Drosophi
c 689	13	26.0	5922	6	ABJ32451	Abj32451 Human imm	762	13	14449	4	ABL11692	Ab111692 Drosophi
c 690	13	26.0	5951	6	AA545409	AA545409 Chemicali	763	13	15059	13	ADP55625	ADP55625 Human PRO
c 691	13	26.0	5951	6	ABK28260	Abk28260 DNA trans	764	13	15059	14	ADY18324	Ady18324 Human enco
c 692	13	26.0	6075	6	ABJ33550	Abj33550 Human imm	765	13	15308	4	ABL27868	Ab127868 Drosophi
c 693	13	26.0	6160	6	ABK31273	Abk31273 Signal tr	766	13	15861	6	ABJ32524	Abj32524 Human imm
c 694	13	26.0	6160	6	ABJ70234	Abj70234 Chemicali	767	13	16329	5	ABJ14411	Abj14411 Human tier
c 695	13	26.0	6276	4	ABJ29886	Abj29886 Drosophi	768	13	16914	6	ABL70316	Ab170316 Chemicali
c 696	13	26.0	6277	4	AA546323	AA546323 Tumour su	769	13	16914	6	AA561254	AA561254 Human gen
c 697	13	26.0	6350	6	ABK31198	Abk31198 Signal tr	770	13	19820	8	AAJ36348	AAJ36348 Human mus
c 698	13	26.0	6350	6	ABJ70165	Abj70165 Chemicali	771	13	19820	8	AAJ59336	AAJ59336 CDNA enco
c 699	13	26.0	6350	6	AA561110	AA561110 Human gen	772	13	19820	12	ADJ30086	Adj30086 Human mus
c 700	13	26.0	6505	10	ADC01390	Adc01390 Enteroha	773	13	24200	4	ABL21182	Ab121182 Drosophi
c 701	13	26.0	6506	9	ACD18988	Ac18988 E. coli 0	774	13	24206	4	ABL21180	Ab121180 Drosophi
c 702	13	26.0	6839	4	ABJ01920	Abj01920 Drosophi	775	13	25800	12	ADQ97464	Adq97464 Mouse can
c 703	13	26.0	6839	4	ABJ01920	Abj01920 Drosophi	776	13	25800	12	AAZ46355	AAZ46355 Haemorrh
c 704	13	26.0	6873	14	ACT64374	Act64374 M. xanthu	777	13	26270	3	ABD23878	Abd23878 Human can
c 705	13	26.0	6973	6	ABJ33778	Abj33778 Human imm	778	13	26278	13	ABD23878	Abd23878 Human can
c 706	13	26.0	7005	13	AD547818	Ad547818 Bacteri	779	13	28854	8	ABX95685	Abx95685 Human gen
c 707	13	26.0	7025	4	ABJ10044	Abj10044 Drosophi	780	13	29392	2	AAV15422	AAV15422 Mouse pol
c 708	13	26.0	7099	4	AAJ04882	AAj04882 Human rep	781	13	32183	5	AAI99267	AAI99267 Human exc
c 709	13	26.0	7099	4	ABJ97776	Abj97776 Human tes	782	13	32187	5	AAI63617	AAI63617 Human kid
c 710	13	26.0	7254	12	ADO07825	Ado07825 FLY poly	783	13	32187	4	AAK42663	AAK42663 Genomic s
c 711	13	26.0	7382	2	AAK87336	AAk87336 Aspergill	784	13	32187	9	AAK60819	AAk60819 Connecti
c 712	13	26.0	7537	4	ABL09602	Ab109602 Drosophi	785	13	32192	4	AAI99266	AAI99266 Human exc
c 713	13	26.0	7675	4	ABJ29692	Abj29692 Drosophi	786	13	32192	5	AAI63616	AAI63616 Human kid
c 714	13	26.0	7682	13	ADR84321	Adr84321 Aspergill	787	13	32193	4	ABK42662	ABK42662 Genomic s
c 715	13	26.0	7784	6	ABJ34425	Abj34425 Human imm	788	13	32193	9	ADB60818	AdB60818 Connecti
c 716	13	26.0	7789	11	ACN88701	Acn88701 Breast ca	789	13	33472	4	ABL19792	Ab119792 Drosophi
c 717	13	26.0	8006	13	ADV87687	Adv87687 Streptoco	790	13	33923	4	AAK67071	AAK67071 Human imm
c 718	13	26.0	8006	13	ADV78940	Adv78940 Streptoco	791	13	36412	10	ADB74383	AdB74383 Mycobacte
c 719	13	26.0	8244	4	AA546395	AA546395 Tumour su	792	13	37476	14	ADM38519	Adm38519 Immunomod
c 720	13	26.0	8244	6	ABJ32982	Abj32982 Human imm	793	13	37973	6	ABJ34196	Abj34196 Human imm
c 721	13	26.0	8244	6	ABO67031	Ab067031 Human ang	794	13	39353	4	AAK67232	AAK67232 Human imm
c 722	13	26.0	8244	10	ADB54261	AdB54261 Pretreate	795	13	39353	4	AAK65396	AAK65396 Human imm
c 723	13	26.0	8244	10	ADB54261	AdB54261 Pretreate	796	13	39358	4	AAK65397	AAK65397 Human imm
c 724	13	26.0	8354	4	ABJ23606	Abj23606 Drosophi	797	13	39358	4	AAK67233	AAK67233 Human imm
c 725	13	26.0	8777	4	ABN80133	Abn80133 Human che	798	13	39780	10	ADB72395	AdB72395 Mouse Sem
c 726	13	26.0	8910	6	AA546730	AA546730 Tumour su	799	13	39780	10	ADB72395	AdB72395 Mouse Sem
c 727	13	26.0	9502	4	AA546730	AA546730 Tumour su	800	13	39780	10	ADB72395	AdB72395 Mouse Sem
c 728	13	26.0	9767	6	ABJ14016	Abj14016 Drosophi	801	13	41170	14	ACT64804	Act64804 M. xanthu
c 729	13	26.0	9810	6	ABJ32427	Abj32427 Human imm	802	13	41188	4	AAK87512	AAK87512 Human imm
c 730	13	26.0	9814	6	ABK31428	Abk31428 Signal tr	803	13	43011	12	ADN01941	Adn01941 Strephilo
c 731	13	26.0	9817	6	ABJ33368	Abj33368 Human imm	804	13	43576	3	AA686809	AA686809 Bacterio
c 732	13	26.0	9822	4	AAK69390	AAK69390 Human imm	805	13	48509	13	ABD33397	ABD33397 Human can
c 733	13	26.0	9859	6	ABJ24132	Abj24132 Human imm	806	13	49806	11	ACN44528	Acn44528 Mouse gen
c 734	13	26.0	10286	6	AA545308	AA545308 Chemicali	807	13	56153	4	AA546794	AA546794 Tumour su
c 735	13	26.0	10286	6	ABK28147	Abk28147 DNA trans	808	13	56737	6	AB566985	AB566985 Human hyp
c 736	13	26.0	10322	3	AAZ46680	AAZ46680 Blast dis	809	13	57763	10	ADK02528	ADK02528 Human MYB
c 737	13	26.0	10820	13	ADRI6680	Adr16680 RNA of at	810	13	57763	10	ADB72266	AdB72266 Human MYB
c 738	13	26.0	11009	13	ADT05535	Adt05535 Haemophi	811	13	64976	2	AAV21409_16	AAV21409_16 Con
c 739	13	26.0	11459	2	AAK06876	AAK06876 Strephilo	812	13	65720	14	AD213747_3	Ad213747_3 Con
c 740	13	26.0	11466	2	AAV74755	AAV74755 Strephilo	813	13	65720	14	AD213747_3	Ad213747_3 Con
c 741	13	26.0	11580	4	ABJ08832	Abj08832 Streptoco	814	13	66886	9	AAK28542	AAK28542 Mouse Itk
c 742	13	26.0	11617	13	ADV87698	Adv87698 Streptoco	815	13	67832	9	ADK02801	ADK02801 Mouse Itk
c 743	13	26.0	11617	13	ADV78951	Adv78951 Streptoco	816	13	67832	10	ADB72539	AdB72539 Mouse Itk
c 744	13	26.0	11774	4	AAK90413	AAK90413 Human dig	817	13	67832	10	ADK85281	ADK85281 Mouse Itk
c 745	13	26.0	11774	4	AAK69391	AAK69391 Human imm	818	13	67832	12	ADM74396	AdM74396 Murine ca
c 746	13	26.0	11774	5	AAK39969	AAK39969 Genomic s	819	13	72592	12	AAK22300	AAK22300 BAC contra
c 747	13	26.0	11774	9	ADB32929	AdB32929 Human nov	820	13	73742	12	ADQ97824	AdQ97824 Human can
c 748	13	26.0	12709	6	AA518570	AA518570 Xylella f	821	13	76138	12	ADQ97824	AdQ97824 Human can
c 749	13	26.0	13225	4	AA559563	AA559563 Propionib	822	13	76363	8	ACF30938	AcF30938 Rice cult



C 823	13	26.0	76363	12	AD109997	Ad109997 Rice cult	C 896	13	26.0	110000	14	AE839175_32	Continuation (33 o
C 824	13	26.0	76363	12	ADK72433	AdK72433 Rice fert	C 897	13	26.0	110000	14	AE842401_03	Continuation (4 of
C 825	13	26.0	76363	14	ADV65783	AdV65783 Rice chro	C 898	13	26.0	110000	14	AE842401_31	Continuation (32 o
C 826	13	26.0	76846	11	ACN44380	Acn44380 Mouse gen	C 899	13	26.0	110000	14	AE835723_0	Continuation (32 o
C 827	13	26.0	80331	4	AAc89599	AAc89599 Human his	C 900	13	26.0	113550	6	ABL34175	ABL34175 Human imm
C 828	13	26.0	86248	10	ADCO0087	ADCO0087 Enterohae	C 901	13	26.0	115050	14	AD212553	Ad212553 Murine ca
C 829	13	26.0	86574	6	ABK83560	ABK83560 Human cdn	C 902	13	26.0	120144	13	ABD33161	Abd33161 Murine ca
C 830	13	26.0	86574	13	ADRS5822	ADRS5822 Drug ther	C 903	13	26.0	127567	14	AE641137	AE641137 Murine ca
C 831	13	26.0	87394	13	ADTS5151	ADTS5151 Nucleotid	C 904	13	26.0	131885	14	AE839176	AE839176 Human BCA
C 832	13	26.0	87563	9	ACD19044	ACd19044 B. coli 0	C 905	13	26.0	135356	13	ADT05646	Adt05646 Haemophil
C 833	13	26.0	89378	12	ADN46845_20	Continuation (21 o	C 906	13	26.0	141503	12	ADOC59464	Adoc59464 Human can
C 834	13	26.0	89378	12	ADN46123_20	Continuation (21 o	C 907	13	26.0	141912	10	ADOC6530	Adoc6530 Human GPC
C 835	13	26.0	89378	12	ADN46464_20	Continuation (21 o	C 908	13	26.0	144179	11	ACN44188	ACn44188 Mouse gen
C 836	13	26.0	91609	12	ADOS9473	Ados9473 Human can	C 909	13	26.0	148567	9	ACA62841	ACA62841 Human kin
C 837	13	26.0	91609	14	ADZ13834	Adz13834 Murine ca	C 910	13	26.0	148567	10	ABSS5500	ABss5500 Gene enco
C 838	13	26.0	92076	13	ABD33368	Abd33368 Murine ca	C 911	13	26.0	148567	12	ADL09163	Adl09163 Human pro
C 839	13	26.0	98686	12	AD180019	Ad180019 Human tra	C 912	13	26.0	148567	14	ADZ58499	Adz58499 Human ser
C 840	13	26.0	98948	13	ABD33256	ABd33256 Human can	C 913	13	26.0	149612	11	ACN45154	ACn45154 Human gen
C 841	13	26.0	101786	3	AAE22293	AAe22293 BAC conta	C 914	13	26.0	158001	12	ADL17884	ADl17884 Human pho
C 842	13	26.0	103747	6	ABO88139	ABq88139 Human ost	C 915	13	26.0	170170	10	ADL13643	ADl13643 Osteoarth
C 843	13	26.0	105295	14	AE835712	AEb35712 L. pneumo	C 916	13	26.0	171398	14	ADZ13359	ADz13359 Human can
C 844	13	26.0	110000	2	AAV42063_07	Continuation (8 of	C 917	13	26.0	180557	6	ABN85750	ABN85750 Human BAC
C 845	13	26.0	110000	2	AAV21209_04	Continuation (5 of	C 918	13	26.0	186510	10	ADZ24797	ADZ24797 Human end
C 846	13	26.0	110000	2	AAV30458_1	Continuation (2 of	C 919	13	26.0	191584	13	ABD33586	ABD33586 Human can
C 847	13	26.0	110000	2	AAV30459_1	Continuation (2 of	C 920	13	26.0	191584	13	ADP67026	ADp67026 Human can
C 848	13	26.0	110000	2	AAZ01425_05	Continuation (6 of	C 921	13	26.0	192992	13	ABD32866	ABd32866 Mouse can
C 849	13	26.0	110000	2	AAZ01425_08	Continuation (7 of	C 922	13	26.0	194588	14	AE835717	AE835717 L. pneumo
C 850	13	26.0	110000	2	AAZ01425_08	Continuation (9 of	C 923	13	26.0	207433	8	ABX74891	ABx74891 Bacterial
C 851	13	26.0	110000	2	AAZ01425_09	Continuation (10 o	C 924	13	26.0	207433	12	ADJ36614	ADj36614 Bacterial
C 852	13	26.0	110000	2	AAZ01425_06	Continuation (7 of	C 925	13	26.0	207433	8	ADJ36614	ADj36614 Bacterial
C 853	13	26.0	110000	4	AA199682_00	AA199682 Mycobacte	C 926	13	26.0	207433	12	ADL81193	ADl81193 BAC109812
C 854	13	26.0	110000	4	AA199682_01	Continuation (2 of	C 927	13	26.0	220895	6	ABK84798	ABk84798 Human cdn
C 855	13	26.0	110000	4	AA199682_14	Continuation (15 o	C 928	13	26.0	220895	13	ADR52737	ADR52737 Drug ther
C 856	13	26.0	110000	4	AA199682_40	Continuation (41 o	C 929	13	26.0	231222	10	ADL13693	ADL13693 Osteoarth
C 857	13	26.0	110000	4	AA199683_00	AA199683 Mycobacte	C 930	13	26.0	248999	12	ADQ97365	ADq97365 Human can
C 858	13	26.0	110000	4	AA199683_01	Continuation (2 of	C 931	13	26.0	256157	11	ACN44650	ACn44650 Human gen
C 859	13	26.0	110000	4	AA199683_14	Continuation (15 o	C 932	13	26.0	256157	13	ABD33570	ABD33570 Human can
C 860	13	26.0	110000	4	AA199683_40	Continuation (41 o	C 933	13	26.0	256157	11	ACN44068	ACn44068 Mouse gen
C 861	13	26.0	110000	6	ABN71527_10	Continuation (11 o	C 934	13	26.0	308766	13	ADT05738	ADt05738 Haemophil
C 862	13	26.0	110000	6	ABN71527_11	Continuation (12 o	C 935	13	26.0	322885	13	ADS93537	ADs93537 Human MRC
C 863	13	26.0	110000	6	ABN71527_12	Continuation (13 o	C 936	13	26.0	326002	13	ABD32843	ABd32843 Human can
C 864	13	26.0	110000	6	ABQ74964_6	Continuation (7 of	C 937	13	26.0	335199	10	ADC24703	ADc24703 Human wil
C 865	13	26.0	110000	6	ABQ67196_3	Continuation (4 of	C 938	13	26.0	342748	14	ADZ13793	ADz13793 Human can
C 866	13	26.0	110000	6	ABQ69245_29	Continuation (30 o	C 939	13	26.0	347814	12	ADQ59440	ADq59440 Human can
C 867	13	26.0	110000	8	AAVS3224_4	Continuation (5 of	C 940	13	26.0	349901	10	ADC86940	ADC86940 Human GPC
C 868	13	26.0	110000	8	AAVS3223_3	Continuation (4 of	C 941	13	26.0	349980	5	AAH41223	AAH41223 Pyrococcu
C 869	13	26.0	110000	10	ACPF6383_3	Continuation (5 of	C 942	13	26.0	349980	5	AAH41223	AAH41223 Pyrococcu
C 870	13	26.0	110000	10	ACPF6367_04	Continuation (4 of	C 943	13	26.0	349999	10	ADC87010	ADC87010 Human GPC
C 871	13	26.0	110000	10	ACPF6367_26	Continuation (27 o	C 944	13	26.0	349999	12	ABT171229	ABt171229 Oligonuc1
C 872	13	26.0	110000	10	ACPF6367_37	Continuation (38 o	C 945	13	26.0	349999	12	ABH64321	ABh64321 Oligonuc1
C 873	13	26.0	110000	10	ACPF6386_10	Continuation (11 o	C 946	13	26.0	349999	13	ABH64320	ABh64320 Oligonuc1
C 874	13	26.0	110000	10	ACPF6386_12	Continuation (3 of	C 947	13	26.0	349999	13	ABH21390	ABh21390 Oligonuc1
C 875	13	26.0	110000	12	ADNA6845_05	Continuation (6 of	C 948	13	26.0	349999	13	ABCT0876	ABc70876 Oligonuc1
C 876	13	26.0	110000	12	ADNA6845_00	Continuation (16 o	C 949	13	26.0	349999	13	ABCT0877	ABc70877 Oligonuc1
C 877	13	26.0	110000	12	ADNA7591_15	Continuation (16 o	C 950	13	26.0	349999	13	ABH21391	ABh21391 Oligonuc1
C 878	13	26.0	110000	12	ADNA7591_15	Continuation (16 o	C 951	13	26.0	349999	13	ABH21391	ABh21391 Oligonuc1
C 879	13	26.0	110000	12	ADNA6123_05	Continuation (6 of	C 952	13	26.0	349999	13	AAV31881	AAv31881 Peptide n
C 880	13	26.0	110000	12	ADNA7209_00	Continuation (16 o	C 953	13	26.0	349999	13	AAZ32650	AAz32650 Murine ca
C 881	13	26.0	110000	12	ADNA7209_15	Continuation (16 o	C 954	13	26.0	349999	21	AAZ32650	AAz32650 Murine ca
C 882	13	26.0	110000	12	ADNA6464_05	Continuation (6 of	C 955	13	26.0	349999	22	ADZ47971	ADz47971 Human LSI
C 883	13	26.0	110000	12	ADNA7960_00	Continuation (16 o	C 956	13	26.0	349999	22	ADZ47971	ADz47971 Human LSI
C 884	13	26.0	110000	12	ADNA7960_15	Continuation (16 o	C 957	13	26.0	349999	24	AAZ719241	AAz719241 Human NOV
C 885	13	26.0	110000	12	ADOS9443_1	Continuation (2 of	C 958	13	26.0	349999	24	ADZ719241	ADz719241 Human NOV
C 886	13	26.0	110000	12	ADQ97331_0	Continuation (9 of	C 959	13	26.0	349999	24	ADZ719241	ADz719241 Human NOV
C 887	13	26.0	110000	13	ABD32966_08	Continuation (9 of	C 960	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 888	13	26.0	110000	13	ABD32966_09	Continuation (10 o	C 961	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 889	13	26.0	110000	13	ADVB1204_12	Continuation (13 o	C 962	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 890	13	26.0	110000	13	ADVB1204_13	Continuation (14 o	C 963	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 891	13	26.0	110000	14	ADZ13754_1	Continuation (14 o	C 964	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 892	13	26.0	110000	14	ADZ12617_1	Continuation (2 of	C 965	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 893	13	26.0	110000	14	ADZ12617_1	Continuation (2 of	C 966	13	26.0	349999	25	AAZ75968	AAz75968 DEN-2 glo
C 894	13	26.0	110000	14	AE61095_0	Continuation (2 of	C 967	13	26.0	349999	26	AAZ75968	AAz75968 DEN-2 glo
C 895	13	26.0	110000	14	AE61095_03	Continuation (4 of	C 968	13	26.0	349999	26	AAZ75968	AAz75968 DEN-2 glo



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969      12      27      12      ADQ30812
C 970      12      27      13      ADG69311
C 971      12      27      13      ADG69250
C 972      12      27      13      ADG69250
973      12      31      4      ABK06610
974      12      31      4      ABK06610
975      12      31      5      ADV49541
976      12      31      6      ACN21829
977      12      31      6      ACN20950
978      12      31      8      ACD54390
979      12      31      8      ACD63094
980      12      31      11      ADM55317
981      12      31      11      AEB62680
982      12      31      11      AEB62742
983      12      31      12      ADM62672
984      12      31      12      ADI90673
C 985      12      34      12      ADJ77939
C 986      12      42      2      AAV59313
C 987      12      42      2      AAZ21029
C 988      12      42      14      AEA52566
C 989      12      42      14      AEA42418
990      12      43      2      AAV59312
991      12      43      2      AAZ21028
992      12      43      14      AEA52565
993      12      43      14      AEA42417
C 994      12      48      5      ADV19143
995      12      50      2      AAV76144
996      12      50      6      ABZ05788
C 997      12      57      6      ABR60410
C 998      12      57      6      ABR60364
C 999      12      57      6      ABR60969
C1000     12      57      6      ABR60741

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## ALIGNMENTS

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RESULT 1
ID      ADR48525 standard; DNA; 50 BP.
XX
AC      ADR48525;
XX
DT      04-NOV-2004 (first entry)
XX
DE      pagA target sequence #3.
XX
KW      Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KW      pXO1; pXO2; target sequence; de.
XX
OS      Bacillus anthracis.
XX
PN      WO2004070001-A2.
XX
PD      19-AUG-2004.
XX
PF      12-NOV-2003; 2003WO-US036240.
XX
PR      15-NOV-2002; 2002US-0426552P.
PR      16-MAY-2003; 2003US-0471082P.
XX
PA      (GENP-) GEN-PROBE INC.
XX
PI      Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX
DR      MPI; 2004-604428/58.
XX
PT      New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT      sequence, useful for detecting cutaneous and respiratory Bacillus anthracis
PT      infections.
XX
PS      Claim 1; SEQ ID NO 23; 61bp; English.
XX

```

CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a Bacillus  
CC anthracis target sequence. The methods and compositions in a Bacillus  
CC anthracis are useful for detecting the presence of Bacillus anthracis  
CC invention are useful for detecting the presence of Bacillus anthracis  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pXO1 and pXO2, without requiring handling of  
CC virulent Bacillus anthracis. The present sequence represents a pagA  
CC target sequence.

XX Sequence 50 BP; 12 A; 12 C; 13 G; 13 T; 0 U; 0 Other;  
XX

Query Match 100.0%; Score 50; DB 13; Length 50;  
Best local Similarity 100.0%; Pred. NO. 2e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Oy      1 GGGACGGCTCCATCTCAACGCTTACCAACGACTTGGTTAGG 50
Db      1 GGGACGGCTCCATCTCAACGCTTACCAACGACTTGGTTAGG 50

```

```

RESULT 2
ID      AAD29118 standard; DNA; 954 BP.
XX
AC      AAD29118;
XX
DT      07-MAY-2002 (first entry)
XX
DE      Bacillus subtilis protective antigen (PA) domain 1b+2 DNA.
XX
KW      Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW      Bacillus anthracis infection; antibacterial; de.
XX
OS      Bacillus subtilis.
XX
PN      WO200204646-A1.
XX
PD      17-JAN-2002.
XX
PF      06-JUL-2001; 2001WO-GB003065.
XX
PR      08-JUL-2000; 2000GB-00016702.
XX
PA      (MINA ) UK SEC FOR DEFENCE.
XX
PI      Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
PI      Flick-Smith HC, Bullifent HL, Tiltball RM, Topping AW;
XX
DR      MPI; 2002-171720/22.
XX
DR      P-PSDB; AAE18286.
XX
PT      New immunogenic reagent having a polypeptide of the full length
PT      Protective Antigen of Bacillus anthracis, useful for treating B.
PT      anthracis infection or in preparing a medicament for the prophylaxis or
PT      treatment of the infection.
XX
PS      Example 5; Fig 3; 40pp; English.
XX

```

CC The present invention relates to an immunogenic reagent, which produces  
CC an immune response that is protective against Bacillus anthracis. The  
CC reagent comprises one or more polypeptides which together represent up to  
CC three domains of the full length Protective Antigen (PA) of Bacillus  
CC anthracis or variants of these, and at least one of the domains comprises



CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
CC vaccine. The immunogenic reagent is useful in the preparation of a  
CC medicament for the prophylaxis or treatment of B. anthracis infection.  
CC The present sequence is Bacillus subtilis protective antigen domain 1b+2  
CC DNA

XX Sequence 954 BP; 351 A; 163 C; 192 G; 248 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 6; Length 954;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 50  
DB 601 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 650

RESULT 3  
ID ADR48535 standard; DNA; 1108 BP.

XX ADR48535;

DT 04-NOV-2004 (first entry)

XX pagA target sequence #5.

KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
KM pXOI; pXO2; target sequence; ds.

OS Bacillus anthracis.

FN WO2004070001-A2.

PD 19-AUG-2004.

PF 12-NOV-2003; 2003WO-US036240.

PR 15-NOV-2002; 2002US-0426552P.

XX 16-MAY-2003; 2003US-0471082P.

PA (GENP-) GEN-PROBE INC.

PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;

DR WPI; 2004-604428/58.

PT New oligonucleotides that hybridize specifically to a Bacillus anthracis  
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax  
PT infections.

PS Claim 21; SEQ ID NO 33; 61pp; English.

CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a Bacillus  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of Bacillus anthracis  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences;  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pXOI and pXO2, without requiring handling of  
CC virulent Bacillus anthracis. The present sequence represents a pagA  
CC target sequence.

XX Sequence 1108 BP; 409 A; 188 C; 224 G; 287 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 13; Length 1108;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 50  
ID 1108 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 50

DB 606 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 655

RESULT 4  
ID ADL16358 standard; DNA; 1272 BP.

XX ADL16358;

DT 06-MAY-2004 (first entry)

DE pBP113 vector DNA for expression of 47kDa PA deletion mutant (PA47).

KW Immunogenic; vaccine; lethal infection; protective antigen; PA;  
KM lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.

OS Bacillus anthracis.

FN Synthetic.

PH Key

FT CDS location/Qualifiers  
FT 1..1272  
FT /\*tag= a  
FT /product= "PA deletion mutant protein (PA47)"  
FT /partial  
FT /note= "No start codon"

FN US2004028695-A1.

PD 12-FEB-2004.

PF 28-MAR-2003; 2003US-00402466.

PR 12-APR-2002; 2002US-0372152P.

PA (PARK/) PARK S.

PA (GIRI/) GIRI L.

PI Park S, Giri L;

DR WPI; 2004-168865/16.

DR P-PSDB; ADL16359.

PT Immunogenic composition for preparing a vaccine against a lethal  
PT infection of Bacillus anthracis in an animal, comprises an immunizing  
PT amount of a recombinant B. anthracis protective antigen protein and/or  
PT lethal factor protein.

PS Disclosure; SEQ ID NO 23; 143pp; English.

CC The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of Bacillus anthracis in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is pBP113 vector DNA for the  
CC expression of Bacillus anthracis 47 kDa N-terminal PA deletion mutant  
CC (PA47). This sequence is used in the invention.

XX Sequence 1272 BP; 507 A; 172 C; 238 G; 355 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 13; Length 1272;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 50  
DB 172 GGGACGGCTCCATCTACACGCTGTACCAACGACTTCGTAGTTAGG 221

RESULT 5  
AAD29119  
ID AAD29119 standard; DNA; 1278 BP.



```

XX AAD29119;
AC 07-MAY-2002 (first entry)
KW Bacillus subtilis protective antigen (PA) domain 1b+2+3 DNA.
XX
XX
XX
XX Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX
XX Bacillus subtilis.
OS
XX
XX Key Location/Qualifiers
FH 1. 1278
FT CDS /tag= a
FT /product= "Domain 1b+2+3"
FT /note= "CDS does not include start and stop codon"
FT /partial
XX
XX WO200204646-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-GB003065.
XX
XX 08-JUL-2000; 2000GB-00016702.
XX
XX (MINA ) UK SEC FOR DEFENCE.
XX
XX Williamson ED, Miller J, Walker NJ, Baillie LMU, Holden PT;
XX Plick-Smith HC, Bullifent HL, Tibball RW, Topping AM;
XX
XX WPI: 2002-171720/22.
XX P-PSDB; AAB18287.
XX
XX New immunogenic reagent having a polypeptide of the full length
XX protective antigen of Bacillus anthracis, useful for treating B.
XX anthracis infection or in preparing a medicament for the prophylaxis or
XX treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
XX an immune response that is protective against Bacillus anthracis. The
XX reagent comprises one or more polypeptides which together represent up to
XX three domains of the full length Protective Antigen (PA) of Bacillus
XX anthracis or variants of these, and at least one of the domains comprises
XX domain 1 or domain 4 of PA or its variant. The invention is used as a
XX vaccine. The immunogenic reagent is useful in the preparation of a
XX medicament for the prophylaxis or treatment of B. anthracis infection.
XX The present sequence is Bacillus subtilis protective antigen domain
XX 1b+2+3 DNA
XX
XX Sequence 1278 BP; 489 A; 210 C; 245 G; 334 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 6; Length 1278;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGACGGCTCCATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50
DB 601 GGGACGGCTCCATCTACACGTTTACCAACGACTTCGTTAGTTAGG 650

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```

XX Antigen; Bacillus anthracis infection; antibacterial; vaccine;
KW protective antigen; PA; ds.
XX
XX Bacillus anthracis.
OS
XX
XX WO2005068493-A1.
XX
XX 28-JUL-2005.
XX
XX 17-JAN-2005; 2005WO-GB000170.
XX
XX 17-JAN-2004; 2004GB-00001036.
XX
XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.
XX
XX Cutting SM;
XX
XX WPI: 2005-563956/57.
XX
XX New non-pathogenic spore comprising an antigenic fragment of anthrax
XX protective antigen, useful as an anthrax vaccine or for manufacturing an
XX anthrax vaccine.
XX
XX Claim 5; SEQ ID NO 10; 90pp; English.
XX
XX The present invention relates to a non-pathogenic spore comprising an
XX antigenic fragment of anthrax protective antigen. Also given is a
XX pharmaceutical composition comprising a non-pathogenic spore comprising
XX at least an antigenic fragment of anthrax protective antigen in
XX association with a pharmaceutical carrier and/or excipient; and methods
XX of inducing immunity to anthrax in a mammal susceptible to anthrax
XX infection. The Bacillus species spore is a spore from many species such
XX as Bacillus alvei; Bacillus badius; Bacillus brevis and preferably a
XX spore from Bacillus subtilis. The spore comprises an antigenic fragment
XX of anthrax protective antigen in the form of a protein attached to the
XX proteinaceous coat of the spore. It comprises an antigenic fragment of
XX anthrax protective antigen encoded in the form of DNA which is adapted to
XX be expressed when the spore germinates. The antigenic fragment is one or
XX more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which
XX comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen
XX which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen
XX which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen
XX which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the
XX protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23
XX which is a sequence of SEQ ID NO: 10. The composition further comprises
XX an adjuvant that potentiates an antigen-specific immune response. The
XX composition (including the spore) is useful as an anthrax vaccine or for
XX manufacturing an anthrax vaccine. The composition and method are used for
XX inducing an immune response against anthrax. The present sequence is DNA
XX encoding anthrax protective antigen domain D1b23.
XX
XX Sequence 1281 BP; 492 A; 210 C; 244 G; 335 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 14; Length 1281;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGGACGGCTCCATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50
DB 607 GGGACGGCTCCATCTACACGTTTACCAACGACTTCGTTAGTTAGG 656

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RESULT 6
AAB63722
ID AAB63722 standard; DNA; 1281 BP.
XX
XX AAB63722;
AC
XX
XX 06-OCT-2005 (first entry)
DT
XX
XX DNA encoding anthrax protective antigen domain D1b23.
DE

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RESULT 7
AAD29117
ID AAD29117 standard; DNA; 1461 BP.
XX
XX AAD29117;
AC
XX
XX 07-MAY-2002 (first entry)
DT
XX
XX Bacillus subtilis protective antigen (PA) domain 1+2 DNA.
DE

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```

KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX Bacillus subtilis.
OS
XX Key Location/Qualifiers
XX CDS 1..1461
XX FT /*tag= a
XX FT /product= "Domain 1+2"
XX FT /note= "CDS does not include start and stop codon"
XX FT /partial
XX WO200204646-A1.
XX PD 17-JAN-2002.
XX PF 06-JUL-2001; 2001WO-GB003065.
XX PR 08-JUL-2000; 2000GB-00016702.
XX PA (MINA ) UK SEC FOR DEFENCE.
XX PI Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
XX PI Flick-Smith HC, Bullifent HL, Titball RW, Topping AW;
XX DR WPI; 2002-171720/22.
XX DR P-PSDB; AAB18285.
XX PS New immunogenic reagent having a polypeptide of the full length
XX PT Protective Antigen of Bacillus anthracis, useful for treating B.
XX PT anthracis infection or in preparing a medicament for the prophylaxis or
XX PT treatment of the infection.
XX PS Example 5; Fig 3; 40pp; English.
XX CC The present invention relates to an immunogenic reagent, which produces
XX CC an immune response that is protective against Bacillus anthracis. The
XX CC reagent comprises one or more polypeptides which together represent up to
XX CC three domains of the full length Protective Antigen (PA) of Bacillus
XX CC anthracis or variants of these, and at least one of the domains comprises
XX CC domain 1 or domain 4 of PA or its variant. The invention is used as a
XX CC vaccine. The immunogenic reagent is useful in the preparation of a
XX CC medicament for the prophylaxis or treatment of B. anthracis infection.
XX CC The present sequence is Bacillus subtilis protective antigen domain 1+2
XX CC DNA
XX SQ Sequence 1461 BP; 548 A; 238 C; 280 G; 395 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 6; Length 1461;
XX Best Local Similarity 100.0%; Pred. No. 1,7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTAGG 50
DB 1108 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTAGG 1157

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FT CDS 1..1704
FT FT /*tag= a
FT FT /partial
FT FT /product= "PA63 fragment"
FT FT /transl_except= (pos:475..477, aa:Xaa)
FT FT /note= "Xaa represents Asn, Phe, Ile, Gly"
XX PN WO2005034841-A2.
XX PD 21-APR-2005.
XX PF 13-MAY-2004; 2004WO-US014971.
XX PR 14-MAY-2003; 2003US-0470563P.
XX PA (MERI ) MERCK & CO INC.
XX PI Heppler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L;
XX PI WPI; 2005-306231/31.
XX DR P-PSDB; ADZ51326.
XX PS Producing recombinant Bacillus anthracis Protective Antigen protein
XX PT encoded by an expression vector having a nucleotide sequence being codon-
XX PT optimized for expression in yeast, useful for manufacturing anthrax
XX PS vaccines.
XX PS Example 1; SEQ ID NO 47; 91pp; English.
XX CC The specification describes a method for producing recombinant Bacillus
XX CC anthracis protective antigen protein. The method comprises providing an
XX CC expression vector having a polynucleotide encoding a Bacillus anthracis
XX CC protective antigen protein which is codon-optimized for expression in
XX CC yeast, transforming a yeast with the vector, fermenting the transformed
XX CC yeast for the expression of the protein, and isolating the protein. The
XX CC protective antigen protein is PA63 or PA83. The method of the invention
XX CC is useful for the produce of antigen protein, which is used for
XX CC prophylactic immunization against anthrax infections. The present
XX CC sequence encodes a PA63 fragment.
XX SQ Sequence 1704 BP; 663 A; 248 C; 328 G; 465 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 14; Length 1704;
XX Best Local Similarity 100.0%; Pred. No. 1,7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTAGG 50
DB 607 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTAGG 656

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RESULT 8
ADZ51325
ID ADZ51325 standard; DNA; 1704 BP.
XX AC ADZ51325;
XX DT 30-JUN-2005 (first entry)
XX DE Nucleotide sequence of a PA63 gene fragment.
XX KW protective antigen protein; PA63; PA83; antibacterial; vaccine;
XX KW prophylactic immunization; anthrax infection; gene; ds.
XX OS Bacillus anthracis.
XX Key Location/Qualifiers

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RESULT 9
AEB63720
ID AEB63720 standard; DNA; 1707 BP.
XX AC AEB63720;
XX DT 06-OCT-2005 (first entry)
XX DE DNA encoding anthrax protective antigen PA63.
XX KW Antigen; bacillus anthracis infection; antibacterial; vaccine;
XX KW protective antigen; PA; ds.
XX OS Bacillus anthracis.
XX PN WO2005068493-A1.
XX PD 28-JUL-2005.
XX PF 17-JAN-2005; 2005WO-GB000170.
XX PR 17-JAN-2004; 2004GB-00001036.

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XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX Cutting SM;  
XX WPI; 2005-563956/57.  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
XX protective antigen, useful as an anthrax vaccine or for manufacturing an  
XX anthrax vaccine.  
XX  
XX Disclosure; SEQ ID NO 8; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
XX antigenic fragment of anthrax protective antigen. Also given is a  
XX pharmaceutical composition comprising a non-pathogenic spore comprising  
XX at least an antigenic fragment of anthrax protective antigen in  
XX association with a pharmaceutical carrier and/or excipient; and methods  
XX of inducing immunity to anthrax in a mammal susceptible to anthrax  
XX infection. The Bacillus species spore is a spore from many species such  
XX as Bacillus alvei; Bacillus baduarius; Bacillus brevis and preferably a  
XX spore from Bacillus subtilis. The spore comprises an antigenic fragment  
XX of anthrax protective antigen in the form of a protein attached to the  
XX proteinaceous coat of the spore. It comprises an antigenic fragment of  
XX anthrax protective antigen encoded in the form of DNA which is adapted to  
XX be expressed when the spore germinates. The antigenic fragment is one or  
XX more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
XX comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
XX which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
XX which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
XX which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
XX protective antigen which has a sequence of SEQ ID NO: 4; and Domain 1b23  
XX which is a sequence of SEQ ID NO: 10. The composition further comprises  
XX an adjuvant that potentiates an antigen-specific immune response. The  
XX composition (including the spore) is useful as an anthrax vaccine or for  
XX manufacturing an anthrax vaccine. The composition and method are used for  
XX inducing an immune response against anthrax. The present sequence is DNA  
XX encoding anthrax protective antigen PA63.  
XX  
XX Sequence 1707 BP; 665 A; 248 C; 327 G; 467 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 50; DB 14; Length 1707;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 GGGAGCGGCTCCAACTTACCAACGTTTACCAACGACTTCGTTAGTGTAGG 50  
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||  
XX 607 GGGACGGCTCCAACTTACCAACGTTTACCAACGACTTCGTTAGTGTAGG 656  
XX  
XX RESULT 10  
XX AA256877 standard; DNA; 1710 BP.  
XX ID AA256877;  
XX AC AA256877;  
XX DT 25-APR-2000 (first entry)  
XX DE B. anthracis PA63 protein encoding DNA.  
XX KW Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
XX tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX OS Bacillus anthracis.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..1710  
XX FT /\*tag= a  
XX FT /product= "MAT-PA protein"  
XX PN WO200002522-A2.  
XX PD 20-JAN-2000.

XX 09-JUL-1999; 99WO-US015568.  
XX 10-JUL-1998; 98US-0092416P.  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX WPI; 2000-182165/16.  
XX P-P6DB; AA556961.  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX  
XX Disclosure; Page 35; 35pp; English.  
XX  
XX The invention provides a recombinant DNA construct that comprises a  
XX vector and at least one nucleic acid (or its fragment) encoding a  
XX combination of Bacillus anthracis proteins, selected from protective  
XX antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
XX with its secretory signals replaced with those of tissue plasminogen  
XX activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
XX for anthrax and in producing infectious alpha virus particles. These  
XX particles, expressing the B. anthracis proteins are useful also as  
XX vaccines for anthrax. Host cells transformed with the construct are  
XX useful for analyzing the effectiveness of drugs and agents that inhibit  
XX anthrax or B. anthracis proteins. The present sequence represents a B.  
XX anthracis PA63 protein encoding DNA  
XX  
XX Sequence 1710 BP; 666 A; 248 C; 329 G; 467 T; 0 U; 0 Other;  
XX  
XX Query Match 100.0%; Score 50; DB 3; Length 1710;  
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 1 GGGAGCGGCTCCAACTTACCAACGTTTACCAACGACTTCGTTAGTGTAGG 50  
XX ||||||||||||||||||||||||||||||||||||||||||||||||||||  
XX 610 GGGACGGCTCCAACTTACCAACGTTTACCAACGACTTCGTTAGTGTAGG 659  
XX  
XX RESULT 11  
XX ADL16356 standard; DNA; 1722 BP.  
XX ID ADL16356;  
XX AC ADL16356;  
XX DT 06-MAY-2004 (first entry)  
XX DE pBP111 vector DNA for expression of 64kDa PA deletion mutant (PA64).  
XX KW Immunogenic; vaccine; lethal infection; protective antigen; PA;  
XX lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.  
XX OS Bacillus anthracis.  
XX  
XX Key Location/Qualifiers  
XX CDS 1..1722  
XX FT /\*tag= a  
XX FT /product= "PA deletion mutant protein (PA64)"  
XX FT /partial  
XX FT /note= "No start codon"  
XX  
XX US2004028695-A1.  
XX 12-FEB-2004.  
XX 28-MAR-2003; 2003US-00402466.  
XX 12-APR-2002; 2002US-0372152P.  
XX (PARK/) PARK S.



```

PA (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI: 2004-168865/16.
XX
XX P-PSDB; ADL16357.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclousure; SEQ ID NO 21; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is pBR11 vector DNA for the
XX expression of Bacillus anthracis 64kDa N-terminal PA deletion mutant
XX (PA64). This sequence is used in the invention.
XX
XX Sequence 1722 BP; 673 A; 251 C; 330 G; 468 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 12; Length 1722;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGGTAGG 50
Db 622 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGGTAGG 671
XX
XX RESULT 12
XX AAD29120
XX ID AAD29120 standard; DNA; 1785 BP.
XX
XX AC AAD29120;
XX
XX DT 07-MAY-2002 (first entry)
XX
XX DE Bacillus subtilis protective antigen (PA) domain 1+2+3 DNA.
XX
XX KW Immunogenic reagent; immune response; protective antigen; PA; vaccine;
XX KW Bacillus anthracis infection; antibacterial; ds.
XX
XX OS Bacillus subtilis.
XX
XX FH Key Location/Qualifiers
XX FT 1..1785
XX FT /*tag= a
XX FT /product= "Domain 1+2+3"
XX FT /note= "CDS does not include start and stop codon"
XX FT /partial
XX
XX WO200204646-A1.
XX
XX EN 17-JAN-2002.
XX
XX PD 06-JUL-2001; 2001WO-GB003065.
XX
XX PF 08-JUL-2000; 2000GB-00016702.
XX
XX PR (MINA ) UK SEC FOR DEFENCE.
XX
XX PA
XX
XX PI Williamson ED, Miller J, Walker NT, Baillie LMJ, Holden PT;
XX PI Flick-Smith HC, Bullifent HL, Tibbitt RW, Topping AW;
XX
XX WPI: 2002-171720/22.
XX
XX DR P-PSDB; AAE18288.
XX
XX

```

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PT New immunogenic reagent having a polypeptide of the full length
PT Protective Antigen of Bacillus anthracis, useful for creating B.
PT anthracis infection or in preparing a medicament for the prophylaxis or
PT treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
XX an immune response that is protective against Bacillus anthracis. The
XX reagent comprises one or more polypeptides which together represent up to
XX three domains of the full length Protective Antigen (PA) of Bacillus
XX anthracis or variants of these, and at least one of the domains comprises
XX domain 1 or domain 4 of PA or its variant. The invention is used as a
XX vaccine. The immunogenic reagent is useful in the preparation of a
XX medicament for the prophylaxis or treatment of B. anthracis infection.
XX The present sequence is Bacillus subtilis protective antigen domain 1+2+3
XX DNA
XX
XX Sequence 1785 BP; 686 A; 285 C; 333 G; 481 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 50; DB 6; Length 1785;
XX Best Local Similarity 100.0%; Pred. No. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
OY 1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGGTAGG 50
Db 1108 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGGTAGG 1157
XX
XX RESULT 13
XX AAQ70189
XX ID AAQ70189 standard; DNA; 2160 BP.
XX
XX AC AAQ70189;
XX
XX DT 25-MAR-2003 (revied)
XX DT 04-APR-1995 (first entry)
XX
XX DE Sequence encoding modified protective antigen of Bacillus anthracis.
XX
XX KW Anthrax; Bacillus anthracis; fusion protein; lethal factor;
XX KW protective antigen; cell killing; targeting; pathogen;
XX KW intracellular; HIV; human immunodeficiency virus; toxin; ss.
XX
XX OS Bacillus anthracis.
XX
XX FH Key Location/Qualifiers
XX FT 1..2160
XX FT /*tag= a
XX FT /product= "Modified anthrax protective antigen."
XX FT /partial
XX
XX WO9418332-A2.
XX
XX PN 18-AUG-1994.
XX
XX PD 14-FEB-1994; 94WO-US001624.
XX
XX PF 12-FEB-1993; 93US-00021601.
XX PR 25-JUN-1993; 93US-00082849.
XX
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX PI Leppla SH, Klimpel K, Arora N, Singh Y, Nichols PJ;
XX
XX WPI: 1994-279753/34.
XX
XX DR P-PSDB; AAR60193.
XX
XX PT Nucleic acid encoding anthrax toxin fusion protein - useful for
XX PT targeting toxin to specific cells, eg for killing tumour cells or HIV-
XX PT infected cells.
XX
XX Example 6; Page 111-113; 124pp; English.
XX
XX

```







CC 1+2+3+4 DNA

XX SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 6; Length 2208;

Best Local Similarity 100.0%; Pred. No. 1.7e-18;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 50

Db 1108 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 1157

RESULT 16

AA199904 ID AA199904 standard; DNA; 2208 BP.

XX AC AA199904;

XX DT 01-FEB-2002 (first entry)

XX DE Anthrax PA encoding polynucleotide.

XX KW Anthrax; PA; protective antigen; antibacterial; pore-forming toxin;

XX KV B moiety; A-B anthrax toxin; Bacillus anthracis; vaccine; ds.

XX OS Bacillus anthracis.

XX Key Location/Qualifiers

FH CDS 1..2211

FT /\*tag= a

FT /product= "PA"

XX WO200182788-A2.

XX PD 08-NOV-2001.

XX PF 04-MAY-2001; 2001WO-US014372.

XX PR 04-MAY-2000; 2000US-0201800P.

XX PA (HARD ) HARVARD COLLEGE.

XX PI Collier RJ, Sellman BR;

XX DR WPI; 2002-017725/02.

XX DR P-PSDB; AAM51483.

XX PT Protecting humans against anthrax using mutant B groups (anthrax

XX PT protective antigens) of the pore-forming binary A-B toxin of Bacillus

XX PT anthracis.

XX PS Disclosure; Fig 14; 77pp; English.

XX CC The invention relates to antibacterial agents comprising mutant forms of

XX CC pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants

XX CC in the B moiety of the pore-forming binary A-B anthrax toxin, where the B

XX CC moiety is anthrax protective antigen (PA) and using these mutants or

XX CC compositions of them for protecting against Bacillus anthracis infections

XX CC in humans, especially as vaccines. The present sequence is that of the

XX CC anthrax PA encoding DNA

SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 6; Length 2208;

Best Local Similarity 100.0%; Pred. No. 1.7e-18;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 50

Db 1108 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 1157

RESULT 17

ADL16343 ID ADL16343 standard; DNA; 2208 BP.

XX AC ADL16343;

XX DT 06-MAY-2004 (first entry)

XX DE Bacillus anthracis wild-type rPA DNA #1.

XX KW Immunogenic; vaccine; lethal infection; protective antigen; PA;

XX KV lethal factor; LF; anthrax; antibacterial; gene; ds.

XX OS Bacillus anthracis.

XX Key Location/Qualifiers

FH CDS 1..2208

FT /\*tag= a

FT /product= "rPA protein"

FT /partial

FT /note= "No start codon"

XX US2004028695-A1.

XX PD 12-FEB-2004.

XX PF 28-MAR-2003; 2003US-00402466.

XX PR 12-APR-2002; 2002US-0372152P.

XX PA (PARK/) PARK S.

XX PA (GIRI/) GIRI L.

XX PI Park S, Giri L;

XX DR WPI; 2004-168865/16.

XX DR P-PSDB; ADL16344.

XX PT Immunogenic composition for preparing a vaccine against a lethal

XX PT infection of Bacillus anthracis in an animal, comprises an immunizing

XX PT amount of a recombinant B. anthracis protective antigen protein and/or

XX PT lethal factor protein.

XX PS Disclosure; SEQ ID NO 8; 143pp; English.

XX CC The present invention relates to immunogenic compositions useful for

XX CC preparing a vaccine against a lethal infection of Bacillus anthracis in

XX CC an animal. The compositions comprise an immunising amount of a

XX CC recombinant B. anthracis protective antigen (rPA) protein and a

XX CC recombinant B. anthracis lethal factor (rLF) protein. The composition and

XX CC methods are useful in protecting against anthrax or lethal infections

XX CC caused by B. anthracis. The present sequence is Bacillus anthracis wild-

XX CC type rPA DNA used in the invention.

SQ Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 12; Length 2208;

Best Local Similarity 100.0%; Pred. No. 1.7e-18;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 50

Db 1108 GGGAGCGCTCCAACTTACCAAGCGTGTACCAAGCACTTGTTAGTGTAGG 1157

RESULT 18

ADL16346 ID ADL16346 standard; DNA; 2208 BP.

XX AC ADL16346;

XX DT 06-MAY-2004 (first entry)



```

DE Bacillus anthracis PA DNA from pBP105 vector.
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
OS Bacillus anthracis.
XX
XX Key Location/Qualifiers
FH 1..2208
FT /*tag= a
FT /product= "PA protein"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16348.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 11; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunizing amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is Bacillus anthracis PA DNA
XX from pBP105 vector used in the invention.
XX
XX Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 50; DB 12; Length 2208;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCTCCAACTACAAAGTGTACCAAGCACTTCGTTAGTGTAGG 50
DB 1108 GGGACGGCTCCAACTACAAAGTGTACCAAGCACTTCGTTAGTGTAGG 1157

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FT CDS 1..2208
FT /*tag= a
FT /product= "Protective antigen"
FT /partial
FT /note= "No start codon shown"
XX
XX WO2005004791-A2.
XX
XX 20-JAN-2005.
XX
XX 10-NOV-2003; 2003WO-US035733.
XX
XX 08-NOV-2002; 2002US-0424987P.
XX
XX (HARD ) HARVARD COLLEGE.
XX (UYOK-) UNIV OKLAHOMA.
XX
XX Collier RJ, Ballard JD, Tweten R, Mourez M;
XX
XX WPI; 2005-091963/10.
XX P-PSDB; ADM05483.
XX
XX New B moiety of pore-forming binary A-B toxin or its fragment, where the
XX moiety has a mutation that inhibits its pore-forming ability, useful for
XX preventing or treating bacterial infection, e.g. anthrax.
XX
XX Disclosure; SEQ ID NO 22; 129pp; English.
XX
XX The invention relates to a B moiety of pore-forming binary A-B toxin or
XX its fragment, where the moiety has a mutation that inhibits its pore-
XX forming ability and is selected from S382, N399, and N422 of the Bacillus
XX anthracis protective antigen (PA) appearing as ADM05483. Also included
XX are a vaccine composition comprising the mutant B moiety or its fragment
XX (and a carrier), preventing or treating a bacterial infection in a mammal
XX by administering the vaccine to the mammal, a nucleic acid encoding the
XX mutant B moiety, a vector comprising the nucleic acid and a purified
XX antibody that specifically binds a B moiety, but fails to bind a
XX naturally occurring B moiety. The B moiety is selected from Clostridium
XX difficile, C. perfringens, C. spiroforme, C. botulinum, and Bacillus
XX cereus. The mutation inhibits the pore-forming ability of the toxin in
XX vivo. The B moiety and vaccine composition are useful for preventing or
XX treating a bacterial infection, e.g. anthrax. The present sequence
XX encodes the wild-type PA protein.
XX
XX Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 50; DB 14; Length 2208;
XX Best Local Similarity 100.0%; Pred. NO. 1.7e-18;
XX Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGACGGCTCCAACTACAAAGTGTACCAAGCACTTCGTTAGTGTAGG 50
DB 1108 GGGACGGCTCCAACTACAAAGTGTACCAAGCACTTCGTTAGTGTAGG 1157

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RESULT 19
ADM05484
ID ADM05484 standard; DNA; 2208 BP.
XX
XX ADM05484;
XX
XX 07-APR-2005 (first entry)
XX
XX B. anthracis wild-type protective antigen, DNA.
XX
XX Protein engineering; Bacillus anthracis infection; protective antigen;
XX toxin; bacterial infection; vaccine; antibacterial; ds; gene.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers

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RESULT 20
AEB63729
ID AEB63729 standard; DNA; 2208 BP.
XX
XX AEB63729;
XX
XX 06-OCT-2005 (first entry)
XX
XX DNA encoding anthrax protective antigen, PA83.
XX
XX Antigen; bacillus anthracis infection; antibacterial; vaccine;
XX protective antigen; PA; ds; gene.
XX
XX Bacillus anthracis.
XX
XX WO2005068493-A1.
XX
XX 28-JUL-2005.

```



XX 17-JAN-2005; 2005MO-GB000170.  
 PF  
 XX  
 PR 17-JAN-2004; 2004GB-00001036.  
 XX  
 PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
 XX  
 PI Cutting SM;  
 XX WPI; 2005-563956/57.  
 DR  
 XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
 PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
 PT anthrax vaccine.  
 XX  
 PS Disclosure; SEQ ID NO 17; 90pp; English.  
 XX  
 CC The present invention relates to a non-pathogenic spore comprising an  
 CC antigenic fragment of anthrax protective antigen. Also given is a  
 CC pharmaceutical composition comprising a non-pathogenic spore comprising  
 CC at least an antigenic fragment of anthrax protective antigen in  
 CC association with a pharmaceutical carrier and/or excipient; and methods  
 CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
 CC infection. The Bacillus species spore is a spore from many species such  
 CC as Bacillus alvei; Bacillus baduus; Bacillus brevis and preferably a  
 CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
 CC of anthrax protective antigen in the form of a protein attached to the  
 CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
 CC anthrax protective antigen encoded in the form of DNA which is adapted to  
 CC be expressed when the spore germinates. The antigenic fragment is one or  
 CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
 CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
 CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
 CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
 CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
 CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
 CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
 CC an adjuvant that potentiates an antigen-specific immune response. The  
 CC composition (including the spore) is useful as an anthrax vaccine or for  
 CC manufacturing an anthrax vaccine. The composition and method are used for  
 CC inducing an immune response against anthrax. The present sequence is DNA  
 CC encoding anthrax protective antigen, PA83.  
 XX  
 SQ Sequence 2208 BP; 859 A; 321 C; 414 G; 614 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 50; DB 14; Length 2208;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGACGGCTCCAAATCTACAAAGTGTACCAAGCACTTGTTAGTTAGG 50  
 Db 1108 GGGACGGCTCCAAATCTACAAAGTGTACCAAGCACTTGTTAGTTAGG 1157  
 RESULT 21  
 AA256875 standard; DNA; 2211 BP.  
 XX  
 AC AA256875;  
 XX  
 DT 25-APR-2000 (first entry)  
 XX  
 DB B. anthracis MAT-PA protein encoding DNA.  
 XX  
 KW Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
 KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
 XX  
 OS Bacillus anthracis.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2211  
 FT /\*tag= a  
 FT /product= "MAT-PA protein"

XX WO200002522-A2.  
 EN  
 XX  
 XX 20-JAN-2000.  
 PD  
 XX  
 XX 09-JUL-1999; 99WO-US015568.  
 PF  
 XX 10-JUL-1998; 98US-0092416P.  
 PR  
 XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
 XX  
 PA Lee JS, Pushko P, Parker MD, Smith JR, Welkos SL;  
 PI WPI; 2000-182165/16.  
 DR  
 XX P-PSDB; AAY56959.  
 DR  
 XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
 PT host cells for analyzing the drugs and agents inhibiting anthrax.  
 PT  
 XX  
 PS Disclosure; Page 34; 35pp; English.  
 XX  
 CC The invention provides a recombinant DNA construct that comprises a  
 CC vector and at least one nucleic acid (or its fragment) encoding a  
 CC combination of Bacillus anthracis proteins, selected from protective  
 CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
 CC with its secretory signals replaced with those of tissue plasminogen  
 CC activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine  
 CC for anthrax and in producing infectious alpha virus particles. These  
 CC particles, expressing the B. anthracis proteins are useful also as  
 CC vaccines for anthrax. Host cells transformed with the construct are  
 CC useful for analyzing the effectiveness of drugs and agents that inhibit  
 CC anthrax or B. anthracis proteins. The present sequence represents a B.  
 CC anthracis MAT-PA protein encoding DNA  
 XX  
 SQ Sequence 2211 BP; 860 A; 322 C; 416 G; 613 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 50; DB 3; Length 2211;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 1 GGGACGGCTCCAAATCTACAAAGTGTACCAAGCACTTGTTAGTTAGG 50  
 Db 1111 GGGACGGCTCCAAATCTACAAAGTGTACCAAGCACTTGTTAGTTAGG 1160  
 RESULT 22  
 ADY84835 standard; DNA; 2211 BP.  
 ID ADY84835  
 XX  
 AC ADY84835;  
 XX  
 DT 02-JUN-2005 (first entry)  
 XX  
 DB Bacillus anthracis protective antigen coding sequence.  
 XX  
 KW Bacillus anthracis infection; vaccine; antibacterial; protective antigen;  
 KW gene; ds.  
 XX  
 OS Bacillus anthracis.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2211  
 FT /\*tag= a  
 FT /product= "Protective antigen"  
 PN WO2005026203-A2.  
 XX  
 PD 24-MAR-2005.  
 XX  
 XX 20-SEP-2004; 2004WO-US030616.  
 PF  
 XX 18-SEP-2003; 2003US-0504504P.  
 PR 18-SEP-2003; 2003US-0504505P.



XX (USNA ) US SEC OF NAVY.  
 XX Kopecko DJ, Osorio M, Bhattacharyya S, Giri CP, Blake M;  
 XX WPI; 2005-233481/24.  
 XX  
 PT New attenuated bacterium capable of expressing a heterologous protein,  
 PT which is under the control of a promoter, useful as a vaccine against  
 PT *Bacillus anthracis* infection, or for treating *Bacillus anthracis*  
 PT infection.  
 XX  
 PS Claim 10; SEQ ID NO 9; 83pp; English.  
 XX  
 CC The invention provides an attenuated bacterium which is capable of  
 CC expressing a heterologous protein. The expression of the heterologous  
 CC protein is under the control of a promoter selected from 8 fully defined  
 CC sequences ADV84827-ADV84834. The attenuated bacterium is preferably  
 CC *Salmonella typhi* or *Salmonella typhimurium*. The heterologous protein  
 CC comprises an antigenic sequence derived from a virus, bacterium, fungus,  
 CC yeast or parasite, and is especially a protective antigen (PA) of  
 CC *Bacillus anthracis*. A claimed live attenuated vaccine for immunization  
 CC against anthrax comprises an attenuated galactose epimerase-less mutant  
 CC strain of *S. typhi* (e.g. strain Ty21a) carrying a *Bacillus anthracis* PA,  
 CC especially a wild-type PA or its immunogenic fragment. The PA is  
 CC preferably encoded by a low-copy plasmid such as pGB2. The plasmid  
 CC promotes expression of the PA by a *nirB* promoter or by a *Sec* signal  
 CC sequence. The vaccine is used in a claimed method of immunizing a  
 CC susceptible host against *B. anthracis* disease. The present sequence is  
 CC the *B. anthracis* PA coding sequence (wild-type).  
 XX  
 SQ Sequence 2211 BP; 860 A; 323 C; 415 G; 613 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 50; DB 14; Length 2211;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGACGGCTCCAACTACACGCTGTACCAAGCACTTCGTTAGTTAGG 50  
 DB 1111 GGGACGGCTCCAACTACACGCTGTACCAAGCACTTCGTTAGTTAGG 1160  
 XX  
 RESULT 23  
 ADV96726  
 ID ADV96726 standard; DNA; 2220 BP.  
 XX  
 AC ADV96726;  
 XX  
 DT 24-FEB-2005 (first entry)  
 XX  
 DE Gene of the invention SEQ ID NO:12.  
 XX  
 KW antineoplastic; chemotherapy; toxin; tumor; cytostatic; ds; gene.  
 XX  
 OS Unidentified.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 1..2220  
 FT /\*tag= a  
 XX  
 PN CN1513878-A.  
 XX  
 PD 21-JUL-2004.  
 XX  
 PF 13-JUN-2003; 2003CN-00143142.  
 XX  
 PR 13-JUN-2003; 2003CN-00143142.  
 XX  
 PA (MIJ/) MI J.  
 XX  
 PI MI J;  
 XX  
 DR WPI; 2004-710658/70.

DR P-PSDB; ADV96725.  
 XX  
 PT Antitumor medicine containing recombination bacterial toxin protein  
 PT Complex substance.  
 XX  
 PS Claim 2; SEQ ID NO 12; 29pp; Chinese.  
 XX  
 CC The invention relates to a novel antineoplastic medicine containing the  
 CC recombinant bacteriotoxin protein composition TPCB whose key components  
 CC are recombinant proteins IP33 and IP14. Under the action of a particular  
 CC enzyme generated by tumor cells, the non-toxic protein can be changed  
 CC into toxic protein to directly kill tumor cells specifically. The present  
 CC sequence encodes a protein of the invention.  
 XX  
 SQ Sequence 2220 BP; 860 A; 326 C; 419 G; 615 T; 0 U; 0 Other;  
 XX  
 Query Match 100.0%; Score 50; DB 13; Length 2220;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGGACGGCTCCAACTACACGCTGTACCAAGCACTTCGTTAGTTAGG 50  
 DB 1120 GGGACGGCTCCAACTACACGCTGTACCAAGCACTTCGTTAGTTAGG 1169  
 XX  
 RESULT 24  
 ADR40459  
 ID ADR40459 standard; DNA; 2235 BP.  
 XX  
 AC ADR40459;  
 XX  
 DT 18-NOV-2004 (first entry)  
 XX  
 DE *Bacillus anthracis* protective antigen double mutant DNA seqid 3.  
 XX  
 KW antibacterial; vaccine; protective antigen; PA; proteolytic degradation;  
 KW *B. anthracis* toxin; *B. anthracis* infection; passive immunisation;  
 KW inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;  
 KW gene; ds.  
 XX  
 OS *Bacillus anthracis*.  
 XX  
 FH Synthetic.  
 XX  
 FT Key Location/Qualifiers  
 FT CDS 88..2235  
 FT /\*tag= a  
 FT /product= "*Bacillus anthracis* protective antigen double  
 mutant"  
 XX  
 PN US2004171121-A1.  
 XX  
 PD 02-SEP-2004.  
 XX  
 PF 08-AUG-2003; 2003US-00638006.  
 XX  
 PR 09-AUG-2002; 2002US-0402285P.  
 XX  
 PA (LEPP/) LEPPPLA S H.  
 PA (ROSO/) ROSOVITZ M J.  
 PA (HSUS/) HSU S D.  
 XX  
 PI Leppla SH, Rosovitz MJ, Hsu SD;  
 XX  
 DR WPI; 2004-625107/60.  
 XX  
 DR P-PSDB; ADR40457.  
 XX  
 PT Novel *Bacillus anthracis* protective antigen having mutations conferring  
 PT enhanced resistance to proteolytic degradation compared to wild type  
 PT antigen, useful for inducing antibodies having neutralizing activity  
 PT anthrax toxin.  
 XX  
 PS Example 5; SEQ ID NO 3; 30pp; English.  
 XX



CC The invention describes a recombinant *Bacillus anthracis* protective  
CC antigen (PA), modified to incorporate one or more mutations comprising an  
CC amino acid deletion or substitution in a flexible, exposed, or loop  
CC segment of the PA protein, where the one or more mutations confers  
CC enhanced resistance to proteolytic degradation compared to wild type PA.  
CC A pharmaceutical composition (i) comprising PA and physiologically  
CC acceptable carrier or a composition (ii) comprising a synthetic construct  
CC encoding PA and a carrier is useful for inducing serum antibodies that  
CC have neutralizing activity for a *B. anthracis* toxin which involves  
CC administering (i) to a mammal (human), sufficient to elicit production of  
CC the antibodies. The antibodies protect the mammal against the infection.  
CC (i) is useful for vaccinating a human against *B. anthracis* infection. An  
CC anti-PA-antibody containing composition is useful for passively  
CC immunizing a mammal against the toxic effect of *B. anthracis*. PA is useful  
CC as vaccines to induce serum antibodies which are useful to prevent, treat  
CC or reduced the severity of infections caused by *B. anthracis*, such as  
CC inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA  
CC exhibits enhanced stability to proteolytic degradation that is increased  
CC by at least 25% compared to proteolytic stability of wild-type PA under  
CC comparable conditions. This sequence encodes an exemplary double  
CC protective antigen (PA) mutant comprising deletion of residues 162-167  
CC and residues 304-317 and substitutions S168I and S319G.  
CC  
SQ Sequence 2235 BP; 873 A; 325 C; 416 G; 621 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 13; Length 2235;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAACTACACGCTGTACCAACGACTTCGTTAGTTAGG 50  
Db 1135 GGGACGGCTCCAACTACACGCTGTACCAACGACTTCGTTAGTTAGG 1184

RESULT 25  
AAZ56876  
ID AAZ56876 standard; DNA; 2292 BP.  
AC AAZ56876;  
XX  
XX 25-APR-2000 (first entry)  
DE B. anthracis TPA-PA protein encoding DNA.  
XX  
XX  
KW *Bacillus anthracis* protein; protective antigen; PA; MAT-PA; TPA-PA;  
KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2292  
FT /\*tag= a  
FT /product= "TPA-PA protein"  
XX  
XX WO200002522-A2.  
XX  
XX 20-JAN-2000.  
XX  
XX 09-JUL-1999; 99WO-US015568.  
XX  
XX 10-JUL-1998; 98US-0092416P.  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX  
XX WPI; 2000-182165/16.  
XX  
XX P-PSDB; AAY56960.  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX  
XX Disclosure; Page 32; 35pp; English.

XX  
CC The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of *Bacillus anthracis* proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the *B. anthracis* proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or *B. anthracis* proteins. The present sequence represents a *B.*  
CC *anthracis* TPA-PA protein encoding DNA  
CC  
SQ Sequence 2292 BP; 874 A; 337 C; 446 G; 635 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 3; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAACTACACGCTGTACCAACGACTTCGTTAGTTAGG 50  
Db 1192 GGGACGGCTCCAACTACACGCTGTACCAACGACTTCGTTAGTTAGG 1241

RESULT 26  
AAZ56874  
ID AAZ56874 standard; DNA; 2295 BP.  
AC AAZ56874;  
XX  
XX 25-APR-2000 (first entry)  
DE B. anthracis protective antigen (PA) protein encoding DNA.  
XX  
XX  
KW *Bacillus anthracis* protein; protective antigen; PA; MAT-PA; TPA-PA;  
KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2295  
FT /\*tag= a  
FT /product= "PA protein"  
XX  
XX WO200002522-A2.  
XX  
XX 20-JAN-2000.  
XX  
XX 09-JUL-1999; 99WO-US015568.  
XX  
XX 10-JUL-1998; 98US-0092416P.  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
XX  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
XX  
XX WPI; 2000-182165/16.  
XX  
XX P-PSDB; AAY56958.  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
XX host cells for analyzing the drugs and agents inhibiting anthrax.  
XX  
XX Disclosure; Page 33; 35pp; English.

XX The invention provides a recombinant DNA construct that comprises a  
XX vector and at least one nucleic acid (or its fragment) encoding a  
XX combination of *Bacillus anthracis* proteins, selected from protective  
XX antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
XX with its secretory signals replaced with those of tissue plasminogen  
XX activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
XX for anthrax and in producing infectious alpha virus particles. These  
XX particles, expressing the *B. anthracis* proteins are useful also as



CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis PA protein encoding DNA  
CC  
SQ Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;  
Query Match 100.0%; Score 50; DB 3; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGACGGCTCCAACTACACGTTTACCAACGACTTGGTGTAGG 50  
DB 1195 GGGACGGCTCCAACTACACGTTTACCAACGACTTGGTGTAGG 1244  
RESULT 27  
AAC86016  
ID AAC86016 standard; cDNA; 2295 BP.  
XX  
AC AAC86016;  
XX  
DT 29-AUG-2001 (first entry)  
XX  
DE Wild type B. anthracis protective antigen coding sequence.  
XX  
KM Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine;  
KM humoral; cell-mediated; immune memory response; 88.  
XX  
OS Bacillus anthracis.  
XX  
FH Key Location/Qualifiers  
FT sig\_peptide 1..87  
FT /tag= a  
FT mat\_peptide 88..2295  
FT /tag= b  
FT /product= "PA"  
FT misc\_RNA 610..2295  
FT /tag= C  
FT /product= "Encodes PCRPA peptide"  
XX  
XX WO200145639-A2.  
XX  
XX 26-JUN-2001.  
XX  
XX 21-DEC-2000; 2000WO-US034912.  
XX  
XX 22-DEC-1999; 99US-0171459P.  
XX  
PA (OHIS ) UNITV OHIO STATE RES FOUND.  
PA (GALL/) GALLOWAY D R.  
PA (MATE/) MATECZUN A J.  
XX  
XX Galloway DR, Mateczun AJ;  
XX  
XX WPI; 2001-408540/43.  
XX P-PSDB; AAB47306.  
XX  
XX Protecting animal against lethal infection with Bacillus anthracis, by  
PT administering wildtype or mutated form of Bacillus anthracis lethal  
PT factor protein or its fragment or a nucleic acid encoding the mutated  
PT protein.  
XX  
PS Claim 25; Fig 2; 33pp; English.  
XX  
XX This sequence encodes the B. anthracis protective antigen (PA). An  
CC immunogenic fragment of PA, PCPA, can be used to produce an immune  
CC response which protects an animal against lethal infection with Bacillus  
CC anthracis. DNA encoding the B. anthracis PA can be used in conjunction  
CC with DNA encoding the lethal factor (LF) in a DNA vaccine. Using a DNA  
CC vaccine which encodes the mutated LF protein or fragment alone or in  
CC combination with a DNA encoding the PA protein or its fragment, both  
CC components (humoral and cell-mediated) of the immune system are

CC stimulated, which results in longer term immune memory response. The  
CC combined use of a mutated LF and PA gene or their fragments results in a  
CC higher level of immune response, as judged by overall serum antibody  
CC titers for LF and PA antigens, than the use of either LF or PA genes in  
CC separate immunizations  
CC  
SQ Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;  
Query Match 100.0%; Score 50; DB 4; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGGACGGCTCCAACTACACGTTTACCAACGACTTGGTGTAGG 50  
DB 1195 GGGACGGCTCCAACTACACGTTTACCAACGACTTGGTGTAGG 1244  
RESULT 28  
ADM29247  
ID ADM29247 standard; DNA; 2295 BP.  
XX  
XX ADM29247;  
XX  
XX 24-MAR-2005 (first entry)  
XX  
XX B. anthracis DNA encoding protective antigen, PA.  
XX  
DE Protective antigen; bacillus anthracis infection; vaccine; infection; de;  
KM antibacterial.  
XX  
XX Bacillus anthracis.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2295  
FT /tag= a  
FT /product= "Protective antigen"  
XX  
XX WO200500684-A1.  
XX  
XX 06-JAN-2005.  
XX  
XX 04-JUN-2004; 2004WO-US017736.  
XX  
XX 05-JUN-2003; 2003US-0476598P.  
XX  
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
XX  
XX Schneerson R, Leppla S, Robbins JB, Shiloach J, Kudler-Kiell J;  
PI Liu D, Majadly F;  
PI  
XX  
XX WPI; 2005-066555/07.  
XX P-PSDB; ADM29248.  
XX  
XX Immunogenic conjugate, useful for inhibiting or treating infection and/or  
PT disease caused by Bacillus anthracis or other bacilli, comprises Bacillus  
PT capsular poly-gamma-glutamic acid polypeptide covalently linked to  
PT carrier.  
XX  
PS Disclosure; SEQ ID NO 2; 66pp; English.  
XX  
XX The invention relates to an immunogenic conjugate comprising a Bacillus  
CC capsular poly-gamma-glutamic acid (gammaPGA) polypeptide covalently  
CC linked to a carrier, where the conjugate elicits an immune response in a  
CC subject. Also included are a composition comprising the conjugate and a  
CC pharmaceutically acceptable carrier (for use in eliciting an immune  
CC response against Bacillus anthracis epitope, preferably Bacillus  
CC anthracis antigenic epitope in a subject) and an isolated antibody that  
CC binds to the Bacillus capsular gammaPGA polypeptide (that recognizes  
CC or that binds Bacillus anthracis capsular gammaPGA polypeptide,  
CC or that binds Bacillus anthracis capsular gammaPGA). The carrier may  
CC comprise recombinant B. anthracis protective antigen. The composition and  
CC conjugate are useful for eliciting an immune response against a Bacillus  
CC antigenic epitope in a subject and for inhibiting or treating infection



CC and/or disease caused by *B. anthracis* or other bacilli. The immune  
CC response comprises opsonophagocytic activity. The composition is useful  
CC for active immunization for preventing *B. anthracis* infections and for  
CC preparation of immune antibodies. The present sequence encodes Bacillus  
CC anthracis protective antigen, PA.  
XX  
SQ Sequence 2295 BP; 892 A; 334 C; 432 G; 637 T; 0 U; 0 Other;  
Query Match 100.0%; Score 50; DB 14; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 50  
Db 1195 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 1244  
RESULT 29  
AEB63728  
ID AEB63728 standard; DNA; 2295 BP.  
XX  
AC AEB63728;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE DNA encoding full length anthrax protective antigen, PA83.  
XX  
KW Antigen; bacillus anthracis infection; antibacterial; vaccine;  
KW protective antigen; PA; ds; gene.  
XX  
OS Bacillus anthracis.  
XX  
PN WO2005068493-A1.  
XX  
XX 28-JUL-2005.  
PD  
PF 17-JAN-2005; 2005WO-GB000170.  
XX  
PR 17-JAN-2004; 2004GB-00001036.  
XX  
PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX  
PI Cutting SM;  
PI  
XX WPI; 2005-563956/57.  
DR  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
PS Claim 5; SEQ ID NO 16; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus baduus; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The

CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding full length anthrax protective antigen, PA83.  
XX  
SQ Sequence 2295 BP; 892 A; 332 C; 432 G; 639 T; 0 U; 0 Other;  
Query Match 100.0%; Score 50; DB 14; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 50  
Db 1195 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 1244  
RESULT 30  
ADE65871  
ID ADE65871 standard; DNA; 2605 BP.  
XX  
AC ADE65871;  
XX  
DT 29-JAN-2004 (first entry)  
XX  
DE Bacillus anthracis PA antigen encoding sequence.  
XX  
KW Antibacterial; Vaccine; immune response; Bacillus anthracis; ds.  
XX  
OS Bacillus anthracis.  
XX  
FH Key Location/Qualifiers  
FH CDS 3..2600  
FT /\*tag= a  
XX  
XX WO2003087378-A1.  
XX  
XX 23-OCT-2003.  
PD  
XX 11-APR-2003; 2003WO-GB001553.  
XX  
PF 11-APR-2002; 2002US-0371416P.  
XX  
PR (POMD-) POWDERJECT RES LTD.  
XX  
PA Schmaljohn C, Fuller J;  
XX  
XX WPI; 2003-877105/81.  
DR P-PSDB; ADE65872.  
XX  
XX New polynucleotide vaccine composition comprising a nucleic acid sequence  
PT that encodes a Bacillus anthracis antigen, useful for eliciting a  
PT protective immune response against Bacillus anthracis.  
XX  
PS Example 1; SEQ ID NO 3; 65pp; English.  
XX  
XX The present invention relates to a new polynucleotide vaccine composition  
CC comprising a nucleic acid sequence that encodes a Bacillus anthracis  
CC antigen and that is operatively linked to a promoter suitable for  
CC expression of the antigen in a mammalian cell. The polynucleotide vaccine  
CC composition is useful for eliciting a protective immune response against  
CC Bacillus anthracis. The present sequence represents Bacillus anthracis PA  
CC antigen encoding sequence.  
XX  
SQ Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;  
Query Match 100.0%; Score 50; DB 10; Length 2605;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 50  
Db 1368 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGCTTAGTGG 1417



RESULT 31  
 AEB20797  
 ID AEB20797 standard; DNA; 2605 BP.  
 AC AEB20797;  
 DT 08-SEP-2005 (first entry)  
 DE Bacillus anthracis Protective Antigen (PA) gene, SEQ ID NO:3.  
 XX Nucleic acid vaccine; Bacillus anthracis infection; Protective Antigen;  
 KM gene; ds.  
 XX Bacillus anthracis.  
 OS  
 XX  
 FH Location/Qualifiers  
 FT 3..2603  
 FT CDS  
 FT /tag= a  
 FT /product= "Translated sequence shown in Fig 1A-O"  
 FT /note= "No start or stop codon given. Xaa corresponds to  
 FT in-frame stop codon"  
 FT /transl\_except= (pos:15..17,aa:Xaa)  
 FT /transl\_except= (pos:63..65,aa:Xaa)  
 FT /transl\_except= (pos:81..83,aa:Xaa)  
 FT /transl\_except= (pos:141..143,aa:Xaa)  
 FT /transl\_except= (pos:147..149,aa:Xaa)  
 FT /transl\_except= (pos:246..248,aa:Xaa)  
 FT /transl\_except= (pos:2481..2483,aa:Xaa)  
 FT /transl\_except= (pos:2556..2558,aa:Xaa)  
 FT /transl\_except= (pos:2568..2570,aa:Xaa)  
 FT /transl\_except= (pos:2586..2588,aa:Xaa)  
 FT /transl\_except= (pos:2598..2600,aa:Xaa)  
 FT /transl\_except= (pos:2604..2605,aa:Pro)  
 FT CDS  
 FT /tag= c  
 FT /product= "Bacillus anthracis Protective Antigen"  
 FT /tag= b  
 FT /tag= d  
 FT /product= "Mature Protective Antigen"  
 FT sig\_peptide  
 FT 174..245  
 FT mat\_peptide  
 FT 246..2465  
 FT /tag= d  
 FT /product= "Mature Protective Antigen"  
 XX  
 PN US2005148529-A1.  
 PD  
 XX 07-JUL-2005.  
 XX  
 PF 05-JAN-2004; 2004US-00751103.  
 XX  
 PR 05-JAN-2004; 2004US-00751103.  
 XX  
 XX (POMD-) POWDERJECT VACCINES INC.  
 PA Schmaljohn CS, Fuller JT;  
 PI  
 XX MPI; 2005-478100/48.  
 DR P-PsDB; AEB20798, AEB20803.  
 XX  
 XX New polynucleotide vaccine composition comprising a nucleic acid sequence  
 PT that encodes a Bacillus anthracis antigen, useful for eliciting an immune  
 PT response against B. anthracis in a subject.  
 XX  
 XX Example 1; SEQ ID NO 3; 40pp; English.  
 XX  
 XX The invention relates to a polynucleotide vaccine composition comprising  
 CC a Bacillus anthracis antigen-encoding nucleic acid which is operatively  
 CC linked to a promoter for expression of the antigen in a mammalian cell.  
 CC The invention also relates to use of the vaccine composition of the  
 CC invention for eliciting an immune response in an individual. Preferably,  
 CC the antigen encoded by the polynucleotide vaccine is obtained or derived  
 CC from the Bacillus anthracis Protective Antigen (PA), a non-toxic factor  
 CC responsible for binding to cell membranes which is known to confer active

CC protection against anthrax. The encoded Bacillus anthracis antigen may  
 CC also be linked to a leader signal peptide (such as the tissue plasminogen  
 CC activator (TPA) signal peptide) which permits its secretion. The vaccine  
 CC composition may additionally comprise an adjuvant component such as a CpG  
 CC sequence, a nucleic acid encoding a polypeptide adjuvant, a lipid, a non-  
 CC protein hormone or a vitamin. The polynucleotide vaccine composition of  
 CC the invention can be administered directly into skin or muscle tissue,  
 CC preferably in particulate form, and is useful for inducing a protective  
 CC immune response against Bacillus anthracis infection. The present  
 CC sequence represents the complete nucleotide sequence encoding the  
 CC Bacillus anthracis Protective Antigen, used in the construction of a  
 CC Bacillus anthracis polynucleotide vaccine in an example of the invention.  
 XX  
 SQ Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 50; DB 14; Length 2605;  
 Best Local Similarity 100.0%; Pred. No. 17e-18;  
 Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GGGACGGCTCCATCTACACGTGTATCCACGACTTGTTAGT 50  
 Db 1368 GGGACGGCTCCATCTACACGTGTATCCACGACTTGTTAGT 1417  
 RESULT 32  
 ID AAQ70184 standard; DNA; 2709 BP.  
 AAQ70184  
 AC AAQ70184;  
 XX  
 AC 25-MAR-2003 (revised)  
 DT 04-APR-1995 (first entry)  
 XX  
 DE PA(1-725)-----Human CD4 fusion protein coding sequence.  
 XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;  
 KM protective antigen; cell killing; targeting; pathogen;  
 KM intracellular; HIV; human immunodeficiency virus; toxin; Pseudomonas;  
 KW exotoxin; ss.  
 XX  
 XX Bacillus anthracis.  
 OS Homo sapiens.  
 OS  
 FH Key Location/Qualifiers  
 FT CDS 1..2709  
 FT /tag= a  
 FT /product= "Anthrax fusion protein."  
 XX  
 PN W09418332-A2.  
 PD  
 XX 18-AUG-1994.  
 XX  
 PF 14-FEB-1994; 94WO-US001624.  
 XX  
 PR 12-FEB-1993; 93US-00021601.  
 PR 25-JUN-1993; 93US-00082849.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 PA  
 XX Lep1a SH, Klimpel K, Aroza N, Singh Y, Nichols PJ;  
 PI  
 XX MPI; 1994-279753/34.  
 DR P-PsDB; AAR60183.  
 XX  
 XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
 PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
 PT infected cells.  
 XX  
 PS Disclosure; Page 97-100; 124pp; English.  
 XX  
 XX This sequence encodes a fusion protein comprising amino acid residues 1-  
 CC 725 of the anthrax protective antigen protein and a sequence encoding  
 CC residues 1-178 of human CD4, the portion which binds to gp120 on HIV



CC infected cells. Such fusion proteins may be useful for the specific  
CC killing of tumour cells or the killing of cells infected with  
CC intracellular pathogens, especially HIV, depending on their components.  
CC (Updated on 25-MAR-2003 to correct PN field.)  
CC  
XX

Sequence 2709 BP; 1006 A; 444 C; 551 G; 708 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 1.7e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 50  
|||||

Db 1108 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 1157

## RESULT 33

AAQ70180 standard; DNA; 4235 BP.

AAQ70180;

25-MAR-2003 (revised)

03-APR-1995 (first entry)

Sequence encoding protective antigen of Bacillus anthracis.

Anthrax; Bacillus anthracis; fusion protein; lethal factor;  
KM protective antigen; cell killing; targeting; targeting; pathogen;  
KM intracellular; HIV; human immunodeficiency virus; toxin; ss.  
XX

Bacillus anthracis.

Location/Qualifiers

1891. .4098

/tag= a  
/product= "Anthrax protective antigen."

WO9418332-A2.

18-AUG-1994.

14-FEB-1994; 94WO-US001624.

12-FEB-1993; 93US-00021601.

25-JUN-1993; 93US-00082849.

(USSH ) US DEPT HEALTH & HUMAN SERVICES.

Leppia SH, Klimpel K, Arora N, Singh Y, Nichols PJ;

WPI; 1994-279753/34.

P-PSDB; AAR60179.

Nucleic acid encoding anthrax toxin fusion protein - useful for  
PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
PT infected cells.

Disclosure; Page 78-81; 124pp; English.

The sequence encoding the protective antigen of Bacillus anthracis may be  
CC used in the construction of a nucleic acid which encodes a fusion protein  
CC comprising the anthrax protective antigen binding domain of the native  
CC anthrax lethal factor and a sequence encoding an activity inducing domain  
CC of a second protein. The fusion proteins are useful for the specific  
CC killing of tumour cells or the killing of cells infected with  
CC intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to  
CC correct PN field.)  
XX

Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 2; Length 4235;

Best Local Similarity 100.0%; Pred. No. 1.6e-18;

Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 50  
|||||

Db 2398 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 3047

## RESULT 34

ACF58207 standard; DNA; 4235 BP.

ACF58207;

12-FEB-2004 (first entry)

B. anthracis protective antigen (PA) encoding DNA.

Molecular modeling; antibacterial; protozoacide; fungicide; vaccine;  
KM protective antigen; PA; gene; ds.  
XX

Bacillus anthracis.

WO2003087129-A2.

23-OCT-2003.

08-APR-2003; 2003WO-US010851.

08-APR-2002; 2002US-0371250P.

08-APR-2002; 2002US-0371256P.

17-APR-2002; 2002US-0373668P.

(PLEX-) PLEXUS VACCINE INC.

Katritch V, Bordner A, Deans RJ, Sumner M;

WPI; 2003-853938/79.

P-PSDB; ABR39189.

Identifying immunogenic peptides representative of a structural element  
PT of a target protein comprising detecting an epitope corresponding to the  
PT molecular model of the three dimensional structure of the epitope in the  
PT target protein.

Example 1; Page 106-108; 0pp; English.

The invention relates to identifying an immunogenic peptide  
CC representative of a structural element of a target protein. The method  
CC involves detecting in a molecular model of a chimeric polypeptide  
CC comprising a selected epitope linked to a scaffold protein, an epitope  
CC having a three dimensional conformation corresponding to the molecular  
CC model of the three dimensional structure of the epitope in the target  
CC protein. The method of the invention are useful for identifying  
CC immunogenic peptides of a target protein having a known three dimensional  
CC structure, or of a target protein having a known amino acid sequence but  
CC unknown three dimensional structure. The immunogenic peptides are useful  
CC as vaccines for stimulating an immune response in a subject against  
CC infectious microorganisms including protozoan (Entamoeba histolytica),  
CC yeast (Candida albicans) or bacterium (Shigella flexneri, Yersinia  
CC pestis, Serratia marcescens or Bacillus anthracis). The present sequence  
CC represents a B. anthracis protective antigen (PA) DNA (GenBank Accession  
CC No. 143280), where the antigen can be used as a target protein  
XX

Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;

Query Match 100.0%; Score 50; DB 10; Length 4235;  
Best Local Similarity 100.0%; Pred. No. 1.6e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 50  
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Db 2398 GGGACGGCTCCATCTACACGCTGTACCAACGAGCTTGTTAGTGG 3047



```
RESULT 35
ADL72868
ID ADL72868 standard; DNA; 4235 BP.
XX
AC ADL72868;
XX
DT 17-JUN-2004 (first entry)
XX
DE Anthrax vaccine polynucleotide SEQ ID NO: 3.
XX
KM ds; gene; anthrax; vaccine; antibacterial; codon optimised.
XX
OS Bacillus anthracis.
XX
PN MO2004024067-A2.
XX
PD 25-MAR-2004.
XX
PF 10-SEP-2003; 2003WO-US028199.
XX
PR 10-SEP-2002; 2002US-0409307P.
XX
PR 18-OCT-2002; 2002US-0419089P.
XX
PA (VICA-) VICAL INC.
XX
PI Hermanson GG;
XX
DR WPI; 2004-269870/25.
XX
DR P-PSDB; ADL72869.
XX
PT Novel isolated codon-optimized polynucleotide encoding Bacillus anthracis
PT protective antigen, useful for treating anthrax infections in vertebrate.
XX
PS Example 1; Page 205-209; 288pp; English.
XX
CC The present invention relates to codon-optimised versions of the Bacillus
CC anthracis protective antigen coding sequence, and vectors containing such
CC sequences. These can be used in vaccines to protect vertebrates against
CC anthrax infection. The present sequence is a polynucleotide of the
CC invention.
XX
SQ Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 50; DB 12; Length 4235;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGACGGCTCCATCTACACGCTGTACCAAGACTTCGTTAGTGTAG 50
DB 2998 GGGACGGCTCCATCTACACGCTGTACCAAGACTTCGTTAGTGTAG 3047
XX
RESULT 36
ADL16342
ID ADL16342 standard; DNA; 8198 BP.
XX
AC ADL16342;
XX
DT 06-MAY-2004 (first entry)
XX
DE pBP103 expression vector DNA for expression of rPA.
XX
KM Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; ds.
XX
OS Unidentified.
XX
PN US2004028695-A1.
XX
PD 12-FEB-2004.
XX
PR 28-MAR-2003; 2003US-00402466.
XX
```

```
XX
PR 12-APR-2002; 2002US-0372152P.
XX
PA (PARK/) PARK S.
PA (GIRI/) GIRI L.
XX
PI Park S, Giri L;
XX
DR WPI; 2004-168865/16.
XX
PT Immunogenic composition for preparing a vaccine against a lethal
PT infection of Bacillus anthracis in an animal, comprises an immunizing
PT amount of a recombinant B. anthracis protective antigen protein and/or
PT lethal factor protein.
XX
PS Disclosure; SEQ ID NO 7; 143pp; English.
XX
CC The present invention relates to immunogenic compositions useful for
CC preparing a vaccine against a lethal infection of Bacillus anthracis in
CC an animal. The compositions comprise an immunizing amount of a
CC recombinant B. anthracis protective antigen (rPA) protein and a
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and
CC methods are useful in protecting against anthrax or lethal infections
CC caused by B. anthracis. The present sequence is pBP103 expression vector
CC DNA for the expression of rPA used in the invention.
XX
SQ Sequence 8198 BP; 2786 A; 1349 C; 1776 G; 2287 T; 0 U; 0 Other;
XX
Query Match 100.0%; Score 50; DB 12; Length 8198;
Best Local Similarity 100.0%; Pred. No. 1.6e-18;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGGACGGCTCCATCTACACGCTGTACCAAGACTTCGTTAGTGTAG 50
DB 4842 GGGACGGCTCCATCTACACGCTGTACCAAGACTTCGTTAGTGTAG 4891
XX
RESULT 37
ADL16345
ID ADL16345 standard; DNA; 9286 BP.
XX
AC ADL16345;
XX
DT 06-MAY-2004 (first entry)
XX
DE pBP105 expression vector DNA for expression of rPA and LF30.
XX
KM Immunogenic; vaccine; lethal infection; protective antigen; PA;
KM lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
OS Bacillus anthracis.
XX
OS Unidentified.
XX
FH Key Location/Qualifiers
FH CDS 3735..5942
FT /*tag= a
FT /product= "LF30 protein"
FT /partial
FT /note= "No start codon"
FT CDS 6391..7161
FT /*tag= b
FT /product= "rPA protein"
FT /partial
FT /note= "No start codon"
XX
PN US2004028695-A1.
XX
PD 12-FEB-2004.
XX
PR 28-MAR-2003; 2003US-00402466.
XX
PR 12-APR-2002; 2002US-0372152P.
XX
```



PA (PARK/) PARK S.  
PA (GIRI/) GIRI L.  
XX  
PI Park S, Giri L;  
XX  
DR WP1; 2004-168865/16.  
DR P-PSDB; ADL16339, ADL16344.  
XX  
PT Immunogenic composition for preparing a vaccine against a lethal  
PT infection of *Bacillus anthracis* in an animal, comprises an immunizing  
PT amount of a recombinant *B. anthracis* protective antigen protein and/or  
PT lethal factor protein.  
XX  
PS Disclosure; SEQ ID NO 10; 143pp; English.  
XX  
CC The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant *B. anthracis* protective antigen (rPA) protein and a  
CC recombinant *B. anthracis* lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by *B. anthracis*. The present sequence is pB105 expression vector  
CC DNA for the expression of *Bacillus anthracis* rPA and LF30 used in the  
CC invention.  
XX  
SQ Sequence 9286 BP; 3228 A; 1474 C; 1973 G; 2611 T; 0 U; 0 Other;  
XX  
Query Match 100.0%; Score 50; DB 12; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 1.6e-18;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Qy 1 GGGACGGCTCCATCTACACGTGTACCAAGACTTGGTAGTGG 50  
Db 4842 GGGACGGCTCCATCTACACGTGTACCAAGACTTGGTAGTGG 4891  
XX  
RESULT 38  
ADR48507/c  
ID ADR48507 standard; DNA; 25 BP.  
XX  
AC ADR48507;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE pagA probe #5.  
XX  
KW *Bacillus anthracis*; cutaneous; respiratory anthrax infection; pagA; capB;  
KW pX01; pX02; probe; ss.  
XX  
OS unidentified.  
XX  
PN WO2004070001-A2.  
XX  
PD 19-AUG-2004.  
XX  
PE 12-NOV-2003; 2003WO-US036240.  
XX  
PR 15-NOV-2002; 2002US-0426552P.  
PR 16-MAY-2003; 2003US-0471082P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Norman SA, Bungo JT, Hogan JT, Weisburg WG;  
XX  
DR WP1; 2004-604428/58.  
XX  
PT New oligonucleotides that hybridize specifically to a *Bacillus anthracis*  
PT sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis*  
PT infections.  
XX  
PS Claim 5; SEQ ID NO 5; 61pp; English.  
XX  
CC The present invention relates to an oligonucleotide of 20-40 nucleotides

CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC *anthracis* target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pX01 and pX02, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a pagA  
CC probe, used in the pX01 and pX02 detection kits.  
XX  
SQ Sequence 25 BP; 5 A; 7 C; 7 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 50.0%; Score 25; DB 13; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
Qy 1 GGGACGGCTCCATCTACACGTGT 25  
Db 25 GGGACGGCTCCATCTACACGTGT 1  
XX  
RESULT 39  
ADR48508/c  
ID ADR48508 standard; DNA; 25 BP.  
XX  
AC ADR48508;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE pagA probe #6.  
XX  
KW *Bacillus anthracis*; cutaneous; respiratory anthrax infection; pagA; capB;  
KW pX01; pX02; probe; ss.  
XX  
OS unidentified.  
XX  
PN WO2004070001-A2.  
XX  
PD 19-AUG-2004.  
XX  
PE 12-NOV-2003; 2003WO-US036240.  
XX  
PR 15-NOV-2002; 2002US-0426552P.  
PR 16-MAY-2003; 2003US-0471082P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Norman SA, Bungo JT, Hogan JT, Weisburg WG;  
XX  
DR WP1; 2004-604428/58.  
XX  
PT New oligonucleotides that hybridize specifically to a *Bacillus anthracis*  
PT sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis*  
PT infections.  
XX  
PS Claim 5; SEQ ID NO 6; 61pp; English.  
XX  
CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC *anthracis* target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pX01 and pX02, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a pagA  
CC probe, used in the pX01 and pX02 detection kits.  
XX  
SQ Sequence 25 BP; 8 A; 6 C; 5 G; 6 T; 0 U; 0 Other;  
XX  
Query Match 50.0%; Score 25; DB 13; Length 25;



Best Local Similarity 100.0%; Pred. No. 0.00031;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Job time : 93.6635 secs

QY 26 TACCAACGACTTCGTTAGTTAGG 50  
DB 25 TACCAACGACTTCGTTAGTTAGG 1

## RESULT 40

ADCS1669/c

ID ADCS1669 standard; DNA; 20 BP.

AC ADCS1669;

DT 18-DEC-2003 (first entry)

DE Bacillus brevis PA (toxin gene), PCR primer #1.

KM Sporulation microbe; anthrax; spore-forming bacteria;

KW sporulation microbe detection; soil; food; sporulating microbe;

OS detection method; toxic sporulating microbe; PA; toxin; PCR; primer; ss.

PN Brevibacillus brevis.

PD JP2003061665-A.

PF 04-MAR-2003.

PR 21-AUG-2001; 2001JP-00250187.

PA 21-AUG-2001; 2001JP-00250187.

DR (YAKU-) ZH YAKULT BIOSCIENCE KENKYU ZAIDAN.

XX WPI; 2003-601344/57.

PT Isolating nucleic acid from spore-forming bacteria e.g. Bacillus

PT anthracis, by culturing microbes in sporulation microbe-containing

PS physical crushing.

PS Disclosure; SEQ ID NO 6; 9pp; Japanese.

CC The present invention relates to a method for detecting a sporulation

CC microbe in a sporulation microbe-containing composition by isolating a

CC nucleic acid and amplifying the nucleic acid using specific PCR primers,

CC and primers for anthrax. Isolating a nucleic acid from a spore-forming

CC bacteria present in a sporulation microbe-containing composition,

CC comprises adding alcohol (70-90 weight % ethanol) to a sporulation

CC microbe-containing composition, culturing the sporulation microbes in the

CC composition and extracting nucleic acids from the culture by physical

CC crushing. The method is useful for isolating nucleic acid from spore-

CC forming bacteria in a sporulation microbe-containing composition, and for

CC detecting the sporulation microbe present in the composition. Preferably,

CC the method is useful for detecting and isolating a nucleic acid from

CC Bacillus anthracis, the causative agent of anthrax, in soil and food

CC stuffs. The method accurately detects the presence of sporulating

CC microbes present in a soil or food sample, and thus provides a sensitive

CC detection method for the toxic sporulating microbe e.g. B. anthracis. The

CC present invention.

SQ Sequence 20 BP; 7 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 38.0%; Score 19; DB 10; Length 20;

Best Local Similarity 100.0%; Pred. No. 0.79;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CGACTTCGTTAGTTAGG 50

DB 20 CGACTTCGTTAGTTAGG 2



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

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#### SUMMARIES

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6	50	100.0	1710 6 US-10-442-502-4	Sequence 4, Appl
7	50	100.0	1722 7 US-10-402-466A-21	Sequence 21, Appl
8	50	100.0	1783 6 US-10-332-282-12	Sequence 12, Appl
9	50	100.0	2208 6 US-09-848-909-22	Sequence 22, Appl
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97	14	28.0	502	4	US-09-925-065A-789154	Sequence 789154,	170	14	28.0	2699	10	US-11-097-143-8455	Sequence 8455, Ap
98	14	28.0	502	4	US-09-925-065A-789155	Sequence 789155,	171	14	28.0	2943	10	US-11-097-143-13601	Sequence 13601, A
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102	14	28.0	540	9	US-10-363-483A-40109	Sequence 40109, A	175	14	28.0	3342	7	US-10-437-963-39503	Sequence 29503, A
103	14	28.0	540	9	US-10-363-483A-40110	Sequence 40110, A	176	14	28.0	3897	7	US-10-437-963-50771	Sequence 50771, A
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105	14	28.0	570	8	US-10-363-345A-7862	Sequence 7862, Ap	178	14	28.0	4159	10	US-11-097-143-31456	Sequence 31456, A
106	14	28.0	570	9	US-10-363-483A-7861	Sequence 7861, Ap	179	14	28.0	4221	7	US-10-437-963-40526	Sequence 40526, A
107	14	28.0	570	9	US-10-363-483A-7862	Sequence 7862, Ap	180	14	28.0	4347	7	US-10-437-963-50692	Sequence 50692, A
108	14	28.0	589	4	US-09-925-065A-286874	Sequence 286874, Ap	181	14	28.0	4497	7	US-10-437-963-50727	Sequence 50727, A
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111	14	28.0	590	9	US-10-363-483A-39395	Sequence 39395, A	184	14	28.0	5151	6	US-10-242-515-2572	Sequence 2572, Ap
112	14	28.0	590	9	US-10-363-483A-39396	Sequence 39396, A	185	14	28.0	5386	6	US-10-311-455-506	Sequence 506, Ap
113	14	28.0	594	3	US-09-903-814-7	Sequence 7, Appl1	186	14	28.0	5634	10	US-11-097-143-13600	Sequence 13600, A
114	14	28.0	594	3	US-10-723-061-7	Sequence 7, Appl1	187	14	28.0	5735	7	US-10-257-166-148	Sequence 148, Ap
115	14	28.0	603	8	US-10-425-115-152053	Sequence 152053, Ap	188	14	28.0	5940	2	US-08-910-386A-10	Sequence 10, Appl1
116	14	28.0	603	8	US-10-363-345A-5763	Sequence 5763, Ap	189	14	28.0	6398	6	US-10-311-455-1073	Sequence 1073, Ap
117	14	28.0	603	8	US-10-363-345A-5764	Sequence 5764, Ap	190	14	28.0	7593	8	US-10-363-345A-4843	Sequence 4843, Ap
118	14	28.0	603	9	US-10-363-483A-5763	Sequence 5763, Ap	191	14	28.0	7593	8	US-10-363-345A-4844	Sequence 4844, Ap
119	14	28.0	603	9	US-10-363-483A-5764	Sequence 5764, Ap	192	14	28.0	7593	8	US-10-363-483A-4843	Sequence 4843, Ap
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121	14	28.0	614	7	US-10-437-963-11766	Sequence 11766, A	194	14	28.0	9767	3	US-09-070-927A-130	Sequence 130, Ap
122	14	28.0	620	7	US-10-424-599-61667	Sequence 61667, A	195	14	10202	10	US-11-097-143-1097	Sequence 1097, Ap	
123	14	28.0	636	8	US-10-425-115-67314	Sequence 67314, A	196	14	28.0	11101	10	US-11-023-888-3	Sequence 3, Appl1
124	14	28.0	655	8	US-10-425-115-9007	Sequence 9007, Ap	197	14	28.0	19603	10	US-11-097-143-1096	Sequence 1096, Ap
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130	14	28.0	689	8	US-10-363-345A-22358	Sequence 22358, A	203	14	28.0	78815	8	US-10-856-218A-36	Sequence 36, Appl1
131	14	28.0	689	9	US-10-363-483A-22357	Sequence 22357, A	204	14	28.0	78815	10	US-11-047-184-36	Sequence 44, Appl1
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134	14	28.0	693	3	US-09-938-842A-1259	Sequence 1259, Ap	207	14	28.0	81684	7	US-10-322-261-673	Sequence 673, Ap
135	14	28.0	732	8	US-10-363-345A-8255	Sequence 8255, Ap	208	14	28.0	90435	7	US-10-322-666-160	Sequence 160, Ap
136	14	28.0	732	8	US-10-363-345A-8256	Sequence 8256, Ap	209	14	28.0	110306	8	US-10-741-600-17721	Sequence 17721, A
137	14	28.0	732	9	US-10-363-483A-8255	Sequence 8255, Ap	210	14	28.0	185548	10	US-10-741-600-17721	Sequence 62, Appl1
138	14	28.0	732	9	US-10-363-483A-8256	Sequence 8256, Ap	211	14	28.0	185548	10	US-11-099-166-62	Sequence 62, Appl1
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140	14	28.0	767	6	US-10-027-633-123516	Sequence 123516, Ap	213	14	28.0	250135	7	US-10-741-600-17721	Sequence 17721, A
141	14	28.0	810	6	US-10-179-382-1	Sequence 1, Appl1	214	14	28.0	316778	6	US-10-027-632-174961	Sequence 174961, A
142	14	28.0	816	7	US-10-724-972A-3256	Sequence 3256, Ap	215	14	28.0	316778	6	US-10-027-632-174961	Sequence 174961, A
143	14	28.0	824	8	US-10-363-345A-11589	Sequence 11589, A	216	14	28.0	3673778	6	US-10-312-841-1	Sequence 1, Appl1
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146	14	28.0	824	9	US-10-363-483A-11590	Sequence 11590, A	219	13	26.0	25	5	US-10-098-263B-9639	Sequence 9639, Ap
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149	14	28.0	844	7	US-10-437-963-77321	Sequence 77321, A	222	13	26.0	25	5	US-10-098-263B-16823	Sequence 16823, A
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152	14	28.0	860	7	US-10-425-114-881	Sequence 881, App	225	13	26.0	25	5	US-10-098-263B-108166	Sequence 108166, A
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154	14	28.0	893	7	US-10-437-963-77319	Sequence 77319, A	227	13	26.0	25	5	US-10-098-263B-118859	Sequence 118859, A
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161	14	28.0	1509	7	US-10-437-963-25424	Sequence 25424, A	234	13	26.0	25	8	US-10-719-956-55777	Sequence 55777, A
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164	14	28.0	1659	7	US-10-437-963-86954	Sequence 86954, A	237	13	26.0	25	9	US-10-843-527-106518	Sequence 106518, A
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166	14	28.0	1815	8	US-10-425-115-45942	Sequence 45942, A	239	13	26.0	25	10	US-11-036-317-456727	Sequence 456727, A
167	14	28.0	2185	7	US-10-398-221-3583	Sequence 3583, Ap	240	13	26.0	25	10	US-11-060-756-173880	Sequence 173880, A
168	14	28.0	2250	7	US-10-437-963-50697	Sequence 50697, A	241	13	26.0	25	10	US-11-060-756-173880	Sequence 173880, A
169	14	28.0	2421	8	US-10-425-115-58383	Sequence 58383, A	242	13	26.0	27	6	US-10-317-444-103	Sequence 103, Ap



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245	13	26.0	46	9	US-10-666-927-28	Sequence 28, Appl	318	13	26.0	477	3	US-09-918-995-6963	Sequence 6963, Ap
C 246	13	26.0	164	8	US-10-425-115-112325	Sequence 112325,	C 319	13	26.0	479	4	US-09-925-065A-558000	Sequence 558000,
C 247	13	26.0	166	3	US-09-728-444-550	Sequence 550, App	C 320	13	26.0	479	4	US-09-925-065A-558001	Sequence 558001,
C 248	13	26.0	190	3	US-09-854-864-325	Sequence 325, App	C 321	13	26.0	480	9	US-10-972-079-38723	Sequence 38723, A
C 249	13	26.0	190	3	US-10-786-970A-325	Sequence 325, App	C 322	13	26.0	486	8	US-10-425-115-18230	Sequence 18230, A
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251	13	26.0	201	7	US-10-741-601-16418	Sequence 16418, A	C 324	13	26.0	490	3	US-09-864-761-1055	Sequence 1055, Ap
252	13	26.0	201	8	US-10-719-993-26200	Sequence 26200, A	C 325	13	26.0	491	3	US-09-292-758-116	Sequence 116, App
C 253	13	26.0	201	8	US-10-719-993-44227	Sequence 44227, A	C 326	13	26.0	492	5	US-10-027-632-58181	Sequence 58181, A
C 254	13	26.0	201	8	US-10-741-600-47070	Sequence 47070, A	C 327	13	26.0	492	5	US-10-027-632-59188	Sequence 59188, A
C 255	13	26.0	210	7	US-10-437-963-11786	Sequence 11786, A	C 328	13	26.0	492	5	US-10-027-632-109161	Sequence 309161,
C 256	13	26.0	212	4	US-09-925-065A-658063	Sequence 658063,	C 329	13	26.0	492	6	US-10-027-632-58181	Sequence 58181, A
C 257	13	26.0	212	4	US-09-925-065A-658064	Sequence 658064,	C 330	13	26.0	492	6	US-10-027-632-59188	Sequence 59188, A
C 258	13	26.0	212	4	US-09-925-065A-658065	Sequence 658065,	C 331	13	26.0	492	6	US-10-027-632-109161	Sequence 309161,
C 259	13	26.0	219	4	US-09-925-065A-221249	Sequence 221249,	C 332	13	26.0	494	5	US-10-027-632-195139	Sequence 195139,
C 260	13	26.0	226	8	US-10-357-930-60294	Sequence 60294, A	C 333	13	26.0	494	6	US-10-027-632-195139	Sequence 195139,
C 261	13	26.0	230	3	US-09-854-867-324	Sequence 324, App	C 334	13	26.0	499	3	US-09-783-580-7617	Sequence 7617, Ap
C 262	13	26.0	230	9	US-10-786-970A-324	Sequence 324, App	C 335	13	26.0	499	4	US-09-925-065A-940088	Sequence 940088,
263	13	26.0	259	3	US-09-923-876-2799	Sequence 2799, Ap	C 336	13	26.0	501	8	US-10-363-345A-29361	Sequence 29361, A
264	13	26.0	259	3	US-09-923-876-2799	Sequence 2799, Ap	C 337	13	26.0	501	8	US-10-363-345A-29362	Sequence 29362, A
265	13	26.0	259	6	US-10-317-444-267	Sequence 267, App	C 338	13	26.0	501	8	US-10-363-345A-36503	Sequence 36503, A
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C 267	13	26.0	273	7	US-10-437-963-28892	Sequence 28892, A	C 340	13	26.0	501	9	US-10-363-483A-29361	Sequence 29361, A
268	13	26.0	276	3	US-09-864-408A-1179	Sequence 1179, Ap	C 341	13	26.0	501	9	US-10-363-483A-29362	Sequence 29362, A
269	13	26.0	277	6	US-10-317-444-269	Sequence 269, App	C 342	13	26.0	501	9	US-10-363-483A-36503	Sequence 36503, A
C 270	13	26.0	277	6	US-10-317-444-270	Sequence 270, App	C 343	13	26.0	507	4	US-09-925-065A-426747	Sequence 426747,
C 271	13	26.0	279	8	US-10-425-115-175293	Sequence 175293,	C 344	13	26.0	507	4	US-09-925-065A-426746	Sequence 426746,
C 272	13	26.0	279	8	US-10-357-930-61424	Sequence 61424, A	C 345	13	26.0	507	4	US-09-925-065A-426746	Sequence 426746,
273	13	26.0	281	3	US-09-968-007A-866	Sequence 866, App	C 346	13	26.0	507	4	US-09-925-065A-426747	Sequence 426747,
274	13	26.0	281	9	US-10-843-641A-7336	Sequence 7336, App	C 347	13	26.0	507	8	US-10-425-115-131774	Sequence 131774,
275	13	26.0	284	7	US-10-767-701-17131	Sequence 17131, A	C 348	13	26.0	507	8	US-10-425-115-164852	Sequence 164852,
C 276	13	26.0	295	7	US-10-424-599-66130	Sequence 66130, A	C 349	13	26.0	509	8	US-10-425-115-173436	Sequence 173436,
C 277	13	26.0	307	8	US-10-425-115-106196	Sequence 106196,	C 350	13	26.0	510	8	US-10-363-345A-11703	Sequence 11703, A
278	13	26.0	311	6	US-10-425-115-168643	Sequence 168643,	C 351	13	26.0	510	8	US-10-363-345A-11703	Sequence 11703, A
279	13	26.0	316	8	US-10-062-674-176	Sequence 176, App	C 352	13	26.0	510	9	US-10-363-483A-11703	Sequence 11703, A
C 280	13	26.0	317	7	US-10-424-599-36435	Sequence 36435, A	C 353	13	26.0	510	9	US-10-363-483A-11704	Sequence 11704, A
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C 282	13	26.0	330	8	US-10-425-115-37946	Sequence 37946, A	C 355	13	26.0	516	8	US-10-363-345A-36119	Sequence 36119, A
C 283	13	26.0	332	7	US-10-767-701-22467	Sequence 22467, A	C 356	13	26.0	516	8	US-10-363-345A-36119	Sequence 36120, A
C 284	13	26.0	336	7	US-10-424-599-62976	Sequence 62976, A	C 357	13	26.0	516	9	US-10-363-483A-36119	Sequence 36120, A
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C 287	13	26.0	355	4	US-09-925-065A-152935	Sequence 152935,	C 360	13	26.0	518	4	US-09-925-065A-533030	Sequence 533030,
C 288	13	26.0	355	4	US-10-767-701-19797	Sequence 19797, A	C 361	13	26.0	519	4	US-09-925-065A-841542	Sequence 841542,
289	13	26.0	363	8	US-10-425-115-171504	Sequence 171504,	C 362	13	26.0	519	7	US-10-767-701-14874	Sequence 14874, A
C 290	13	26.0	380	3	US-10-357-930-59168	Sequence 59168, A	C 363	13	26.0	519	9	US-10-487-901-6778	Sequence 6778, Ap
C 291	13	26.0	380	3	US-09-924-035A-786	Sequence 786, App	C 364	13	26.0	528	8	US-10-653-487-850	Sequence 850, App
C 292	13	26.0	393	9	US-10-487-901-1440	Sequence 1440, App	C 365	13	26.0	529	4	US-09-925-065A-475321	Sequence 475321,
C 293	13	26.0	393	9	US-10-487-901-5550	Sequence 5550, Ap	C 366	13	26.0	532	4	US-09-925-065A-36671	Sequence 36671, A
294	13	26.0	401	8	US-10-767-795-1064	Sequence 1064, Ap	C 367	13	26.0	532	4	US-09-925-065A-36672	Sequence 36672, A
295	13	26.0	407	3	US-09-867-701-10203	Sequence 10203, A	C 368	13	26.0	532	4	US-09-925-065A-36673	Sequence 36673, A
296	13	26.0	412	8	US-10-674-124A-5050	Sequence 5050, App	C 369	13	26.0	536	4	US-09-925-065A-537635	Sequence 537635,
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298	13	26.0	432	8	US-10-425-115-47869	Sequence 47869, A	C 371	13	26.0	536	6	US-10-027-632-93418	Sequence 93418, A
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C 300	13	26.0	432	7	US-10-282-122A-27996	Sequence 27996, A	C 373	13	26.0	537	4	US-09-925-065A-356312	Sequence 356312,
C 301	13	26.0	432	7	US-10-425-115-113806	Sequence 113806,	C 374	13	26.0	538	4	US-09-925-065A-426743	Sequence 426743,
302	13	26.0	443	3	US-09-732-627A-2550	Sequence 2550, App	C 375	13	26.0	538	5	US-10-027-632-288689	Sequence 288689,
303	13	26.0	443	8	US-10-425-115-148402	Sequence 148402,	C 376	13	26.0	538	6	US-10-027-632-288689	Sequence 288689,
C 304	13	26.0	446	8	US-10-425-115-36665	Sequence 36665, A	C 377	13	26.0	540	4	US-09-925-065A-303760	Sequence 303760,
C 305	13	26.0	450	3	US-09-918-995-33025	Sequence 33025, A	C 378	13	26.0	541	4	US-09-925-065A-184467	Sequence 184467,
C 306	13	26.0	453	6	US-10-032-585-6182	Sequence 6182, App	C 379	13	26.0	542	4	US-09-925-065A-504806	Sequence 504806,
307	13	26.0	454	4	US-10-425-114-6532	Sequence 6532, App	C 380	13	26.0	544	8	US-10-363-345A-13693	Sequence 13693, A
308	13	26.0	458	4	US-09-925-065A-654491	Sequence 654491,	C 381	13	26.0	544	8	US-10-363-345A-13694	Sequence 13694, A
309	13	26.0	459	7	US-09-732-627A-4260	Sequence 4260, App	C 382	13	26.0	544	9	US-10-363-483A-13693	Sequence 13693, A
C 310	13	26.0	459	7	US-10-425-114-16964	Sequence 16964, A	C 383	13	26.0	544	9	US-10-363-483A-13694	Sequence 13694, A
C 311	13	26.0	461	4	US-09-925-065A-499063	Sequence 499063,	C 384	13	26.0	550	9	US-10-972-079-29195	Sequence 29195, A
312	13	26.0	461	5	US-10-027-632-42581	Sequence 42581, A	C 385	13	26.0	552	4	US-09-925-065A-830643	Sequence 830643,
313	13	26.0	461	6	US-10-027-632-42581	Sequence 42581, A	C 386	13	26.0	555	8	US-10-363-345A-6995	Sequence 6995, App
C 314	13	26.0	462	7	US-10-424-599-11809	Sequence 11809, A	C 387	13	26.0	555	8	US-10-363-345A-6996	Sequence 6996, App
C 315	13	26.0	468	5	US-10-027-632-221354	Sequence 221354,	C 388	13	26.0	555	9	US-10-363-483A-6995	Sequence 6995, App



389	13	26.0	555	9	US-10-363-483A-6996	Sequence 6996, Ap	C 462	13	26.0	602	4	US-09-925-065A-823276	Sequence 823276,
390	13	26.0	556	4	US-09-925-065A-10881	Sequence 10881, A	463	13	26.0	602	8	US-10-425-115-138921	Sequence 138921,
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393	13	26.0	557	8	US-10-357-930-49841	Sequence 49841, A	466	13	26.0	603	8	US-10-357-930-56354	Sequence 56354, A
C 394	13	26.0	562	4	US-09-925-065A-361958	Sequence 361958,	C 467	13	26.0	604	4	US-09-925-065A-233199	Sequence 233199,
C 395	13	26.0	562	4	US-09-925-065A-361959	Sequence 361959,	468	13	26.0	605	4	US-09-925-065A-433123	Sequence 433123,
C 396	13	26.0	562	7	US-10-767-701-14872	Sequence 14872, A	469	13	26.0	607	7	US-10-425-114-18923	Sequence 18923, A
C 397	13	26.0	562	9	US-10-779-543-16714	Sequence 16714, A	470	13	26.0	607	7	US-10-425-114-28199	Sequence 28199, A
C 398	13	26.0	562	9	US-10-425-114-7180	Sequence 7180, Ap	C 471	13	26.0	607	7	US-10-021-332-2490	Sequence 2490, Ap
C 399	13	26.0	564	7	US-10-767-701-29765	Sequence 29765, A	472	13	26.0	609	4	US-09-925-065A-63783	Sequence 63783, A
C 400	13	26.0	566	4	US-09-925-065A-348690	Sequence 348690,	473	13	26.0	609	4	US-09-925-065A-63784	Sequence 63784, A
C 401	13	26.0	566	4	US-09-925-065A-348691	Sequence 348691,	C 474	13	26.0	611	4	US-09-925-065A-111150	Sequence 111150,
C 402	13	26.0	567	4	US-09-925-065A-368374	Sequence 368374,	C 475	13	26.0	611	5	US-10-027-632-204635	Sequence 204635,
C 403	13	26.0	567	4	US-09-925-065A-368375	Sequence 368375,	C 476	13	26.0	611	6	US-10-027-632-204635	Sequence 204635,
C 404	13	26.0	568	4	US-09-925-065A-332097	Sequence 332097,	477	13	26.0	612	4	US-09-925-065A-339822	Sequence 339822,
C 405	13	26.0	568	4	US-09-925-065A-932098	Sequence 932098,	C 478	13	26.0	612	4	US-09-925-065A-668370	Sequence 668371,
C 406	13	26.0	569	4	US-09-925-065A-932098	Sequence 932098,	C 479	13	26.0	612	4	US-09-925-065A-668371	Sequence 668372,
C 407	13	26.0	571	4	US-09-925-065A-46061	Sequence 46061,	C 480	13	26.0	612	4	US-10-425-114-28575	Sequence 28575, A
C 408	13	26.0	571	4	US-09-925-065A-01034	Sequence 401034,	481	13	26.0	613	7	US-10-425-114-28575	Sequence 95239, A
C 409	13	26.0	572	4	US-09-925-065A-950429	Sequence 950429,	C 482	13	26.0	614	7	US-10-425-114-18588	Sequence 18588, A
C 410	13	26.0	572	7	US-10-021-323-2544	Sequence 2544, Ap	483	13	26.0	614	7	US-10-425-114-13	Sequence 13, Ap
C 411	13	26.0	573	4	US-09-925-065A-929888	Sequence 929888,	484	13	26.0	615	7	US-10-425-114-24703	Sequence 24703, A
C 412	13	26.0	573	4	US-09-925-065A-929889	Sequence 929889,	485	13	26.0	615	7	US-10-425-114-28301	Sequence 28301, A
C 413	13	26.0	573	8	US-10-468-488-6	Sequence 6, Ap	486	13	26.0	615	7	US-10-425-115-152058	Sequence 152058,
C 414	13	26.0	575	4	US-09-925-065A-929877	Sequence 929877,	487	13	26.0	615	8	US-10-425-115-152058	Sequence 146680,
C 415	13	26.0	575	4	US-09-925-065A-929878	Sequence 929878,	C 488	13	26.0	616	8	US-10-425-115-148680	Sequence 641799,
C 416	13	26.0	576	4	US-09-925-065A-372623	Sequence 372623,	C 489	13	26.0	617	4	US-09-925-065A-846868	Sequence 846868,
C 417	13	26.0	576	4	US-09-925-065A-372625	Sequence 372625,	C 490	13	26.0	618	4	US-09-925-065A-113275	Sequence 113275,
C 418	13	26.0	578	4	US-09-925-065A-313679	Sequence 313679,	C 491	13	26.0	619	4	US-09-925-065A-921691	Sequence 921691,
C 419	13	26.0	579	7	US-10-021-323-15422	Sequence 15422,	C 492	13	26.0	619	4	US-09-925-065A-308559	Sequence 308559,
C 420	13	26.0	581	8	US-10-653-047-1387	Sequence 1387, Ap	C 493	13	26.0	620	7	US-10-425-114-28133	Sequence 28133, A
C 421	13	26.0	581	8	US-10-363-345A-33199	Sequence 33199, A	C 494	13	26.0	621	4	US-09-925-065A-913223	Sequence 913223,
C 422	13	26.0	581	9	US-10-363-483A-33199	Sequence 33200, A	C 495	13	26.0	621	7	US-10-425-114-28116	Sequence 28116, A
C 423	13	26.0	581	9	US-10-363-483A-33200	Sequence 33200, A	C 496	13	26.0	621	7	US-10-425-114-28116	Sequence 28116, A
C 424	13	26.0	584	6	US-10-029-386-103	Sequence 1003, Ap	C 497	13	26.0	623	7	US-10-425-114-28273	Sequence 28273, A
C 425	13	26.0	587	4	US-09-925-065A-110035	Sequence 110035,	C 498	13	26.0	623	7	US-10-425-114-28273	Sequence 237222,
C 426	13	26.0	587	4	US-09-925-065A-372624	Sequence 372624,	C 499	13	26.0	624	5	US-10-027-632-237222	Sequence 237222,
C 427	13	26.0	588	4	US-09-925-065A-302312	Sequence 302312,	C 500	13	26.0	624	6	US-10-027-632-237222	Sequence 954138,
C 428	13	26.0	589	8	US-10-425-115-83336	Sequence 83336, A	C 501	13	26.0	625	4	US-09-925-065A-954138	Sequence 28109, A
C 429	13	26.0	590	8	US-10-425-115-165330	Sequence 165330,	C 502	13	26.0	627	7	US-10-425-114-28204	Sequence 28204, A
C 430	13	26.0	590	9	US-10-487-901-4165	Sequence 4165, Ap	C 503	13	26.0	627	7	US-10-425-114-28204	Sequence 5441, Ap
C 431	13	26.0	591	4	US-09-925-065A-303761	Sequence 4690, Ap	C 504	13	26.0	628	8	US-10-363-345A-5441	Sequence 5441, Ap
C 432	13	26.0	591	5	US-10-066-543-157	Sequence 157, Ap	C 505	13	26.0	628	8	US-10-363-345A-5442	Sequence 5442, Ap
C 433	13	26.0	592	4	US-09-925-065A-108989	Sequence 108989,	C 506	13	26.0	628	9	US-10-363-483A-5441	Sequence 5441, Ap
C 434	13	26.0	592	4	US-09-925-065A-108990	Sequence 108990,	C 507	13	26.0	628	9	US-10-363-483A-5441	Sequence 542339,
C 435	13	26.0	592	4	US-09-925-065A-108990	Sequence 108990,	C 508	13	26.0	634	4	US-09-925-065A-442339	Sequence 148404,
C 436	13	26.0	593	4	US-10-972-079-38722	Sequence 38722, A	C 509	13	26.0	634	8	US-10-425-115-18494	Sequence 954135,
C 437	13	26.0	593	4	US-09-925-065A-291539	Sequence 291539,	C 510	13	26.0	635	4	US-09-925-065A-954135	Sequence 954135,
C 438	13	26.0	594	4	US-09-925-065A-292621	Sequence 292621,	C 511	13	26.0	635	4	US-09-925-065A-954135	Sequence 47431, A
C 439	13	26.0	596	6	US-10-029-386-10012	Sequence 10012, A	C 512	13	26.0	636	8	US-10-425-115-152056	Sequence 152056,
C 440	13	26.0	597	4	US-09-925-065A-54389	Sequence 54389, A	C 513	13	26.0	636	8	US-10-425-115-152056	Sequence 707919,
C 441	13	26.0	597	7	US-10-437-963-55901	Sequence 55901, A	C 514	13	26.0	639	4	US-09-925-065A-707919	Sequence 707919,
C 442	13	26.0	597	8	US-10-363-345A-10927	Sequence 10927, A	C 515	13	26.0	639	4	US-09-925-065A-707919	Sequence 707919,
C 443	13	26.0	597	8	US-10-363-345A-10928	Sequence 10928, A	C 516	13	26.0	639	4	US-09-925-065A-707920	Sequence 707920,
C 444	13	26.0	597	9	US-10-363-483A-10927	Sequence 10927, A	C 517	13	26.0	639	4	US-09-925-065A-781238	Sequence 781238,
C 445	13	26.0	597	9	US-10-363-483A-10928	Sequence 10928, A	C 518	13	26.0	639	4	US-09-925-065A-842361	Sequence 842361,
C 446	13	26.0	598	4	US-09-925-065A-150640	Sequence 150640,	C 519	13	26.0	640	5	US-10-369-499-31317	Sequence 31317, A
C 447	13	26.0	599	4	US-09-925-065A-920427	Sequence 920427,	C 520	13	26.0	640	5	US-10-027-632-233094	Sequence 233094,
C 448	13	26.0	599	4	US-09-925-065A-920428	Sequence 920428,	C 521	13	26.0	640	5	US-10-027-632-233095	Sequence 233095,
C 449	13	26.0	600	4	US-09-925-065A-53929	Sequence 53929, A	C 522	13	26.0	640	5	US-10-027-632-233096	Sequence 233096,
C 450	13	26.0	600	4	US-09-925-065A-53930	Sequence 53930, A	C 523	13	26.0	640	6	US-10-027-632-233094	Sequence 233094,
C 451	13	26.0	600	9	US-10-972-079-56474	Sequence 56474, A	C 524	13	26.0	640	6	US-10-027-632-233095	Sequence 233095,
C 452	13	26.0	600	9	US-10-972-079-56475	Sequence 56475, A	C 525	13	26.0	640	6	US-10-027-632-233096	Sequence 862834,
C 453	13	26.0	600	9	US-10-972-079-58094	Sequence 58094, A	C 526	13	26.0	641	4	US-09-925-065A-662894	Sequence 897750,
C 454	13	26.0	600	9	US-10-972-079-65324	Sequence 65324, A	C 527	13	26.0	644	4	US-10-425-114-22885	Sequence 22885, A
C 455	13	26.0	600	9	US-10-972-079-65325	Sequence 65325, A	C 528	13	26.0	644	7	US-10-363-345A-7423	Sequence 7423, Ap
C 456	13	26.0	600	9	US-10-972-079-80103	Sequence 80103, A	C 529	13	26.0	645	8	US-10-363-345A-7424	Sequence 7424, Ap
C 457	13	26.0	600	9	US-10-972-079-80104	Sequence 80104, A	C 530	13	26.0	645	9	US-10-363-483A-7424	Sequence 7424, Ap
C 458	13	26.0	600	9	US-10-972-079-95954	Sequence 95954, A	C 531	13	26.0	645	9	US-10-363-483A-7424	Sequence 683922,
C 459	13	26.0	600	9	US-10-972-079-95955	Sequence 95955, A	C 532	13	26.0	646	4	US-09-925-065A-683882	Sequence 683882,
C 460	13	26.0	602	4	US-09-925-065A-221124	Sequence 221124,	C 533	13	26.0	646	4	US-09-925-065A-683883	Sequence 683883,
C 461	13	26.0	602	4	US-09-925-065A-221125	Sequence 221125,	C 534	13	26.0	646	4	US-09-925-065A-683883	Sequence 683883,



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538	13	26.0	648	7	US-10-437-963-80254	Sequence 80254, A	C 611	13	26.0	789	8	US-10-357-920-10055	Sequence 20055, A
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C 541	13	26.0	649	7	US-09-925-065A-905561	Sequence 905561, A	614	13	26.0	802	7	US-10-424-599-91828	Sequence 91828, A
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C 544	13	26.0	650	4	US-09-925-065A-453118	Sequence 453118, A	C 617	13	26.0	822	5	US-10-027-632-162886	Sequence 162886, A
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547	13	26.0	653	7	US-10-425-114-28262	Sequence 28262, A	C 620	13	26.0	822	6	US-10-027-632-162886	Sequence 162887, A
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549	13	26.0	654	6	US-10-363-483A-12347	Sequence 12347, A	C 622	13	26.0	825	7	US-10-425-114-35108	Sequence 35108, A
550	13	26.0	654	6	US-09-925-065A-415746	Sequence 415746, A	C 623	13	26.0	839	8	US-10-425-115-20965	Sequence 20965, A
C 551	13	26.0	656	7	US-10-424-599-20039	Sequence 20039, A	624	13	26.0	849	5	US-10-027-632-161306	Sequence 161306, A
C 552	13	26.0	657	4	US-09-925-065A-638388	Sequence 638388, A	C 625	13	26.0	849	6	US-10-027-632-161306	Sequence 161306, A
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558	13	26.0	660	8	US-10-425-115-152057	Sequence 152057, A	C 631	13	26.0	882	8	US-10-363-345A-16400	Sequence 16400, A
559	13	26.0	660	8	US-10-363-345A-12347	Sequence 12347, A	C 632	13	26.0	882	8	US-10-363-345A-16400	Sequence 16399, A
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C 561	13	26.0	660	9	US-10-363-483A-12347	Sequence 12347, A	C 634	13	26.0	882	9	US-10-363-483A-16400	Sequence 16400, A
C 562	13	26.0	660	9	US-10-363-483A-12348	Sequence 12348, A	C 635	13	26.0	886	8	US-10-425-115-102934	Sequence 102934, A
C 563	13	26.0	664	8	US-10-425-115-40467	Sequence 40467, A	C 636	13	26.0	893	5	US-10-027-632-8195	Sequence 8194, Ap
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C 565	13	26.0	664	8	US-10-363-345A-7710	Sequence 7710, Ap	C 638	13	26.0	893	6	US-10-027-632-8195	Sequence 8195, Ap
566	13	26.0	664	9	US-10-363-483A-7709	Sequence 7709, Ap	C 639	13	26.0	894	6	US-10-027-632-8195	Sequence 8195, Ap
C 567	13	26.0	664	9	US-10-363-483A-7710	Sequence 7710, Ap	C 640	13	26.0	894	6	US-10-425-115-148424	Sequence 148424, A
568	13	26.0	666	4	US-10-425-115-152055	Sequence 152055, A	C 641	13	26.0	911	9	US-10-950-095-43	Sequence 43, App1
569	13	26.0	667	4	US-09-925-065A-837933	Sequence 837933, A	C 642	13	26.0	922	7	US-10-425-114-4491	Sequence 4491, Ap
C 570	13	26.0	670	7	US-10-424-599-101483	Sequence 101483, A	643	13	26.0	930	4	US-09-925-065A-65518	Sequence 65518, A
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573	13	26.0	676	7	US-10-424-599-45304	Sequence 45304, A	C 646	13	26.0	956	4	US-09-925-065A-48848	Sequence 48848, A
C 574	13	26.0	677	7	US-10-767-701-11408	Sequence 11408, A	647	13	26.0	956	4	US-09-925-065A-681045	Sequence 681045, A
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C 578	13	26.0	690	5	US-10-027-632-26525	Sequence 26525, A	C 651	13	26.0	959	9	US-10-363-483A-16227	Sequence 16227, A
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583	13	26.0	696	8	US-10-425-115-152049	Sequence 152049, A	656	13	26.0	991	7	US-10-425-114-4016	Sequence 4016, Ap
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C 586	13	26.0	699	9	US-10-363-345A-17111	Sequence 17111, A	659	13	26.0	1005	3	US-09-974-300-1184	Sequence 1184, Ap
587	13	26.0	705	9	US-10-363-483A-17112	Sequence 17112, A	660	13	26.0	1005	6	US-10-369-493-35214	Sequence 35214, A
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C 594	13	26.0	714	8	US-10-363-345A-15102	Sequence 15102, A	C 666	13	26.0	1022	6	US-10-027-632-160228	Sequence 260228, A
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685	13	1120	4	US-09-925-065A-62374	Sequence 62374, A	c 758	13	1701	7	US-10-425-114-1106	Sequence 1106, Ap
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C 856	13	26.0	2664	4	US-09-925-065A-67334	Sequence 67325, A	C 929	13	26.0	4199	10	US-11-097-143-30811	Sequence 30811, A
C 857	13	26.0	2664	4	US-09-925-065A-67336	Sequence 67326, A	C 930	13	26.0	4233	7	US-10-282-122A-31630	Sequence 31630, A
C 858	13	26.0	2664	6	US-10-241-596-111	Sequence 111, App	C 931	13	26.0	4236	7	US-10-437-963-80897	Sequence 80897, A
C 859	13	26.0	2694	7	US-10-437-963-79039	Sequence 79039, A	C 932	13	26.0	4266	6	US-10-241-596-109	Sequence 109, App
C 860	13	26.0	2720	8	US-10-425-115-99348	Sequence 99348, A	C 933	13	26.0	4266	7	US-10-437-963-80429	Sequence 80429, A
C 861	13	26.0	2726	6	US-10-264-213-30	Sequence 30, App	C 934	13	26.0	4278	7	US-10-437-963-78814	Sequence 78814, A
C 862	13	26.0	2726	8	US-10-264-213-42	Sequence 42, App	C 935	13	26.0	4325	7	US-10-437-963-80838	Sequence 80838, A
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C 864	13	26.0	2756	6	US-10-062-674-1625	Sequence 1625, Ap	C 937	13	26.0	4371	5	US-10-208-721-8	Sequence 8, App
C 865	13	26.0	2757	7	US-10-437-963-80398	Sequence 80398, A	C 938	13	26.0	4398	7	US-10-437-963-82453	Sequence 82453, A
C 866	13	26.0	2774	10	US-11-097-143-42154	Sequence 12154, A	C 939	13	26.0	4470	7	US-10-437-963-85427	Sequence 85427, A
C 867	13	26.0	2895	7	US-10-437-963-63578	Sequence 63578, A	C 940	13	26.0	4626	7	US-10-437-963-80440	Sequence 80440, A
C 868	13	26.0	2902	10	US-11-097-143-38758	Sequence 38758, A	C 941	13	26.0	4656	7	US-10-437-963-80401	Sequence 79051, A
C 869	13	26.0	2939	10	US-11-097-143-35362	Sequence 35362, A	C 942	13	26.0	4668	6	US-10-172-118-969	Sequence 969, App
C 870	13	26.0	3007	7	US-10-041-018-364	Sequence 364, App	C 943	13	26.0	4668	7	US-10-342-880-765	Sequence 880, App
C 871	13	26.0	3042	7	US-10-437-963-79790	Sequence 79790, A	C 944	13	26.0	4684	8	US-10-723-867-1454	Sequence 1454, App
C 872	13	26.0	3096	8	US-10-425-115-40860	Sequence 40860, A	C 945	13	26.0	4734	7	US-10-437-963-78929	Sequence 78929, A
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C 875	13	26.0	3195	7	US-10-437-963-80243	Sequence 80243, A	C 948	13	26.0	4776	7	US-10-437-963-82303	Sequence 82303, A
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C 878	13	26.0	3315	7	US-10-437-963-82084	Sequence 82084, A	C 951	13	26.0	4828	7	US-10-437-963-80480	Sequence 80480, A
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C 881	13	26.0	3405	5	US-10-027-632-264805	Sequence 264805, A	C 954	13	26.0	4851	5	US-10-194-163-939	Sequence 939, App
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C 884	13	26.0	3474	7	US-10-437-963-80864	Sequence 80864, A	C 957	13	26.0	4859	8	US-10-357-930-28981	Sequence 28981, A
C 885	13	26.0	3501	7	US-10-437-963-79987	Sequence 79987, A	C 958	13	26.0	4859	8	US-10-357-930-29335	Sequence 29335, A
C 886	13	26.0	3513	7	US-10-437-963-47222	Sequence 47222, A	C 959	13	26.0	4861	10	US-11-097-143-41746	Sequence 41746, A
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C 888	13	26.0	3546	8	US-10-474-792-673	Sequence 673, App	C 961	13	26.0	4873	7	US-10-437-963-79033	Sequence 79033, A
C 889	13	26.0	3553	8	US-10-857-673-1	Sequence 1, App	C 962	13	26.0	4876	7	US-10-437-963-81295	Sequence 81295, A
C 890	13	26.0	3575	10	US-11-097-143-16990	Sequence 16990, A	C 963	13	26.0	4977	7	US-10-437-963-79826	Sequence 79826, A
C 891	13	26.0	3594	7	US-10-437-963-78932	Sequence 78932, A	C 964	13	26.0	4997	7	US-10-282-122A-35506	Sequence 35506, A
C 892	13	26.0	3621	7	US-10-437-963-80558	Sequence 80558, A	C 965	13	26.0	5051	10	US-11-097-143-41780	Sequence 41780, A
C 893	13	26.0	3656	10	US-11-097-143-34189	Sequence 34189, A	C 966	13	26.0	5163	7	US-10-437-963-79006	Sequence 79006, A
C 894	13	26.0	3797	10	US-11-097-143-32713	Sequence 32713, A	C 967	13	26.0	5184	7	US-10-221-613-384	Sequence 384, App
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C 897	13	26.0	3924	7	US-10-437-963-80402	Sequence 80402, A	C 970	13	26.0	5244	8	US-10-473-126-111	Sequence 111, App
C 898	13	26.0	3968	7	US-10-451-467A-173	Sequence 173, App	C 971	13	26.0	5252	6	US-10-240-453-176	Sequence 176, App
C 899	13	26.0	3970	7	US-10-437-963-82261	Sequence 82261, A	C 972	13	26.0	5259	7	US-10-437-963-79930	Sequence 79930, A



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C 977 13 26.0 5424 7 US-10-437-963-78841 Sequence 78841, A
C 978 13 26.0 5425 7 US-10-437-963-79004 Sequence 79004, A
979 13 26.0 5476 5 US-10-239-676-208 Sequence 208, App
980 13 26.0 5476 6 US-10-311-455-2088 Sequence 2088, App
C 981 13 26.0 5493 7 US-10-437-963-65429 Sequence 65429, A
C 982 13 26.0 5499 7 US-10-437-963-793-2 Sequence 2, App11
983 13 26.0 5520 7 US-10-437-963-78860 Sequence 78860, A
984 13 26.0 5523 7 US-10-437-963-80477 Sequence 80477, A
985 13 26.0 5569 9 US-10-450-763-8364 Sequence 8364, A
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C 990 13 26.0 5816 5 US-10-198-846-12711 Sequence 12711, A
C 991 13 26.0 5904 7 US-10-437-963-79940 Sequence 79940, A
C 992 13 26.0 5908 7 US-10-437-963-78844 Sequence 78844, A
C 993 13 26.0 5914 7 US-10-437-963-83129 Sequence 83129, A
994 13 26.0 5920 7 US-10-437-963-82271 Sequence 82271, A
C 995 13 26.0 5922 6 US-10-311-455-424 Sequence 424, App
996 13 26.0 5951 5 US-10-239-676-116 Sequence 116, App
997 13 26.0 5951 6 US-10-240-453-134 Sequence 134, App
998 13 26.0 6030 7 US-10-437-963-80489 Sequence 80489, A
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C1000 13 26.0 6045 7 US-10-437-963-78937 Sequence 78937, A
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## ALIGNMENTS

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RESULT 1
US-10-442-502-13
; Sequence 13, Application US/10442502
; Publication No. US20040009945A1
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; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSKHO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: PARKER, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 693
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; US-10-442-502-13
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Best Local Similarity 100.0%; Pred. No. 4,8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 340 GGGACGGCTCCAACTTACCAAGCGTGTACCAAGCACTTCGTTAGTGTAGG 389
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RESULT 2
US-10-332-282-8
; Sequence 8, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
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; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 954
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 7
US-10-332-282-8
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Best Local Similarity 100.0%; Pred. No. 4,8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 601 GGGACGGCTCCAACTTACCAAGCGTGTACCAAGCACTTCGTTAGTGTAGG 650
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RESULT 3
US-10-402-466A-23
; Sequence 23, Application US/10402466A
; Publication No. US20040028695A1
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; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gil, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 23
; LENGTH: 1272
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP113 for a PA deletion mutant PA47.
US-10-402-466A-23
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Query Match 100.0%; Score 50; DB 7; Length 1272;
Best Local Similarity 100.0%; Pred. No. 4,8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 172 GGGACGGCTCCAACTTACCAAGCGTGTACCAAGCACTTCGTTAGTGTAGG 221
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RESULT 4
US-10-332-282-10
; Sequence 10, Application US/10332282
; Publication No. US20030170263A1
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; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Echel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 1278
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 9
US-10-332-282-10
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Query Match          100.0%; Score 50; DB 6; Length 1278;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 50
Db 601 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 650
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RESULT 5
US-10-332-282-6
; Sequence 6, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Echel D
; APPLICANT: Miller, Julie
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; PRIOR FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 1461
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 5
US-10-332-282-6
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Query Match          100.0%; Score 50; DB 6; Length 1461;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 50
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Db 1108 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 1157
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RESULT 6
US-10-442-502-4
; Sequence 4, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1710
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-4
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Query Match          100.0%; Score 50; DB 6; Length 1710;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 50
Db 610 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 659
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RESULT 7
US-10-402-466A-21
; Sequence 21, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gilt, Lillian
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTIN
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 21
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP11 for a PA deletion mutant PA64.
US-10-402-466A-21
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Query Match          100.0%; Score 50; DB 7; Length 1722;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 1 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 50
Db 622 GGGAGCGCTCCAACTCTACCAAGCTGTACCAAGCACTTGTTAGTGG 671
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RESULT 8
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US-10-332-282-12
; Sequence 12, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Walker, Julie
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 11
US-10-332-282-12

Query Match          100.0%; Score 50; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 50
Db 1108 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 1157

RESULT 9
US-09-848-909-22
; Sequence 22, Application US/09848909
; Publication No. US20020039588A1
; GENERAL INFORMATION:
; APPLICANT: Collier, R. John
; APPLICANT: Sellman, Brett R.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; FILE REFERENCE: 00742/060002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; OTHER INFORMATION:
US-09-848-909-22

Query Match          100.0%; Score 50; DB 3; Length 2208;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 50
Db 1108 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 1157

RESULT 10
US-10-332-282-14
; Sequence 14, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Ethel D
; APPLICANT: Walker, Julie
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Tibball, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
; OTHER INFORMATION: used to encode SEQ ID NO: 13
US-10-332-282-14

Query Match          100.0%; Score 50; DB 6; Length 2208;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 50
Db 1108 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 1157

RESULT 11
US-10-402-466A-8
; Sequence 8, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giri, Lallan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 8
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence for B. anthracis PA.
US-10-402-466A-8

Query Match          100.0%; Score 50; DB 7; Length 2208;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 50
Db 1108 GGGACGGCTCCAAATCTACACGCTGTTACCAACGACTTCGTTAGTGTAGG 1157

RESULT 12
US-10-402-466A-11
```



```
; Sequence 11, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gil, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 11
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBPI05 for B. anthracis PA. The DNA cod
; OTHER INFORMATION: sequences for rPA (2208 bases) is identical to Sequence 8.
US-10-402-466A-11
```

```
Query Match          100.0%; Score 50; DB 7; Length 2208;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 50
Db 1108 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 1157
```

```
RESULT 13
US-10-442-502-2
; Sequence 2, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-2
```

```
Query Match          100.0%; Score 50; DB 6; Length 2211;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 50
Db 1111 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 1160
```

```
RESULT 14
US-10-638-006-3
; Sequence 3, Application US/10638006
; Publication No. US2004017121A1
; GENERAL INFORMATION:
```

```
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA as
; APPLICANT: represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Leppia, Stephen H.
; APPLICANT: Rosovitz, Mary Jo
; APPLICANT: Hsu, S. Dana
; TITLE OF INVENTION: METHODS FOR PREPARING BACILLUS ANTHRACIS SPOULATION DEFICIENT
; TITLE OF INVENTION: MUTANTS AND FOR PRODUCING RECOMBINANT BACILLUS ANTHRACIS
; TITLE OF INVENTION: PROTECTIVE ANTIGEN FOR USE IN VACCINES
; FILE REFERENCE: 4239-66891
; CURRENT APPLICATION NUMBER: US/10/638,006
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: 60/402,285
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2235
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Mature double mutant protective antigen
US-10-638-006-3
```

```
Query Match          100.0%; Score 50; DB 7; Length 2235;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 50
Db 1135 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 1184
```

```
RESULT 15
US-10-442-502-3
; Sequence 3, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1998-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 2292
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-3
```

```
Query Match          100.0%; Score 50; DB 6; Length 2292;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 1 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 50
Db 1192 GGGACGGCTCCATCTACACGCTGTACCAAGCACTTGTTAGTGTAGG 1241
```

```
RESULT 16
US-09-747-521-3
; Sequence 3, Application US/09747521
; Patent No. US20020051791A1
; GENERAL INFORMATION:
```



```

; APPLICANT: Galloway, Darrel
; APPLICANT: Mateczun, Alfred
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04079
; CURRENT APPLICATION NUMBER: US/09/747,521
; CURRENT FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-09-747-521-3

Query Match          100.0%; Score 50; DB 3; Length 2295;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 50
DB 1195 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 1244

RESULT 17
US-10-106-014-3
; Sequence 3, Application US/10106014
; Publication No. US20020142002A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04114
; CURRENT APPLICATION NUMBER: US/10/106,014
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-106-014-3

Query Match          100.0%; Score 50; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 50
DB 1195 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 1244

RESULT 18
US-10-105-695-3
; Sequence 3, Application US/10105695
; Publication No. US20020197272A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Ant
; FILE REFERENCE: 22727/04115
; CURRENT APPLICATION NUMBER: US/10/105,695
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
```

```

; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-105-695-3

Query Match          100.0%; Score 50; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 50
DB 1195 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 1244

RESULT 19
US-10-105-694-3
; Sequence 3, Application US/10105694
; Publication No. US20030003109A1
; GENERAL INFORMATION:
; APPLICANT: Galloway, Darrel R.
; APPLICANT: Mateczun, Alfred J.
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus An
; FILE REFERENCE: 22727/04116
; CURRENT APPLICATION NUMBER: US/10/105,694
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: US 09/747,521
; PRIOR FILING DATE: 2000-12-21
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(2295)
; OTHER INFORMATION:
US-10-105-694-3

Query Match          100.0%; Score 50; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 50
DB 1195 GGGACGGCTCCAACTTACACAGCGTTACCAAGCACTTGGTTAGTGTAGG 1244

RESULT 20
US-10-442-502-1
; Sequence 1, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
```



```
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-1
```

```
Query Match          100.0%; Score 50; DB 6; Length 2295;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 50
Db      1195 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 1244
```

```
RESULT 21
US-10-751-103-3
; Sequence 3, Application US/10751103
; Publication No. US20050148529A1
; GENERAL INFORMATION:
; APPLICANT: Schmaljohn, Connie S.
; APPLICANT: Fuller, James T.
; TITLE OF INVENTION: Nucleic Acid Immunization
; FILE REFERENCE: 033267-021
; CURRENT APPLICATION NUMBER: US/10/751,103
; CURRENT FILING DATE: 2004-01-05
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 2605
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (174)...(2465)
US-10-751-103-3
```

```
Query Match          100.0%; Score 50; DB 9; Length 2605;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 50
Db      1368 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 1417
```

```
RESULT 22
US-10-410-647-29
; Sequence 29, Application US/10410647
; Publication No. US20030235818A1
; GENERAL INFORMATION:
; APPLICANT: PLEXUS VACCINE, INC.
; APPLICANT: Kevitch, Vasevold
; APPLICANT: Bordner, Andrew
; APPLICANT: Deans, Robert
; APPLICANT: Sumner, Mary
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME
; FILE REFERENCE: PLEX110-1
; CURRENT APPLICATION NUMBER: US/10/410,647
; CURRENT FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/373,668
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/371,256
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/371,250
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 4235
; TYPE: DNA
```

```
; ORGANISM: Bacillus anthracis
US-10-410-647-29
```

```
Query Match          100.0%; Score 50; DB 6; Length 4235;
Best Local Similarity 100.0%; Pred. No. 4.8e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 50
Db      2998 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 3047
```

```
RESULT 23
US-10-402-466A-7
; Sequence 7, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giri, Laljan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTION
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 7
; LENGTH: 8198
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Expression vector for B. anthracis Protective Antigen (PA). B.
; OTHER INFORMATION: sequence is shown since the vector sequence is different from
; OTHER INFORMATION: of the pBP vectors. The PA coding sequence is from 3735 to 59
US-10-402-466A-7
```

```
Query Match          100.0%; Score 50; DB 7; Length 8198;
Best Local Similarity 100.0%; Pred. No. 4.7e-19;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 50
Db      4842 GGGACGGCTCCATCTACACGCTGTACCAACGACTTGTAGTGTAGG 4891
```

```
RESULT 24
US-10-402-466A-10
; Sequence 10, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giri, Laljan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTION
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 10
; LENGTH: 9286
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Dual expression vector pBP105 for B. anthracis PA and LF30. B.
; OTHER INFORMATION: sequence is shown since the vector sequence contains two coding
; OTHER INFORMATION: regions. The coding region for PA is from 3735 to 5942 and the
```



OTHER INFORMATION: region for LF30 is from 6391 to 7161.  
US-10-402-466A-10

Query Match 100.0%; Score 50; DB 7; Length 9286;  
Best Local Similarity 100.0%; Pred. No. 4,76-19;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCATCTACAGCTGTACCAAGCACTTGTTAGTGG 50  
Db 4842 GGGACGGCTCCATCTACAGCTGTACCAAGCACTTGTTAGTGG 4891

## RESULT 25

US-09-925-065A-472627  
Sequence 472627, Application US/09925065A  
Publication No. US20050228172A9

GENERAL INFORMATION:  
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 472627  
LENGTH: 547

TYPE: DNA  
ORGANISM: Homo sapiens

US-09-925-065A-472627

Query Match 36.0%; Score 18; DB 4; Length 547;  
Best Local Similarity 100.0%; Pred. No. 2,3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AATCTACACGTTTACC 29  
Db 300 AATCTACACGTTTACC 317

## RESULT 26

US-09-925-065A-472628  
Sequence 472628, Application US/09925065A  
Publication No. US20050228172A9

GENERAL INFORMATION:  
APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135

CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08

PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24

PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20

PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30

PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16

PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09

NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 472628  
LENGTH: 547  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-472628

Query Match 36.0%; Score 18; DB 4; Length 547;  
Best Local Similarity 100.0%; Pred. No. 2,3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 12 AATCTACACGTTTACC 29  
Db 300 AATCTACACGTTTACC 317

## RESULT 27

US-10-437-963-84993  
Sequence 84993, Application US/10437963  
Publication No. US20040123343A1

GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua

APPLICANT: Cao, Yongwei  
APPLICANT: Wu, Wei

APPLICANT: Boukharov, Andrey A.  
APPLICANT: Barbazuk, Brad

TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53221)B  
CURRENT APPLICATION NUMBER: US/10/437,963

CURRENT FILING DATE: 2003-05-14  
NUMBER OF SEQ ID NOS: 204966

SEQ ID NO 84993  
LENGTH: 1605

TYPE: DNA  
ORGANISM: Oryza sativa

FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT4530\_84175C.1

US-10-437-963-84993

Query Match 36.0%; Score 18; DB 7; Length 1605;  
Best Local Similarity 100.0%; Pred. No. 2,3;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 ACGGCTCCATCTACAC 21  
Db 819 ACGGCTCCATCTACAC 836

## RESULT 28

US-10-424-599-35666  
Sequence 35666, Application US/10424599  
Publication No. US20040031072A1

GENERAL INFORMATION:  
APPLICANT: La Rosa, Thomas J.

APPLICANT: Kovalic, David K.  
APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement

FILE REFERENCE: 38-21(53222)B  
CURRENT APPLICATION NUMBER: US/10/424,599

CURRENT FILING DATE: 2003-04-28  
NUMBER OF SEQ ID NOS: 285684

SEQ ID NO 35666  
LENGTH: 295

TYPE: DNA  
ORGANISM: Glycine max

FEATURE:  
OTHER INFORMATION: Clone ID: PAT\_MRT3847\_13220C.1

US-10-424-599-35666



Query Match 34.0%; Score 17; DB 7; Length 295;  
Best Local Similarity 100.0%; Pred. No. 9;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AACGTGTACCAACGAC 35  
Db 255 AACGTGTACCAACGAC 271

RESULT 29  
US-11-036-317-401757/C  
; Sequence 401757, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036,317  
; PRIOR FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536,639  
; PRIOR FILING DATE: 2004-01-13  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 401757  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-401757

Query Match 32.0%; Score 16; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGCACGGCTCCCATCT 16  
Db 17 GGCACGGCTCCCATCT 2

RESULT 30  
US-09-925-065A-242591  
; Sequence 242591, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 242591  
; LENGTH: 554  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-242591

Query Match 32.0%; Score 16; DB 4; Length 554;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TGTACCAACGACTTC 38  
Db 536 TGTACCAACGACTTC 551

RESULT 31  
US-09-925-065A-102353/C  
; Sequence 102353, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 102353  
; LENGTH: 563  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-102353

Query Match 32.0%; Score 16; DB 4; Length 563;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TGTACCAACGACTTC 38  
Db 28 TGTACCAACGACTTC 13

RESULT 32  
US-09-925-065A-611993  
; Sequence 611993, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 611993  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-611993

Query Match 32.0%; Score 16; DB 4; Length 577;



Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 ACGGCTCAATCTACA 19  
|||||  
Db 356 ACGGCTCAATCTACA 371

RESULT 33  
US-09-119-900-14  
; Sequence 14, Application US/09119900  
; Patent No. US20020081622A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Craig W.  
; APPLICANT: Pang, Patty P.-Y.  
; APPLICANT: Belei, Marina  
; TITLE OF INVENTION: Recombinant DNase B Derived from  
; TITLE OF INVENTION: Streptococcus pyogenes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/119,900  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,845  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farber, Michael B.  
; REGISTRATION NUMBER: 32,612  
; REFERENCE/DOCKET NUMBER: 9521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 937 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..819  
; US-09-119-900-14

Query Match 32.0%; Score 16; DB 3; Length 937;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCATCTACACG 22  
|||||  
Db 667 GCTCCATCTACACG 682

RESULT 34  
US-10-453-032-14  
; Sequence 14, Application US/10453032

; Publication No. US20040023305A1

; GENERAL INFORMATION:  
; APPLICANT: Adams, Craig W.  
; APPLICANT: Pang, Patty P.-Y.  
; APPLICANT: Belei, Marina  
; TITLE OF INVENTION: Recombinant DNase B Derived from  
; TITLE OF INVENTION: Streptococcus pyogenes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor  
; CITY: Pasadena  
; STATE: California  
; COUNTRY: USA  
; ZIP: 91001  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/453,032  
; FILING DATE: 03-JUNE-2003  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/082,845  
; FILING DATE: 23-JUNE-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Farber, Michael B.  
; REGISTRATION NUMBER: 32,612  
; REFERENCE/DOCKET NUMBER: 9521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (818) 796-4000  
; TELEFAX: (818) 795-6321  
; INFORMATION FOR SEQ ID NO: 14:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 937 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: double  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; ORIGINAL SOURCE:  
; ORGANISM: Streptococcus pyogenes  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 1..819  
; US-10-453-032-14

Query Match 32.0%; Score 16; DB 7; Length 937;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCATCTACACG 22  
|||||  
Db 667 GCTCCATCTACACG 682

RESULT 35  
US-09-119-900-11  
; Sequence 11, Application US/09119900  
; Patent No. US20020081622A1  
; GENERAL INFORMATION:  
; APPLICANT: Adams, Craig W.  
; APPLICANT: Pang, Patty P.-Y.  
; APPLICANT: Belei, Marina  
; TITLE OF INVENTION: Recombinant DNase B Derived from  
; TITLE OF INVENTION: Streptococcus pyogenes  
; NUMBER OF SEQUENCES: 16  
; CORRESPONDENCE ADDRESS:  
; ADDRESSER: Sheldon & Mak  
; STREET: 225 South Lake Avenue, Ninth Floor



CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/119,900  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
US-09-119-900-11

Query Match 32.0%; Score 16; DB 3; Length 940;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCAATCTACAACG 22  
|||||  
Db 670 GCTCCAATCTACAACG 685

RESULT 36  
US-10-453-032-11  
Sequence 11, Application US/10453032  
Publication No. US20040023305A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belal, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
TITLE OF INVENTION: Streptococcus pyogenes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/453,032  
FILING DATE: 03-JUNE-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/082,845  
FILING DATE: 23-JUNE-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 940 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
US-10-453-032-11

Query Match 32.0%; Score 16; DB 7; Length 940;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCAATCTACAACG 22  
|||||  
Db 670 GCTCCAATCTACAACG 685

RESULT 37  
US-09-119-900-7  
Sequence 7, Application US/09119900  
Patent No. US20020081622A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belal, Marina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
TITLE OF INVENTION: Streptococcus pyogenes  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/119,900  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double



TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..944  
US-09-119-900-7

Query Match 32.0%; Score 16; DB 3; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTCCATCTACACG 22  
Db 792 GCTCCATCTACACG 807

RESULT 38  
US-10-453-032-7  
Sequence 7, Application US/10453032  
Publication No. US20040023305A1  
GENERAL INFORMATION:  
APPLICANT: Adams, Craig W.  
APPLICANT: Pang, Patty P.-Y.  
APPLICANT: Belet, Martina  
TITLE OF INVENTION: Recombinant DNase B Derived from  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Sheldon & Mak  
STREET: 225 South Lake Avenue, Ninth Floor  
CITY: Pasadena  
STATE: California  
COUNTRY: USA  
ZIP: 91001  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/453, 032  
FILING DATE: 03-JUNE-2003  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/082,845  
FILING DATE: 23-JUNE-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Farber, Michael B.  
REGISTRATION NUMBER: 32,612  
REFERENCE/DOCKET NUMBER: 9521  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (818) 796-4000  
TELEFAX: (818) 795-6321  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1083 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pyogenes  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 129..944  
US-10-453-032-7

Query Match 32.0%; Score 16; DB 7; Length 1083;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTCCATCTACACG 22  
Db 792 GCTCCATCTACACG 807

RESULT 39  
US-11-097-143-22159  
Sequence 22159, Application US/11097143  
Publication No. US20050208558A1  
GENERAL INFORMATION:  
APPLICANT: Venter, J. Craig  
APPLICANT: et al.  
TITLE OF INVENTION: DETECTION KIT, SUCH AS NUCLEIC ACID  
TITLE OF INVENTION: ARRAYS, FOR DETECTING EXPRESSION OF 10,000 OR MORE  
FILE REFERENCE: CL000728  
CURRENT APPLICATION NUMBER: US/11/097,143  
CURRENT FILING DATE: 2005-04-04  
PRIOR APPLICATION NUMBER: 60/157,832  
PRIOR FILING DATE: 1999-10-05  
PRIOR APPLICATION NUMBER: 60/160,191  
PRIOR FILING DATE: 1999-10-19  
PRIOR APPLICATION NUMBER: 60/161,932  
PRIOR FILING DATE: 1999-10-28  
PRIOR APPLICATION NUMBER: 60/164,769  
PRIOR FILING DATE: 1999-11-12  
PRIOR APPLICATION NUMBER: 60/173,383  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 60/175,693  
PRIOR FILING DATE: 2000-01-12  
PRIOR APPLICATION NUMBER: 60/184,831  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: 60/191,637  
PRIOR FILING DATE: 2000-03-23  
NUMBER OF SEQ ID NOS: 43008  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 22159  
LENGTH: 3257  
TYPE: DNA  
ORGANISM: DROSOPHILA  
US-11-097-143-22159

Query Match 32.0%; Score 16; DB 10; Length 3257;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTGTTACCAAGACTT 37  
Db 166 GTGTTACCAAGACTT 181

RESULT 40  
US-10-174-677-110/C  
Sequence 110, Application US/10174677  
Publication No. US20030190704A1  
GENERAL INFORMATION:  
APPLICANT: Xie, Ting  
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR ANCHORING STEM CELLS IN A MICROENV  
FILE REFERENCE: 40716(IP-012)  
CURRENT APPLICATION NUMBER: US/10/174,677  
CURRENT FILING DATE: 2002-06-19  
NUMBER OF SEQ ID NOS: 117  
SOFTWARE: Patentin version 3.1  
SEQ ID NO 110  
LENGTH: 5414  
TYPE: DNA  
ORGANISM: DROSOPHILA  
US-10-174-677-110



Query Match 32.0%; Score 16; DB 6; Length 5414;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTGTTACCAACGACTT 37  
|||  
Db 130 GTGTTACCAACGACTT 175

Search completed: April 12, 2006, 06:02:41  
Job time : 160.436 secs



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C 93	13	26.0	518	6	US-09-925-065A-533030	Sequence 533030,	C 166	13	26.0	573	6	US-09-925-065A-929888	Sequence 929888,
C 94	13	26.0	519	6	US-09-925-065A-841582	Sequence 841582,	C 167	13	26.0	573	6	US-09-925-065A-929889	Sequence 929889,
C 95	13	26.0	528	14	US-11-112-908-244	Sequence 244, App	C 168	13	26.0	575	6	US-09-925-065A-929877	Sequence 929877,
C 96	13	26.0	529	6	US-09-925-065A-475321	Sequence 475321,	C 169	13	26.0	575	6	US-09-925-065A-929878	Sequence 929878,
C 97	13	26.0	529	10	US-10-301-480-490186	Sequence 490186,	C 170	13	26.0	576	6	US-09-925-065A-372823	Sequence 372823,
C 98	13	26.0	529	10	US-10-301-480-490187	Sequence 490187,	C 171	13	26.0	576	6	US-09-925-065A-372825	Sequence 372825,
C 99	13	26.0	529	10	US-10-301-480-490188	Sequence 490188,	C 172	13	26.0	578	6	US-09-925-065A-113679	Sequence 113679,
C 100	13	26.0	529	10	US-10-301-480-1103595	Sequence 1103595,	C 173	13	26.0	578	10	US-10-301-480-188788	Sequence 188788,
C 101	13	26.0	529	10	US-10-301-480-1103596	Sequence 1103596,	C 174	13	26.0	578	10	US-10-301-480-1002197	Sequence 1002197,
C 102	13	26.0	529	10	US-10-301-480-1103597	Sequence 1103597,	C 175	13	26.0	579	10	US-10-301-480-442551	Sequence 442551,
C 103	13	26.0	531	10	US-10-301-480-1103597	Sequence 1103597,	C 176	13	26.0	579	10	US-10-301-480-1055960	Sequence 1055960,
C 104	13	26.0	531	10	US-10-301-480-427765	Sequence 427765,	C 177	13	26.0	579	10	US-10-301-480-1055962	Sequence 1055962,
C 105	13	26.0	532	6	US-09-925-065A-16671	Sequence 16671, A	C 178	13	26.0	582	10	US-10-301-480-904128	Sequence 904128,
C 106	13	26.0	532	6	US-09-925-065A-36672	Sequence 36672, A	C 179	13	26.0	582	10	US-10-301-480-904128	Sequence 904128,
C 107	13	26.0	532	6	US-09-925-065A-36673	Sequence 36673, A	C 180	13	26.0	582	10	US-09-925-065A-110035	Sequence 110035,
C 108	13	26.0	532	6	US-09-925-065A-36673	Sequence 36673, A	C 181	13	26.0	587	6	US-09-925-065A-372824	Sequence 372824,
C 109	13	26.0	532	9	US-10-301-480-137909	Sequence 137909,	C 182	13	26.0	587	6	US-09-925-065A-372824	Sequence 372824,
C 110	13	26.0	532	9	US-10-301-480-137910	Sequence 137910,	C 183	13	26.0	588	6	US-09-925-065A-202312	Sequence 202312,
C 111	13	26.0	532	9	US-10-301-480-137911	Sequence 137911,	C 184	13	26.0	591	6	US-09-925-065A-303761	Sequence 303761,
C 112	13	26.0	532	10	US-10-301-480-751318	Sequence 751318,	C 185	13	26.0	591	10	US-10-301-480-379892	Sequence 379892,
C 113	13	26.0	532	10	US-10-301-480-751319	Sequence 751319,	C 186	13	26.0	591	10	US-10-301-480-993301	Sequence 993301,
C 114	13	26.0	532	10	US-10-301-480-751320	Sequence 751320,	C 187	13	26.0	592	6	US-09-925-065A-108889	Sequence 108889,
C 115	13	26.0	536	6	US-09-925-065A-537635	Sequence 537635,	C 188	13	26.0	592	6	US-09-925-065A-108890	Sequence 108890,
C 116	13	26.0	537	6	US-09-925-065A-356312	Sequence 356312,	C 189	13	26.0	592	6	US-09-925-065A-291539	Sequence 291539,
C 117	13	26.0	538	6	US-09-925-065A-426743	Sequence 426743,	C 190	13	26.0	592	10	US-10-301-480-468196	Sequence 468196,
C 118	13	26.0	538	10	US-10-301-480-443231	Sequence 444321,	C 191	13	26.0	592	10	US-10-301-480-1081605	Sequence 1081605,
C 119	13	26.0	538	10	US-10-301-480-470575	Sequence 470575,	C 192	13	26.0	593	10	US-10-301-480-373113	Sequence 373113,
C 120	13	26.0	538	10	US-10-301-480-470576	Sequence 470576,	C 193	13	26.0	593	10	US-10-301-480-986522	Sequence 986522,
C 121	13	26.0	538	10	US-10-301-480-1057730	Sequence 1057730,	C 194	13	26.0	594	6	US-09-925-065A-296261	Sequence 296261,
C 122	13	26.0	538	10	US-10-301-480-1083984	Sequence 1083984,	C 195	13	26.0	594	10	US-10-301-480-368425	Sequence 368425,
C 123	13	26.0	538	10	US-10-301-480-1083985	Sequence 1083985,	C 196	13	26.0	594	10	US-10-301-480-981884	Sequence 981884,
C 124	13	26.0	539	10	US-10-301-480-490183	Sequence 490183,	C 197	13	26.0	595	9	US-10-301-480-76645	Sequence 76645, A
C 125	13	26.0	539	10	US-10-301-480-1103592	Sequence 1103592,	C 198	13	26.0	595	10	US-10-301-480-690054	Sequence 690054, A
C 126	13	26.0	540	6	US-09-925-065A-303760	Sequence 303760,	C 199	13	26.0	596	9	US-10-301-480-56767	Sequence 56767, A
C 127	13	26.0	540	10	US-10-301-480-379891	Sequence 379891,	C 200	13	26.0	596	9	US-10-301-480-209608	Sequence 209608,
C 128	13	26.0	541	6	US-09-925-065A-184467	Sequence 184467,	C 201	13	26.0	596	10	US-10-301-480-670176	Sequence 670176,
C 129	13	26.0	542	6	US-09-925-065A-504806	Sequence 504806,	C 202	13	26.0	596	10	US-10-301-480-823017	Sequence 823017,
C 130	13	26.0	548	10	US-10-301-480-274795	Sequence 274795,	C 203	13	26.0	597	6	US-09-925-065A-54389	Sequence 54389, A
C 131	13	26.0	548	10	US-10-301-480-888204	Sequence 888204,	C 204	13	26.0	597	9	US-10-301-480-155627	Sequence 155627,
C 132	13	26.0	549	9	US-10-932-182A-1599	Sequence 1599, Ap	C 205	13	26.0	597	10	US-10-301-480-769036	Sequence 769036,
C 133	13	26.0	549	9	US-10-932-182A-1599	Sequence 1599, Ap	C 206	13	26.0	598	6	US-09-925-065A-190640	Sequence 190640,
C 134	13	26.0	552	6	US-09-925-065A-830643	Sequence 830643,	C 207	13	26.0	598	9	US-10-301-480-208693	Sequence 208693,
C 135	13	26.0	556	6	US-09-925-065A-10821	Sequence 10821, A	C 208	13	26.0	598	10	US-10-301-480-880335	Sequence 880335,
C 136	13	26.0	556	9	US-10-301-480-21176	Sequence 21176, A	C 209	13	26.0	598	10	US-10-301-480-442552	Sequence 442552,
C 137	13	26.0	556	9	US-10-301-480-112058	Sequence 112058,	C 210	13	26.0	598	10	US-10-301-480-822102	Sequence 822102,
C 138	13	26.0	556	10	US-10-301-480-634585	Sequence 634585,	C 211	13	26.0	598	10	US-10-301-480-893744	Sequence 893744,
C 139	13	26.0	556	10	US-10-301-480-725467	Sequence 725467,	C 212	13	26.0	598	10	US-10-301-480-105361	Sequence 105361,
C 140	13	26.0	557	6	US-09-925-065A-278439	Sequence 278439,	C 213	13	26.0	599	6	US-09-925-065A-920427	Sequence 920427,
C 141	13	26.0	559	10	US-10-301-480-355457	Sequence 355457,	C 214	13	26.0	599	6	US-09-925-065A-53929	Sequence 53929, A
C 142	13	26.0	559	10	US-10-301-480-968866	Sequence 968866,	C 215	13	26.0	600	6	US-09-925-065A-53930	Sequence 53930, A
C 143	13	26.0	560	10	US-10-301-480-438523	Sequence 438523,	C 216	13	26.0	600	6	US-09-925-065A-3964	Sequence 3964, Ap
C 144	13	26.0	560	10	US-10-301-480-438524	Sequence 438524,	C 217	13	26.0	600	8	US-10-750-185-3964	Sequence 3964, Ap
C 145	13	26.0	560	10	US-10-301-480-1051932	Sequence 1051932,	C 218	13	26.0	600	8	US-10-750-623-3964	Sequence 3964, Ap
C 146	13	26.0	562	6	US-10-301-480-1051933	Sequence 1051933,	C 219	13	26.0	600	9	US-10-301-480-155167	Sequence 155167,
C 147	13	26.0	562	6	US-09-925-065A-361958	Sequence 361958,	C 220	13	26.0	600	9	US-10-301-480-768576	Sequence 768576,
C 148	13	26.0	562	6	US-09-925-065A-361959	Sequence 361959,	C 221	13	26.0	600	10	US-10-301-480-768577	Sequence 768577,
C 149	13	26.0	566	6	US-09-925-065A-348690	Sequence 348690,	C 222	13	26.0	602	6	US-09-925-065A-221124	Sequence 221124,
C 150	13	26.0	566	6	US-09-925-065A-348691	Sequence 348691,	C 223	13	26.0	602	6	US-09-925-065A-221125	Sequence 221125,
C 151	13	26.0	566	10	US-10-301-480-420821	Sequence 420821,	C 224	13	26.0	602	6	US-09-925-065A-823276	Sequence 823276,
C 152	13	26.0	566	10	US-10-301-480-1034220	Sequence 1034220,	C 225	13	26.0	603	10	US-10-301-480-306500	Sequence 306500,
C 153	13	26.0	567	6	US-09-925-065A-368274	Sequence 368274,	C 226	13	26.0	603	10	US-10-301-480-306501	Sequence 306501,
C 154	13	26.0	567	6	US-09-925-065A-368275	Sequence 368275,	C 227	13	26.0	603	10	US-10-301-480-919909	Sequence 919909,
C 155	13	26.0	568	6	US-09-925-065A-932097	Sequence 932097,	C 228	13	26.0	603	10	US-10-301-480-919910	Sequence 919910,
C 156	13	26.0	568	6	US-09-925-065A-932098	Sequence 932098,	C 229	13	26.0	604	6	US-09-925-065A-223159	Sequence 223159,
C 157	13	26.0	569	6	US-09-925-065A-646061	Sequence 646061,	C 230	13	26.0	605	6	US-09-925-065A-433123	Sequence 433123,
C 158	13	26.0	571	6	US-09-925-065A-401034	Sequence 401034,	C 231	13	26.0	607	10	US-10-301-480-495489	Sequence 495489,
C 159	13	26.0	571	6	US-09-925-065A-950429	Sequence 950429,	C 232	13	26.0	607	10	US-10-301-480-1108898	Sequence 1108898,
C 160	13	26.0	571	10	US-10-301-480-420822	Sequence 420822,	C 233	13	26.0	609	6	US-09-925-065A-63783	Sequence 63783, A
C 161	13	26.0	571	10	US-10-301-480-1034231	Sequence 1034231,	C 234	13	26.0	609	6	US-09-925-065A-63784	Sequence 63784, A
C 162	13	26.0	572	10	US-10-301-480-432916	Sequence 432916,	C 235	13	26.0	609	9	US-10-301-480-165021	Sequence 165021,
C 163	13	26.0	572	10	US-10-301-480-432917	Sequence 432917,	C 236	13	26.0	609	9	US-10-301-480-165022	Sequence 165022,
C 164	13	26.0	572	10	US-10-301-480-1046325	Sequence 1046325,	C 237	13	26.0	609	9	US-10-301-480-165022	Sequence 165022,



C 238	13	26.0	609	10	US-10-301-480-316420	Sequence 316420,	311	13	26.0	869	6	US-09-925-065A-946485	Sequence 946485,
C 239	13	26.0	609	10	US-10-301-480-778430	Sequence 778430,	312	13	26.0	869	6	US-09-925-065A-946486	Sequence 946486,
C 240	13	26.0	609	10	US-10-301-480-778431	Sequence 778431,	C 313	13	26.0	911	8	US-10-667-295-54918	Sequence 54918, A
C 241	13	26.0	609	10	US-10-301-480-929829	Sequence 929829,	314	13	26.0	930	6	US-09-925-065A-65918	Sequence 65918, A
C 242	13	26.0	611	6	US-09-925-065A-311110	Sequence 311110,	315	13	26.0	930	10	US-10-301-480-177157	Sequence 177157,
C 243	13	26.0	612	6	US-09-925-065A-319822	Sequence 319822,	316	13	26.0	930	9	US-10-301-480-177157	Sequence 177157,
C 244	13	26.0	612	6	US-09-925-065A-668370	Sequence 668370,	317	13	26.0	956	6	US-09-925-065A-488448	Sequence 488448, A
C 245	13	26.0	612	6	US-09-925-065A-668371	Sequence 668371,	318	13	26.0	956	6	US-09-925-065A-681045	Sequence 681045,
C 246	13	26.0	612	6	US-09-925-065A-668372	Sequence 668372,	319	13	26.0	956	9	US-10-301-480-150086	Sequence 150086,
C 247	13	26.0	612	9	US-10-301-480-210561	Sequence 210561,	320	13	26.0	956	9	US-10-301-480-150086	Sequence 150086,
C 248	13	26.0	612	10	US-10-301-480-823970	Sequence 823970,	321	13	26.0	965	10	US-10-301-480-763495	Sequence 763495,
C 249	13	26.0	614	9	US-10-301-480-74178	Sequence 74178, A	322	13	26.0	965	10	US-10-301-480-550794	Sequence 550794,
C 250	13	26.0	614	9	US-10-301-480-74179	Sequence 74179, A	323	13	26.0	965	10	US-10-301-480-1160520	Sequence 1160520,
C 251	13	26.0	614	9	US-10-301-480-74180	Sequence 74180, A	324	13	26.0	974	10	US-10-301-480-1173351	Sequence 1173351,
C 252	13	26.0	614	9	US-10-301-480-212464	Sequence 212464,	C 325	13	26.0	985	10	US-10-301-480-547111	Sequence 547111,
C 253	13	26.0	614	10	US-10-301-480-687587	Sequence 687587,	C 326	13	26.0	985	10	US-10-301-480-1160520	Sequence 1160520,
C 254	13	26.0	614	10	US-10-301-480-687588	Sequence 687588,	C 327	13	26.0	999	6	US-09-925-065A-171751	Sequence 171751, A
C 255	13	26.0	614	10	US-10-301-480-687589	Sequence 687589,	C 328	13	26.0	999	9	US-10-301-480-172990	Sequence 172990,
C 256	13	26.0	614	10	US-10-301-480-825873	Sequence 825873,	C 329	13	26.0	999	10	US-10-301-480-554553	Sequence 554553,
C 257	13	26.0	617	6	US-09-925-065A-641799	Sequence 641799,	C 330	13	26.0	999	10	US-10-301-480-554553	Sequence 554553,
C 258	13	26.0	618	6	US-09-925-065A-846868	Sequence 846868,	C 331	13	26.0	999	10	US-10-301-480-786399	Sequence 786399,
C 259	13	26.0	619	6	US-09-925-065A-113275	Sequence 113275,	C 332	13	26.0	999	10	US-10-301-480-1167962	Sequence 1167962,
C 260	13	26.0	619	6	US-09-925-065A-321691	Sequence 321691,	C 333	13	26.0	999	10	US-10-301-480-1202527	Sequence 1202527,
C 261	13	26.0	619	6	US-09-925-065A-909859	Sequence 909859,	C 334	13	26.0	1000	10	US-10-301-480-599527	Sequence 599527,
C 262	13	26.0	621	6	US-09-925-065A-913223	Sequence 913223,	C 335	13	26.0	1000	10	US-10-301-480-1212936	Sequence 1212936,
C 263	13	26.0	622	10	US-10-301-480-396312	Sequence 396312,	C 336	13	26.0	1012	14	US-11-024-959-57	Sequence 57, Appl
C 264	13	26.0	622	10	US-10-301-480-1009721	Sequence 1009721,	C 337	13	26.0	1022	9	US-10-301-480-95037	Sequence 95037, A
C 265	13	26.0	625	6	US-09-925-065A-954138	Sequence 954138,	C 338	13	26.0	1022	10	US-10-301-480-708446	Sequence 708446,
C 266	13	26.0	633	11	US-11-096-568A-31065	Sequence 31065, A	C 339	13	26.0	1031	8	US-10-750-185-27241	Sequence 27241, A
C 267	13	26.0	634	6	US-09-925-065A-542339	Sequence 542339,	C 340	13	26.0	1031	8	US-10-750-185-27241	Sequence 27241, A
C 268	13	26.0	635	6	US-09-925-065A-954134	Sequence 954134,	C 341	13	26.0	1071	9	US-10-933-182A-2822	Sequence 2822, A
C 269	13	26.0	635	6	US-09-925-065A-954135	Sequence 954135,	C 342	13	26.0	1071	9	US-10-933-182A-2822	Sequence 2822, A
C 270	13	26.0	639	6	US-09-925-065A-707918	Sequence 707918,	C 343	13	26.0	1084	14	US-11-024-959-167	Sequence 167, Appl
C 271	13	26.0	639	6	US-09-925-065A-707919	Sequence 707919,	C 344	13	26.0	1108	6	US-09-925-065A-37760	Sequence 37760, A
C 272	13	26.0	639	6	US-09-925-065A-707920	Sequence 707920,	C 345	13	26.0	1108	6	US-10-301-480-138998	Sequence 138998,
C 273	13	26.0	639	6	US-09-925-065A-781238	Sequence 781238,	C 346	13	26.0	1108	10	US-10-301-480-752407	Sequence 752407,
C 274	13	26.0	639	6	US-09-925-065A-842361	Sequence 842361,	C 347	13	26.0	1118	14	US-11-024-959-166	Sequence 166, Appl
C 275	13	26.0	641	6	US-09-925-065A-862824	Sequence 862824,	C 348	13	26.0	1120	6	US-09-925-065A-62371	Sequence 62371, A
C 276	13	26.0	641	6	US-09-925-065A-897750	Sequence 897750,	C 349	13	26.0	1120	6	US-09-925-065A-62371	Sequence 62371, A
C 277	13	26.0	641	10	US-10-301-480-412834	Sequence 412834,	C 350	13	26.0	1120	6	US-09-925-065A-62373	Sequence 62373, A
C 278	13	26.0	641	10	US-10-301-480-1026243	Sequence 1026243,	C 351	13	26.0	1120	6	US-09-925-065A-62373	Sequence 62373, A
C 279	13	26.0	646	6	US-09-925-065A-683822	Sequence 683822,	C 352	13	26.0	1120	9	US-10-301-480-163609	Sequence 163609,
C 280	13	26.0	646	6	US-09-925-065A-683823	Sequence 683823,	C 353	13	26.0	1120	9	US-10-301-480-163610	Sequence 163610,
C 281	13	26.0	648	6	US-09-925-065A-774055	Sequence 774055,	C 354	13	26.0	1120	9	US-10-301-480-163611	Sequence 163611,
C 282	13	26.0	648	6	US-09-925-065A-838261	Sequence 838261,	C 355	13	26.0	1120	9	US-10-301-480-163612	Sequence 163612,
C 283	13	26.0	649	6	US-09-925-065A-905561	Sequence 905561,	C 356	13	26.0	1120	10	US-10-301-480-777018	Sequence 777018,
C 284	13	26.0	650	6	US-09-925-065A-453118	Sequence 453118,	C 357	13	26.0	1120	10	US-10-301-480-777019	Sequence 777019,
C 285	13	26.0	650	6	US-09-925-065A-766411	Sequence 766411,	C 358	13	26.0	1120	10	US-10-301-480-777020	Sequence 777020,
C 286	13	26.0	650	10	US-10-301-480-481429	Sequence 481429,	C 359	13	26.0	1120	10	US-10-301-480-777021	Sequence 777021,
C 287	13	26.0	650	10	US-10-301-480-511883	Sequence 511883,	C 360	13	26.0	1166	14	US-11-024-959-164	Sequence 164, Appl
C 288	13	26.0	650	10	US-10-301-480-1094838	Sequence 1094838,	C 361	13	26.0	1169	8	US-10-750-185-52370	Sequence 52370, A
C 289	13	26.0	650	10	US-10-301-480-1125292	Sequence 1125292,	C 362	13	26.0	1169	8	US-10-750-185-52370	Sequence 52370, A
C 290	13	26.0	656	6	US-09-925-065A-906748	Sequence 906748,	C 363	13	26.0	1194	8	US-10-517-939-209	Sequence 209, Appl
C 291	13	26.0	656	6	US-09-925-065A-415746	Sequence 415746,	C 364	13	26.0	1251	9	US-10-933-182A-5904	Sequence 5904, Appl
C 292	13	26.0	657	6	US-09-925-065A-638388	Sequence 638388,	C 365	13	26.0	1251	9	US-10-933-182A-5904	Sequence 5904, Appl
C 293	13	26.0	657	6	US-09-925-065A-741263	Sequence 741263,	C 366	13	26.0	1262	8	US-10-750-185-61626	Sequence 61626, A
C 294	13	26.0	667	6	US-09-925-065A-837933	Sequence 837933,	C 367	13	26.0	1262	8	US-10-750-185-61626	Sequence 61626, A
C 295	13	26.0	682	6	US-09-925-065A-912630	Sequence 912630,	C 368	13	26.0	1279	6	US-09-925-065A-67663	Sequence 67663, A
C 296	13	26.0	707	8	US-10-750-185-38930	Sequence 38930, A	C 369	13	26.0	1279	6	US-09-925-065A-67663	Sequence 67663, A
C 297	13	26.0	707	8	US-10-750-623-38930	Sequence 38930, A	C 370	13	26.0	1279	9	US-10-301-480-168921	Sequence 168921,
C 298	13	26.0	757	9	US-09-925-065A-68622	Sequence 68622, A	C 371	13	26.0	1279	9	US-10-301-480-168922	Sequence 168922,
C 299	13	26.0	757	9	US-10-301-480-169861	Sequence 169861,	C 372	13	26.0	1279	10	US-10-301-480-782330	Sequence 782330,
C 300	13	26.0	757	10	US-10-301-480-783270	Sequence 783270,	C 373	13	26.0	1279	10	US-10-301-480-782331	Sequence 782331,
C 301	13	26.0	811	8	US-10-667-295-211	Sequence 211, Appl	C 374	13	26.0	1287	14	US-11-024-959-165	Sequence 165, Appl
C 302	13	26.0	820	11	US-11-096-568A-29511	Sequence 29511, A	C 375	13	26.0	1290	6	US-09-925-065A-725691	Sequence 725691,
C 303	13	26.0	842	10	US-10-301-480-555330	Sequence 555330,	C 376	13	26.0	1302	11	US-11-079-463-1827	Sequence 1827, Appl
C 304	13	26.0	842	10	US-10-301-480-1168769	Sequence 1168769,	C 377	13	26.0	1314	11	US-11-079-463-1827	Sequence 1827, Appl
C 305	13	26.0	845	11	US-11-172-740-79	Sequence 79, Appl	C 378	13	26.0	1316	6	US-09-925-065A-725791	Sequence 725791,
C 306	13	26.0	851	10	US-10-301-480-544782	Sequence 544782,	C 379	13	26.0	1320	9	US-10-301-480-37063	Sequence 37063, A
C 307	13	26.0	851	10	US-10-301-480-1158191	Sequence 1158191,	C 380	13	26.0	1320	9	US-10-301-480-37064	Sequence 37064, A
C 308	13	26.0	866	8	US-10-750-185-45245	Sequence 45245, A	C 381	13	26.0	1320	9	US-10-301-480-37065	Sequence 37065, A
C 309	13	26.0	866	8	US-10-750-623-45245	Sequence 45245, A	C 382	13	26.0	1320	9	US-10-301-480-37066	Sequence 37066, A
C 310	13	26.0	869	6	US-09-925-065A-921325	Sequence 921325,	C 383	13	26.0	1320	10	US-10-301-480-650472	Sequence 650472,



384	13	26.0	1320	10	US-10-301-480-650473	Sequence 650473,
385	13	26.0	1320	10	US-10-301-480-650474	Sequence 650474,
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387	13	26.0	1351	14	US-11-136-527-1770	Sequence 1770, Ap
388	13	26.0	1351	14	US-11-136-527-5866	Sequence 5866, A
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390	13	26.0	1417	8	US-10-750-623-39110	Sequence 39110, A
391	13	26.0	1418	14	US-11-193-981-1	Sequence 1, Appl
392	13	26.0	1437	11	US-11-096-568A-31218	Sequence 31218, A
393	13	26.0	1479	11	US-11-096-568A-10978	Sequence 10978, A
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395	13	26.0	1521	8	US-10-750-185-35442	Sequence 35442, A
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397	13	26.0	1587	8	US-10-750-185-47647	Sequence 47647, A
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466	13	26.0	86374	8	US-10-775-165-173	Sequence 173, Ap
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C 823	12	24.0	562	10	US-10-301-480-1137061	Sequence 1137061,	896	12	24.0	577	10	US-10-301-480-483305	Sequence 483305,
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C 858	12	24.0	568	6	US-09-925-065A-310523	Sequence 310523,	C 931	12	24.0	583	6	US-09-925-065A-272491	Sequence 272491,
C 859	12	24.0	568	6	US-09-925-065A-310503	Sequence 310503,	C 932	12	24.0	583	6	US-09-925-065A-404655	Sequence 404655,
C 860	12	24.0	568	6	US-09-925-065A-310505	Sequence 310505,	C 933	12	24.0	583	6	US-09-925-065A-462646	Sequence 462646,
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C 875	12	24.0	572	6	US-09-925-065A-175071	Sequence 175071,	C 948	12	24.0	583	10	US-10-301-480-651311	Sequence 651311,
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C 884	12	24.0	573	10	US-10-301-480-1118384	Sequence 1118384,	C 957	12	24.0	586	6	US-09-925-065A-260680	Sequence 260680,
C 885	12	24.0	575	6	US-09-925-065A-104310	Sequence 304310,	C 958	12	24.0	586	6	US-09-925-065A-413267	Sequence 413267,
C 886	12	24.0	575	6	US-09-925-065A-776008	Sequence 776008,	C 959	12	24.0	586	6	US-09-925-065A-487820	Sequence 487820,
C 887	12	24.0	575	10	US-10-301-480-380396	Sequence 380396,	C 960	12	24.0	586	6	US-09-925-065A-620793	Sequence 620793,
C 888	12	24.0	575	10	US-10-301-480-439943	Sequence 439943,	C 961	12	24.0	586	6	US-09-925-065A-942101	Sequence 942101,
C 889	12	24.0	575	10	US-10-301-480-439944	Sequence 439944,	C 962	12	24.0	586	6	US-09-925-065A-942102	Sequence 942102,
C 890	12	24.0	575	10	US-10-301-480-993805	Sequence 993805,	C 963	12	24.0	586	10	US-10-301-480-408903	Sequence 408903,
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C 892	12	24.0	575	10	US-10-301-480-1053353	Sequence 1053353,	C 965	12	24.0	587	6	US-09-925-065A-444173	Sequence 444173,
C 893	12	24.0	577	6	US-09-925-065A-517363	Sequence 517363,	C 966	12	24.0	587	6	US-09-925-065A-444174	Sequence 444174,
C 894	12	24.0	577	10	US-10-301-480-479297	Sequence 479297,	C 967	12	24.0	587	10	US-10-301-480-471581	Sequence 471581,



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c 968      12      24.0      587      10      US-10-301-480-1084990      Sequence 1084990,
c 969      12      24.0      588      6      US-09-925-065A-343211      Sequence 343211,
c 970      12      24.0      588      6      US-09-925-065A-343212      Sequence 343212,
c 971      12      24.0      588      9      US-10-301-480-55882      Sequence 55882, A
c 972      12      24.0      588      10      US-10-301-480-669291      Sequence 669291,
c 973      12      24.0      589      6      US-09-925-065A-248364      Sequence 248364,
c 974      12      24.0      589      6      US-09-925-065A-731647      Sequence 731647,
c 975      12      24.0      589      9      US-10-301-480-54800      Sequence 54800, A
c 976      12      24.0      589      9      US-10-301-480-203658      Sequence 203658,
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c 978      12      24.0      589      10      US-10-301-480-361995      Sequence 361995,
c 979      12      24.0      589      10      US-10-301-480-668209      Sequence 668209,
c 980      12      24.0      589      10      US-10-301-480-817067      Sequence 817067,
c 981      12      24.0      589      10      US-10-301-480-941772      Sequence 941772,
c 982      12      24.0      589      10      US-10-301-480-975404      Sequence 975404,
c 983      12      24.0      590      6      US-09-925-065A-459978      Sequence 459978,
c 984      12      24.0      590      6      US-09-925-065A-459979      Sequence 459979,
c 985      12      24.0      591      6      US-09-925-065A-158588      Sequence 158588,
c 986      12      24.0      591      8      US-10-467-657-4651      Sequence 4651, Ap
c 987      12      24.0      591      10      US-10-301-480-230088      Sequence 230088,
c 988      12      24.0      591      10      US-10-301-480-315527      Sequence 315527,
c 989      12      24.0      591      10      US-10-301-480-843497      Sequence 843497,
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c 992      12      24.0      592      6      US-09-925-065A-391106      Sequence 391106,
c 993      12      24.0      592      10      US-10-301-480-580471      Sequence 580471,
c 994      12      24.0      592      10      US-10-301-480-1193880      Sequence 1193880,
c 995      12      24.0      593      6      US-09-925-065A-284994      Sequence 284994,
c 996      12      24.0      593      6      US-09-925-065A-682291      Sequence 682291,
c 997      12      24.0      593      6      US-09-925-065A-682292      Sequence 682292,
c 998      12      24.0      593      9      US-10-301-480-92007      Sequence 92007, A
c 999      12      24.0      593      10      US-10-301-480-705416      Sequence 705416,
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## ALIGNMENTS

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RESULT 1
US-11-055-557-11
; Sequence 11, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; OTHER INFORMATION: wild-type homo-oligomeric anthrax toxin protective
; OTHER INFORMATION: antigen (PrAg)
US-11-055-557-11

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Query Match      100.0%; Score 50; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 5,1e-21;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      1195 GGGAGCGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTTAGG 1244

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RESULT 2
US-11-055-557-15
; Sequence 15, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-R200A
US-11-055-557-15

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Query Match      100.0%; Score 50; DB 14; Length 2295;
Best Local Similarity 100.0%; Pred. No. 5,1e-21;
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||
Db      1195 GGGAGCGCTCCATCTACACGCTGTACCAAGCACTTCGTTAGTTAGG 1244
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RESULT 3
US-11-055-557-19
; Sequence 19, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 19
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-I210A
US-11-055-557-19

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Query Match      100.0%; Score 50; DB 14; Length 2295;

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Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 50

Db 1195 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 1244

#### RESULT 4

US-11-055-557-1  
; Sequence 1, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:

; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui

; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics

; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557

; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 2304

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified

; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (PrAg) PrAg-U2-R200A

US-11-055-557-1

Query Match 100.0%; Score 50; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 50

Db 1204 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 1253

#### RESULT 5

US-11-055-557-9  
; Sequence 9, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:

; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui

; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics

; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557

; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 9

; LENGTH: 2304

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified

; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (PrAg) PrAg-U2-K197A (PrA-U-K197A)  
US-11-055-557-9

Query Match 100.0%; Score 50; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 50

Db 1204 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 1253

#### RESULT 6

US-11-055-557-13  
; Sequence 13, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:

; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui

; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics

; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557

; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 13

; LENGTH: 2304

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified

; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (PrAg) PrAg-U2

US-11-055-557-13

Query Match 100.0%; Score 50; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 50

Db 1204 GGGACGGCTCCCAATCTACACAGCTGTACCAAGCACTTCGTAGTTAGG 1253

#### RESULT 7

US-11-055-557-3  
; Sequence 3, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:

; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui

; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America

; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services

; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics

; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557

; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417

; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 3



LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-11-1210A (PA-M-1210A)  
US-11-055-557-3

Query Match 100.0%; Score 50; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50  
DB 1207 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 1256

RESULT 8  
US-11-055-557-5  
Sequence 5, Application US/11055557  
Publication No. US2005025083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT FILING DATE: 2005-02-09  
PRIORITY FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 5  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-11-K214A (PA-M-K214A)  
US-11-055-557-5

Query Match 100.0%; Score 50; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50  
DB 1207 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 1256

RESULT 9  
US-11-055-557-7  
Sequence 7, Application US/11055557  
Publication No. US2005025083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT FILING DATE: 2005-02-09

PRIOR APPLICATION NUMBER: US 60/543,417  
PRIOR FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 7  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-11-R178A (PA-M-R178A)  
US-11-055-557-7

Query Match 100.0%; Score 50; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50  
DB 1207 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 1256

RESULT 10  
US-11-055-557-17  
Sequence 17, Application US/11055557  
Publication No. US2005025083A1  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Liu, Shi-Hui  
APPLICANT: Bugge, Thomas H.  
APPLICANT: The Government of the United States of America  
APPLICANT: as represented by The Secretary of the  
APPLICANT: Department of Health and Human Services  
TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
FILE REFERENCE: 015280-501100US  
CURRENT FILING DATE: 2005-02-09  
PRIORITY FILING DATE: 2004-02-09  
NUMBER OF SEQ ID NOS: 42  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 2307  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:modified  
OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
OTHER INFORMATION: (PrAg) PrAg-11  
US-11-055-557-17

Query Match 100.0%; Score 50; DB 14; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 5.1e-21;  
Matches 50; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 50  
DB 1207 GGAGCGGCTCCAAATCTACACGTTTACCAACGACTTCGTTAGTTAGG 1256

RESULT 11  
US-09-925-065A-472627  
Sequence 472627, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT FILING DATE: 2001-08-08



;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 472627  
;; LENGTH: 547  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-472627

Query Match 36.0%; Score 18; DB 6; Length 547;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AATCTACACGCTTACC 29  
Db 300 AATCTACACGCTTACC 317

RESULT 12  
US-09-925-065A-472628  
;; Sequence 472628, Application US/09925065A  
;; Publication No. US20040181048A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single  
;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925,065A  
;; CURRENT FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 472628  
;; LENGTH: 547  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-472628

Query Match 36.0%; Score 18; DB 6; Length 547;  
Best Local Similarity 100.0%; Pred. No. 0.33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 AATCTACACGCTTACC 29  
Db 300 AATCTACACGCTTACC 317

RESULT 13  
US-09-925-065A-242591  
;; Sequence 242591, Application US/09925065A  
;; Publication No. US20040181048A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single  
;; Nucleotide Polymorphisms in the Human Genome

;; FILE REFERENCE: 108827.135  
;; CURRENT APPLICATION NUMBER: US/09/925,065A  
;; CURRENT FILING DATE: 2001-08-08  
;; PRIOR APPLICATION NUMBER: US 60/243,096  
;; PRIOR FILING DATE: 2000-10-24  
;; PRIOR APPLICATION NUMBER: US 60/252,147  
;; PRIOR FILING DATE: 2000-11-20  
;; PRIOR APPLICATION NUMBER: US 60/250,092  
;; PRIOR FILING DATE: 2000-11-30  
;; PRIOR APPLICATION NUMBER: US 60/261,766  
;; PRIOR FILING DATE: 2001-01-16  
;; PRIOR APPLICATION NUMBER: US 60/289,846  
;; PRIOR FILING DATE: 2001-05-09  
;; NUMBER OF SEQ ID NOS: 957086  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 242591  
;; LENGTH: 554  
;; TYPE: DNA  
;; ORGANISM: Homo sapiens  
US-09-925-065A-242591

Query Match 32.0%; Score 16; DB 6; Length 554;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGTTCACACGACTTC 38  
Db 536 TGTTCACACGACTTC 551

RESULT 14  
US-10-301-480-202732/c  
;; Sequence 202732, Application US/10301480  
;; Publication No. US20060057564A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
;; FILE REFERENCE: 108827.137  
;; CURRENT APPLICATION NUMBER: US/10/301,480  
;; CURRENT FILING DATE: 2002-11-21  
;; PRIOR APPLICATION NUMBER: US 10/215,598  
;; PRIOR FILING DATE: 2002-08-09  
;; PRIOR APPLICATION NUMBER: US 60/311,695  
;; PRIOR FILING DATE: 2001-08-10  
;; NUMBER OF SEQ ID NOS: 1226818  
;; SOFTWARE: FastSeq for Windows Version 4.0  
;; SEQ ID NO 202732  
;; LENGTH: 556  
;; TYPE: DNA  
;; ORGANISM: Homo sapien  
US-10-301-480-202732

Query Match 32.0%; Score 16; DB 9; Length 556;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGTTCACACGACTTC 38  
Db 21 TGTTCACACGACTTC 6

RESULT 15  
US-10-301-480-816141/c  
;; Sequence 816141, Application US/10301480  
;; Publication No. US20060057564A1  
;; GENERAL INFORMATION:  
;; APPLICANT: Wang, David G.  
;; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
;; FILE REFERENCE: 108827.137  
;; CURRENT APPLICATION NUMBER: US/10/301,480  
;; CURRENT FILING DATE: 2002-11-21



```
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 816141
; LENGTH: 556
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-816141
```

```
Query Match          32.0%; Score 16; DB 10; Length 556;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 TGTACCAACGACTTC 38
      |||||
Db      21 TGTACCAACGACTTC 6
```

```
RESULT 16
US-10-301-480-323616
; Sequence 323616, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 323616
; LENGTH: 560
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-323616
```

```
Query Match          32.0%; Score 16; DB 10; Length 560;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 TGTACCAACGACTTC 38
      |||||
Db      533 TGTACCAACGACTTC 548
```

```
RESULT 17
US-09-925-065A-102353/c
; Sequence 102353, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
```

```
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 102353
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-102353
```

```
Query Match          32.0%; Score 16; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 TGTACCAACGACTTC 38
      |||||
Db      28 TGTACCAACGACTTC 13
```

```
RESULT 18
US-10-301-480-937025
; Sequence 937025, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 937025
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-937025
```

```
Query Match          32.0%; Score 16; DB 10; Length 563;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      23 TGTACCAACGACTTC 38
      |||||
Db      536 TGTACCAACGACTTC 551
```

```
RESULT 19
US-09-925-065A-611993
; Sequence 611993, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```



```
; SEQ ID NO 611993
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-611993
```

```
Query Match          32.0%; Score 16; DB 6; Length 577;
Best Local Similarity 100.0%; Pred. No. 5-7;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      4 ACGGCTCCATCTACA 19
         |||||
Db      356 ACGGCTCCATCTACA 371
```

```
RESULT 20
US-11-101-244-235510/c
; Sequence 235510, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 235510
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-235510
```

```
Query Match          30.0%; Score 15; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGACGGCTCCATC 15
         |||||
Db      15 GGGACGGCTCCATC 1
```

```
RESULT 21
US-11-101-244-235580/c
; Sequence 235580, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 235580
```

```
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-235580
```

```
Query Match          30.0%; Score 15; DB 12; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGACGGCTCCATC 15
         |||||
Db      16 GGGACGGCTCCATC 2
```

```
RESULT 22
US-11-083-784-235510/c
; Sequence 235510, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 235510
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-235510
```

```
Query Match          30.0%; Score 15; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      1 GGGACGGCTCCATC 15
         |||||
Db      15 GGGACGGCTCCATC 1
```

```
RESULT 23
US-11-083-784-235580/c
; Sequence 235580, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
```



```
/ NUMBER OF SEQ ID NOS: 1591911
/ SOFTWARE: Proprietary
/ SEQ ID NO 235580
/ LENGTH: 19
/ TYPE: RNA
/ ORGANISM: Homo sapiens
US-11-083-784-235580
```

```
Query Match      30.0%; Score 15; DB 13; Length 19;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCCAATC 15
DB      16 GGGACGGCTCCCAATC 2
```

```
RESULT 24
US-10-301-480-571745/c
/ Sequence 571745, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 571745
/ LENGTH: 983
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-571745
```

```
Query Match      30.0%; Score 15; DB 10; Length 983;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCCAATC 15
DB      666 GGGACGGCTCCCAATC 652
```

```
RESULT 25
US-10-301-480-571747/c
/ Sequence 571747, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 571747
/ LENGTH: 983
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-571747
```

```
Query Match      30.0%; Score 15; DB 10; Length 983;
```

```
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCCAATC 15
DB      666 GGGACGGCTCCCAATC 652
```

```
RESULT 26
US-10-301-480-1185154/c
/ Sequence 1185154, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1185154
/ LENGTH: 983
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-1185154
```

```
Query Match      30.0%; Score 15; DB 10; Length 983;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCCAATC 15
DB      666 GGGACGGCTCCCAATC 652
```

```
RESULT 27
US-10-301-480-1185156/c
/ Sequence 1185156, Application US/10301480
/ Publication No. US20060057564A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, David G.
/ TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
/ FILE REFERENCE: 108827.137
/ CURRENT APPLICATION NUMBER: US/10/301,480
/ PRIOR FILING DATE: 2002-11-21
/ PRIOR APPLICATION NUMBER: US 10/215,598
/ PRIOR FILING DATE: 2002-08-09
/ PRIOR APPLICATION NUMBER: US 60/311,695
/ PRIOR FILING DATE: 2001-08-10
/ NUMBER OF SEQ ID NOS: 1226818
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1185156
/ LENGTH: 983
/ TYPE: DNA
/ ORGANISM: Homo sapien
US-10-301-480-1185156
```

```
Query Match      30.0%; Score 15; DB 10; Length 983;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 GGGACGGCTCCCAATC 15
DB      666 GGGACGGCTCCCAATC 652
```

```
RESULT 28
```



```
US-10-301-480-571746/c
; Sequence 571746, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571746
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-571746

Query Match          30.0%; Score 15; DB 10; Length 984;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAATC 15
Db 661 GGGACGGCTCCAATC 647

RESULT 29
US-10-301-480-571748/c
; Sequence 571748, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 571748
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-571748

Query Match          30.0%; Score 15; DB 10; Length 984;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAATC 15
Db 661 GGGACGGCTCCAATC 647

RESULT 30
US-10-301-480-1185155/c
; Sequence 1185155, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
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; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185155
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1185155

Query Match          30.0%; Score 15; DB 10; Length 984;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAATC 15
Db 661 GGGACGGCTCCAATC 647

RESULT 31
US-10-301-480-1185157/c
; Sequence 1185157, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1185157
; LENGTH: 984
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1185157

Query Match          30.0%; Score 15; DB 10; Length 984;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGACGGCTCCAATC 15
Db 661 GGGACGGCTCCAATC 647

RESULT 32
US-10-932-182A-82659
; Sequence 82659, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHIISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 82659
; LENGTH: 1809
; TYPE: DNA
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ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-82659

Query Match 30.0%; Score 15; DB 9; Length 1809;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ACAACGTGTACCA 31  
DB 1071 ACAACGTGTACCA 1085

RESULT 33  
US-10-932-182A-82659  
Sequence 82659, Application US/10932182A  
Publication No. US20060046253A1

GENERAL INFORMATION:  
APPLICANT: NAKAO, YOSHIHIRO  
APPLICANT: NAKAMURA, NORIHISA  
APPLICANT: KODAMA, YUKIKO  
APPLICANT: FUJIMURA, TOMOKO  
APPLICANT: ASHIKARI, TOSHIHIRO  
TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS  
FILE REFERENCE: 030685-043  
CURRENT APPLICATION NUMBER: US/10/932,182A  
CURRENT FILING DATE: 2004-09-02  
NUMBER OF SEQ ID NOS: 197023  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 82659  
LENGTH: 1809  
TYPE: DNA  
ORGANISM: Saccharomyces pastorianus  
US-10-932-182A-82659

Query Match 30.0%; Score 15; DB 9; Length 1809;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 ACAACGTGTACCA 31  
DB 1071 ACAACGTGTACCA 1085

RESULT 34

US-09-925-065A-410737/C  
Sequence 410737, Application US/09925065A  
Publication No. US20040181048A1

GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 410737  
LENGTH: 492  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-410737

Query Match 28.0%; Score 14; DB 6; Length 492;

Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 CAACGTGTACCA 31  
DB 465 CAACGTGTACCA 452

RESULT 35  
US-09-925-065A-789154  
Sequence 789154, Application US/09925065A  
Publication No. US20040181048A1

GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 789154  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-789154

Query Match 28.0%; Score 14; DB 6; Length 502;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCAATCTACCA 20  
DB 112 GCTCAATCTACCA 125

RESULT 36  
US-09-925-065A-789155  
Sequence 789155, Application US/09925065A  
Publication No. US20040181048A1

GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 789155  
LENGTH: 502  
TYPE: DNA  
ORGANISM: Homo sapiens

Query Match 28.0%; Score 14; DB 6; Length 502;



US-09-925-065A-789155

Query Match 28.0%; Score 14; DB 6; Length 502;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GCTCCATCTACAA 20  
Db 112 GCTCCATCTACAA 125

RESULT 37

US-10-301-480-477027/c  
; Sequence 477027, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 477027  
; LENGTH: 511  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-477027

Query Match 28.0%; Score 14; DB 10; Length 511;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CAACGTGTACCA 31  
Db 465 CAACGTGTACCA 452

RESULT 38

US-10-301-480-1090436/c  
; Sequence 1090436, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1090436  
; LENGTH: 511  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1090436

Query Match 28.0%; Score 14; DB 10; Length 511;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 CAACGTGTACCA 31  
Db 465 CAACGTGTACCA 452

RESULT 39

US-10-301-480-543620/c  
; Sequence 543620, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 543620  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-543620

Query Match 28.0%; Score 14; DB 10; Length 513;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 TCGTTAGTGTAGG 50  
Db 217 TCGTTAGTGTAGG 204

RESULT 40

US-10-301-480-1157029/c  
; Sequence 1157029, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1157029  
; LENGTH: 513  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1157029

Query Match 28.0%; Score 14; DB 10; Length 513;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 37 TCGTTAGTGTAGG 50  
Db 217 TCGTTAGTGTAGG 204

Search completed: April 12, 2006, 07:07:01  
Job time : 211.206 secs



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GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 688.433 Seconds  
(without alignments)  
3398.084 Million cell updates/sec

Title: US-10-712-654-23

Perfect score: 50

Sequence: 1 gggagcgctccatctacaa.....acgacttcgtagtgtagg 50

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339354128 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

BST: \*  
1: gb\_eat1: \*  
2: gb\_eat2: \*  
3: gb\_eat3: \*  
4: gb\_hic: \*  
5: gb\_eat4: \*  
6: gb\_eat5: \*  
7: gb\_eat6: \*  
8: gb\_eat7: \*  
9: gb\_g881: \*  
10: gb\_g882: \*  
11: gb\_g883: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	19	38.0	412	9	B97774
2	18	36.0	2319	10	CL944845
3	17	34.0	245	1	AV282492
4	17	34.0	298	2	BF043113
5	17	34.0	426	1	AV590963
6	17	34.0	459	2	BG689655
7	17	34.0	593	7	CJ395784
8	17	34.0	630	1	AM289342
9	17	34.0	781	7	CK773609
10	17	34.0	787	7	CK776895
11	17	34.0	1133	10	CG749587
12	16	32.0	187	3	BP719333
13	16	32.0	318	2	BG234864
14	16	32.0	330	2	BB559488
15	16	32.0	356	2	BI214804
16	16	32.0	387	5	BM165338
17	16	32.0	387	5	BY403337
18	16	32.0	446	6	CB398775
19	16	32.0	460	10	CG993295
20	16	32.0	463	2	BI229863
21	16	32.0	498	11	DR13P12T
22	16	32.0	500	7	CK545847

23	16	32.0	507	9	CE123069
24	16	32.0	509	9	AZ156816
25	16	32.0	533	8	CX856756
26	16	32.0	540	1	AI294195
27	16	32.0	550	1	AV677273
28	16	32.0	552	6	CA697847
29	16	32.0	577	5	BU803375
30	16	32.0	585	6	CB402237
31	16	32.0	585	6	CB402242
32	16	32.0	586	7	CK103491
33	16	32.0	588	7	CK533266
34	16	32.0	597	5	AZ151143
35	16	32.0	598	5	BM398361
36	16	32.0	613	2	BI240948
37	16	32.0	628	6	CE645307
38	16	32.0	629	3	CC157381
39	16	32.0	645	5	BM012882
40	16	32.0	647	5	BM344262
41	16	32.0	672	10	CM404423
42	16	32.0	674	1	AI958973
43	16	32.0	678	10	CE794797
44	16	32.0	680	3	BI371999
45	16	32.0	707	10	CM386620
46	16	32.0	722	9	BZ466461
47	16	32.0	733	5	BM076434
48	16	32.0	734	10	CM351789
49	16	32.0	742	5	BM420879
50	16	32.0	742	10	CL418608
51	16	32.0	743	5	BM152379
52	16	32.0	748	5	BM494671
53	16	32.0	748	10	CM351788
54	16	32.0	749	5	BM098639
55	16	32.0	757	4	AY813598
56	16	32.0	762	5	BM424927
57	16	32.0	766	5	BM379671
58	16	32.0	781	9	CC745366
59	16	32.0	803	9	CC900445
60	16	32.0	822	10	CL253437
61	16	32.0	831	10	CG288904
62	16	32.0	848	10	CG037535
63	16	32.0	869	10	CG226158
64	16	32.0	869	9	CC617016
65	16	32.0	889	9	BZ817915
66	16	32.0	893	10	CG021222
67	16	32.0	903	10	CG882963
68	16	32.0	915	10	CL509696
69	16	32.0	935	10	CG037533
70	16	32.0	942	7	CK404486
71	16	32.0	1025	11	CNS0695D
72	16	32.0	1498	9	AQ900942
73	16	32.0	2774	4	AK087904
74	16	32.0	78	1	AJ966563
75	15	30.0	125	1	AA158947
76	15	30.0	127	5	BM251930
77	15	30.0	236	5	BM796356
78	15	30.0	238	1	AV313614
79	15	30.0	279	7	CO854605
80	15	30.0	292	8	Z21025
81	15	30.0	297	9	AQ551622
82	15	30.0	300	2	BE776864
83	15	30.0	312	10	CM186106
84	15	30.0	319	10	CNS009TV
85	15	30.0	350	5	BM812290
86	15	30.0	350	10	CM124478
87	15	30.0	368	8	CX727501
88	15	30.0	370	3	BP623098
89	15	30.0	373	9	BM478067
90	15	30.0	395	5	BM811241
91	15	30.0	395	5	BM632660
92	15	30.0	409	3	AQ042421
93	15	30.0	411	7	CO849264
94	15	30.0	414	3	BP668588
95	15	30.0			



96	15	30.0	435	1	AV809338	AV809338	AV809338	169	15	30.0	734	10	CZ208036	CZ208036	ALNA-ae3
97	15	30.0	435	7	CO819736	CO819736	LM GB5_00	170	15	30.0	736	9	BH12847	BH12847	RPCI-24-3
98	15	30.0	471	9	AZ143442	AZ143442	SP_001E_A	171	15	30.0	738	10	AG42866	AG42866	Mus muscu
99	15	30.0	487	6	CF588446	CF588446	3E8 Albetr	172	15	30.0	742	10	AG139740	AG139740	Par trogl
100	15	30.0	490	11	TA122F04Q	TA122F04Q	bruce1	173	15	30.0	744	6	CG349357	CG349357	CAB25G00
101	15	30.0	500	5	BM808355	BM808355	BM808355	174	15	30.0	744	10	AG441123	AG441123	Mus muscu
102	15	30.0	503	1	AU273994	AU273994	AU273994	175	15	30.0	745	10	CL544207	CL544207	SP_1012_A
103	15	30.0	505	2	BF434950	BF434950	7075G03_x	176	15	30.0	748	9	AZ188440	AZ188440	SP_1012_A
104	15	30.0	507	1	AU272894	AU272894	AU272894	177	15	30.0	749	8	DT066870	DT066870	AGENCOURT
105	15	30.0	507	6	CF588482	CF588482	4C3 Albetr	178	15	30.0	750	10	CG917745	CG917745	ZMMBB038
106	15	30.0	509	10	CM212465	CM212465	104_643_1	179	15	30.0	751	10	CM086143	CM086143	104_429_1
107	15	30.0	511	10	CM212464	CM212464	104_643_1	180	15	30.0	751	10	CM017931	CM017931	ZMMBC001
108	15	30.0	512	7	CK591069	CK591069	estc_1_van	181	15	30.0	755	7	CO137200	CO137200	EST31871
109	15	30.0	522	9	AZ072213	AZ072213	RPCI-23-3	182	15	30.0	778	10	CZ328300	CZ328300	HS_3106_B
110	15	30.0	530	5	BM809405	BM809405	BM809405	183	15	30.0	781	9	AG782032	AG782032	HS_3106_B
111	15	30.0	530	10	CL580773	CL580773	OB_Ba004	184	15	30.0	782	2	BR665357	BR665357	HS_5440_A
112	15	30.0	531	7	CO849263	CO849263	LM_SH5_00	185	15	30.0	785	2	BR665357	BR665357	HS_5440_A
113	15	30.0	544	2	BM745001	BM745001	BM745001	186	15	30.0	788	10	DU031926	DU031926	13313_Tom
114	15	30.0	546	1	BI175565	BI175565	OSTR048H4	187	15	30.0	789	9	BZ806512	BZ806512	PURP52TD
115	15	30.0	546	1	AI862429	AI862429	td16d01_x	188	15	30.0	789	9	CC834051	CC834051	ZMMBB018
116	15	30.0	549	10	CG678161	CG678161	ZMMBB028	189	15	30.0	791	10	CL817157	CL817157	OR_CBA003
117	15	30.0	551	10	CZ266571	CZ266571	be804_CH2	190	15	30.0	799	10	AG444407	AG444407	Mus muscu
118	15	30.0	552	11	TA183H07Q	TA183H07Q	T_bruce1	191	15	30.0	800	10	CM516121	CM516121	OP_Ba001
119	15	30.0	553	3	BM545101	BM545101	BM545101	192	15	30.0	806	10	CG024215	CG024215	OP_Ba001
120	15	30.0	560	6	CF588458	CF588458	3F12 Albtr	193	15	30.0	808	10	CG059490	CG059490	ZMMBB056
121	15	30.0	561	10	CM306600	CM306600	104_792_1	194	15	30.0	808	10	CG278881	CG278881	PUBBG48TD
122	15	30.0	568	9	B95925	B95925	F23B8TF_1GF	195	15	30.0	810	10	CM385559	CM385559	OGXAM94TH
123	15	30.0	569	7	CO849265	CO849265	LM_SH5_00	196	15	30.0	821	9	BH112892	BH112892	RPCI-24-3
124	15	30.0	570	10	CZ266564	CZ266564	be804_CH2	197	15	30.0	822	9	BH721027	BH721027	RPCI-24-3
125	15	30.0	572	3	BM402801	BM402801	SLA008D03	198	15	30.0	825	9	CC824511	CC824511	OR_CBA003
126	15	30.0	578	5	BY424578	BY424578	BY424578	199	15	30.0	825	10	CG277040	CG277040	Mus muscu
127	15	30.0	589	10	CM174047	CM174047	104_586_1	200	15	30.0	828	2	BG705181	BG705181	OG2CL43TV
128	15	30.0	590	9	AQ944233	AQ944233	Sheated_D	201	15	30.0	832	7	CG637641	CG637641	602688104
129	15	30.0	595	10	CI580463	CI580463	OB_Ba004	202	15	30.0	836	8	DR407878	DR407878	mn33601_
130	15	30.0	601	9	AQ330475	AQ330475	nbx0047C	203	15	30.0	840	9	BZ437548	BZ437548	BORNY18TR
131	15	30.0	602	7	CO849261	CO849261	LM_SH5_00	204	15	30.0	846	10	AG552609	AG552609	Mus muscu
132	15	30.0	602	9	BH788022	BH788022	fm02020E0	205	15	30.0	847	10	DU029634	DU029634	10682_Tom
133	15	30.0	602	10	CL333401	CL333401	RPCI44_24	206	15	30.0	850	9	AQ289633	AQ289633	nbx0019K
134	15	30.0	607	5	BM708364	BM708364	BM708364	207	15	30.0	852	9	B12856	B12856	TA
135	15	30.0	614	9	BH616642	BH616642	BMBAC309B	208	15	30.0	859	10	AG895501	AG895501	Oryza sat
136	15	30.0	614	9	BZ387754	BZ387754	EINBGLTF	209	15	30.0	862	10	CG297245	CG297245	Oryza sat
137	15	30.0	622	9	BZ103964	BZ103964	CH230-238	210	15	30.0	875	10	CG297261	CG297261	OG3AB59TV
138	15	30.0	623	11	DR1A13T	DR1A13T	Danilo_rer	211	15	30.0	877	10	CZ702372	CZ702372	OG3AB59TV
139	15	30.0	626	10	CG739562	CG739562	ZMMBB019	212	15	30.0	884	2	BF790351	BF790351	602249587
140	15	30.0	627	10	CM208568	CM208568	104_638_1	213	15	30.0	885	10	CL392287	CL392287	ZMMBB028
141	15	30.0	630	7	CO849262	CO849262	LM_SH5_00	214	15	30.0	891	10	CG875203	CG875203	end of
142	15	30.0	630	9	AZ036539	AZ036539	RPCI-23-2	215	15	30.0	895	11	CNS06RX1	CNS06RX1	end of
143	15	30.0	631	10	CZ825124	CZ825124	OC_Ba020	216	15	30.0	896	10	CNS00D2U	CNS00D2U	end of
144	15	30.0	631	10	CL777322	CL777322	OR_BBa009	217	15	30.0	912	10	CG310388	CG310388	DIOGPH11
145	15	30.0	634	10	CM686974	CM686974	OG_BBa004	218	15	30.0	912	10	CL474526	CL474526	OGXGH43TH
146	15	30.0	643	10	CZ413651	CZ413651	1009354_R	219	15	30.0	913	10	CG277032	CG277032	SAIL_220
147	15	30.0	645	10	CM216719	CM216719	104_649_1	220	15	30.0	915	7	CV281009	CV281009	OG2CL43TH
148	15	30.0	650	10	CM132101	CM132101	104_515_1	221	15	30.0	918	10	CG822514	CG822514	MS0138_B2
149	15	30.0	653	10	CM2578189	CM2578189	OA_BBa018	222	15	30.0	929	2	BF538331	BF538331	SOYAD25TH
150	15	30.0	654	11	CR349699	CR349699	mtel-8412	223	15	30.0	930	10	DU006518	DU006518	602053820
151	15	30.0	657	9	AZ570859	AZ570859	279PvB10	224	15	30.0	937	10	CG454366	CG454366	PURP061TD
152	15	30.0	668	5	BM704693	BM704693	BM704693	225	15	30.0	942	10	CG310400	CG310400	OGXGH43TV
153	15	30.0	678	10	CM431967	CM431967	f8db001f1	226	15	30.0	952	10	CG455800	CG455800	PURP062TB
154	15	30.0	679	10	CM618737	CM618737	OA_ABa016	227	15	30.0	964	10	CG905580	CG905580	ZMMBB051
155	15	30.0	683	10	CZ420104	CZ420104	1015807_R	228	15	30.0	983	10	CG360136	CG360136	OG3CG27TV
156	15	30.0	688	9	AZ569353	AZ569353	259PvE07	229	15	30.0	985	10	CG886332	CG886332	OG3CG27TV
157	15	30.0	690	2	BE392807	BE392807	601307909	230	15	30.0	989	10	CG875232	CG875232	ZMMBB050
158	15	30.0	691	5	BK320352	BK320352	BK320352	231	15	30.0	991	9	CG82705	CG82705	ZMMBB028
159	15	30.0	693	5	BK320353	BK320353	BK320353	232	15	30.0	998	4	AK017920	AK017920	Mus muscu
160	15	30.0	698	10	CM252265	CM252265	104_715_1	233	15	30.0	1002	10	CG909318	CG909318	ZMMBB052
161	15	30.0	711	9	BH978805	BH978805	ode71c10_	234	15	30.0	1004	10	CL012146	CL012146	ZMMBB053
162	15	30.0	712	9	BH435378	BH435378	BOGIC07TR	235	15	30.0	1007	10	CL255599	CL255599	ZMMBB060
163	15	30.0	716	5	BM748436	BM748436	BM748436	236	15	30.0	1008	10	CNS00HXXF	CNS00HXXF	DIOGPH11
164	15	30.0	718	10	CL764170	CL764170	OR_BBa013	237	15	30.0	1019	2	BF693151	BF693151	602080187
165	15	30.0	719	10	CZ037214	CZ037214	OM_Ba001	238	15	30.0	1024	10	CL052941	CL052941	CH216-76M
166	15	30.0	720	10	CZ121865	CZ121865	OA_BBa000	239	15	30.0	1024	10	CL052941	CL052941	CH216-76M
167	15	30.0	730	10	CZ670926	CZ670926	OM_Ba022	240	15	30.0	1061	8	DNS63616	DNS63616	92224204
168	15	30.0	734	6	CA186922	CA186922	SCUTST308	241	15	30.0	1070	11	CNS078P0	CNS078P0	end of



242	15	30.0	1093	8	DN706053	DN706053	CLJ63-C11	c 315	14	28.0	296	9	A0967773	A0967773	LBRU90TR
243	15	30.0	1099	3	BM415247	BM415247	OP20319 M	c 316	14	28.0	299	1	B1646414	B1646414	
C 244	15	30.0	1101	10	CNS002ZH	AL064269	Drosophila	c 317	14	28.0	300	1	A1936497	A1936497	w28EF05.x
C 245	15	30.0	1201	10	CNS001KK	AL061123	Drosophila	c 318	14	28.0	302	1	AA855421	AA855421	NHTBCae05
C 246	15	30.0	1236	10	CG750597	CG750597	P045-1-F0	c 319	14	28.0	306	2	B1209092	B1209092	EST527132
C 247	15	30.0	1284	2	BG863987	BG863987	602797247	c 320	14	28.0	307	7	CN249284	CN249284	EST015199
C 248	15	30.0	1295	8	DN690876	DN690876	CGX73-A11	c 321	14	28.0	309	6	CF490122	CF490122	MAL1-0009P
C 249	15	30.0	1345	8	DN628674	DN628674	CFW100-E0	c 322	14	28.0	317	2	BB206490	BB206490	BB206490
C 250	15	30.0	1347	10	AG287366	AG287366	Mus muscu	c 323	14	28.0	318	7	CN814174	CN814174	FG06_07g1
C 251	15	30.0	1355	8	DN728378	DN728378	CN841-D01	c 324	14	28.0	319	2	BB338559	BB338559	BB338559
C 252	15	30.0	1358	3	B1835865	B1835865	603087874	c 325	14	28.0	322	7	CK900627	CK900627	FT_2_A08
C 253	15	30.0	1368	5	BU398751	BU398751	603536154	c 326	14	28.0	323	9	CC813675	CC813675	ZMMBBC051
C 254	15	30.0	1375	8	DN706063	DN706063	CLJ63-D04	c 327	14	28.0	328	7	CO320802	CO320802	EX288303.
C 255	15	30.0	1406	2	BG774857	BG774857	602649953	c 328	14	28.0	332	6	CP658566	CP658566	tac55c01.
C 256	14	28.0	51	3	BP128995	BP128995	BP128995	c 329	14	28.0	338	2	BG693478	BG693478	BA
C 257	14	28.0	98	10	AL948871	AL948871	Arabidops	c 330	14	28.0	341	1	AA756767	AA756767	vve5d10.T
C 258	14	28.0	128	10	AJ587766	AJ587766	Arabidops	c 331	14	28.0	343	6	CD184590	CD184590	MS1-0048P
C 259	14	28.0	138	10	AL948872	AL948872	Arabidops	c 332	14	28.0	349	1	AA509134	AA509134	MBAPCX7F1
C 260	14	28.0	149	10	AL765901	AL765901	Arabidops	c 333	14	28.0	353	9	CC066936	CC066936	CSU-K33x.
C 261	14	28.0	156	6	CA918836	CA918836	EST636554	c 334	14	28.0	354	8	CX184607	CX184607	E09_45-23
C 262	14	28.0	157	7	CO294448	CO294448	EK206951.	c 335	14	28.0	355	10	CM793992	CM793992	W18GBLox
C 263	14	28.0	170	10	AL951730	AL951730	Arabidops	c 336	14	28.0	355	11	CR298793	CR298793	meE1-16B1
C 264	14	28.0	172	8	R86614	R86614	RABEST38T	c 337	14	28.0	359	6	CF527767	CF527767	UI-1-BC0-
C 265	14	28.0	177	7	CV311486	CV311486	CM0-HT129	c 338	14	28.0	359	9	B99195	B99195	CIT-HSP-228
C 266	14	28.0	188	9	AZ845817	AZ845817	2M0145113	c 339	14	28.0	360	1	AJ465586	AJ465586	
C 267	14	28.0	197	11	CNS07FT0	AL608490	Anopheles	c 340	14	28.0	360	5	CG4713	CG4713	
C 268	14	28.0	214	6	CB817570	CB817570	d3m1Opz.F	c 341	14	28.0	360	8	D35983	D35983	CE7312 Yuji
C 269	14	28.0	220	3	BM897430	BM897430	p4h1c08.Y	c 342	14	28.0	360	5	N96433	N96433	CE7312 Yuji
C 270	14	28.0	227	2	BB234604	BB234604	BB234604	c 343	14	28.0	360	8	BM528367	BM528367	BM528367
C 271	14	28.0	231	9	CC068007	CC068007	CSU-K33x.	c 344	14	28.0	361	5	BM528367	BM528367	OSTR212C6
C 272	14	28.0	236	9	AQ846798	AQ846798	LMJTFV1.1	c 345	14	28.0	361	6	CB398939	CB398939	
C 273	14	28.0	240	9	AZ769423	AZ769423	IM0570005	c 346	14	28.0	362	7	CN781944	CN781944	EST70039 S
C 274	14	28.0	248	10	CM428485	CM428485	fbdb001f1	c 347	14	28.0	362	8	BY126395	BY126395	BY126395
C 275	14	28.0	248	10	CM428486	CM428486	fbdb001f1	c 348	14	28.0	371	5	BJ660450	BJ660450	BJ660450
C 276	14	28.0	250	10	CE734885	CE734885	tigr-g88-	c 349	14	28.0	375	6	CD098036	CD098036	ME1-0018T
C 277	14	28.0	253	5	BM559964	BM559964	ND5.75A7.	c 350	14	28.0	375	6	DN387083	DN387083	LI83893-0
C 278	14	28.0	254	4	CC142692	CC142692	ND5.75A7.	c 351	14	28.0	378	4	AK208689	AK208689	Mus muscu
C 279	14	28.0	256	1	AV294479	AV294479	AV294479	c 352	14	28.0	380	7	CB889228	CB889228	laa48901.
C 280	14	28.0	258	2	BE772209	BE772209	CM2-FT011	c 353	14	28.0	380	6	CN026709	CN026709	UMC-p4c1v
C 281	14	28.0	258	6	CD179268	CD179268	MS1-0015T	c 354	14	28.0	382	7	CK884643	CK884643	SGP165002
C 282	14	28.0	260	8	TI9683	TI9683	886R Heart	c 355	14	28.0	382	10	CM789947	CM789947	SP_Ba006
C 283	14	28.0	262	4	AK200715	AK200715	Mus muscu	c 356	14	28.0	384	1	AL811971	AL811971	AL811971
C 284	14	28.0	262	4	AK205599	AK205599	Mus muscu	c 357	14	28.0	385	1	AA544468	AA544468	VK33g12.T
C 285	14	28.0	262	4	AK205928	AK205928	Mus muscu	c 358	14	28.0	389	1	AA562411	AA562411	EST374484
C 286	14	28.0	262	4	AK207342	AK207342	Mus muscu	c 360	14	28.0	390	1	AA509144	AA509144	MBAPCX7G1
C 287	14	28.0	262	4	AK207468	AK207468	Mus muscu	c 361	14	28.0	390	10	CG133199	CG133199	PICD42TB
C 288	14	28.0	262	4	AK208541	AK208541	Mus muscu	c 362	14	28.0	393	6	CB081702	CB081702	hk55e003.G
C 289	14	28.0	262	4	AK208620	AK208620	Mus muscu	c 363	14	28.0	395	9	AQ190867	AQ190867	HS_3231.B
C 290	14	28.0	262	4	AK209126	AK209126	Mus muscu	c 364	14	28.0	396	3	BP863144	BP863144	BP863144
C 291	14	28.0	262	4	AK210837	AK210837	Mus muscu	c 365	14	28.0	397	3	BP644364	BP644364	BP644364
C 292	14	28.0	262	4	AK211703	AK211703	Mus muscu	c 366	14	28.0	399	3	BM079225	BM079225	ME8T91-F1
C 293	14	28.0	262	4	AK213222	AK213222	Mus muscu	c 367	14	28.0	402	7	CN071566	CN071566	1021014F0
C 294	14	28.0	262	4	AK215738	AK215738	Mus muscu	c 368	14	28.0	404	1	AA571443	AA571443	xx12b05.X
C 295	14	28.0	262	4	AK215892	AK215892	Mus muscu	c 369	14	28.0	405	6	CD535731	CD535731	LeukONS_7
C 296	14	28.0	262	4	AK216377	AK216377	Mus muscu	c 370	14	28.0	406	5	BQ857071	BQ857071	QGB6112.Y
C 297	14	28.0	262	4	AK217035	AK217035	Mus muscu	c 371	14	28.0	406	10	CM970775	CM970775	ATAA-aa3
C 298	14	28.0	262	4	AK219440	AK219440	Mus muscu	c 372	14	28.0	407	9	CO505790	CO505790	Shaired D
C 299	14	28.0	262	4	AK219889	AK219889	Mus muscu	c 373	14	28.0	410	9	AO650425	AO650425	Sheared D
C 300	14	28.0	263	4	AK206746	AK206746	Mus muscu	c 374	14	28.0	411	7	BP071714	BP071714	BP071714
C 301	14	28.0	263	4	AK219805	AK219805	Mus muscu	c 375	14	28.0	412	7	CO534882	CO534882	3530_1_23
C 302	14	28.0	264	7	CN995483	CN995483	MdEF300Im	c 376	14	28.0	415	1	AV438059	AV438059	AV438059
C 303	14	28.0	265	4	AK209399	AK209399	Mus muscu	c 377	14	28.0	418	1	AI614184	AI614184	v177a10.Y
C 304	14	28.0	268	7	CV402505	CV402505	PC0-AN004	c 378	14	28.0	420	3	BP100021	BP100021	BP100021
C 305	14	28.0	273	2	BG521091	BG521091	R54c07.Y	c 379	14	28.0	420	7	BP694780	BP694780	BP694780
C 306	14	28.0	274	6	CF507424	CF507424	USDA-PR.1	c 380	14	28.0	420	7	CO308213	CO308213	EK257020.
C 307	14	28.0	275	10	AJ594131	AJ594131	Arabidops	c 381	14	28.0	420	8	W03349	W03349	z663f07.r1
C 308	14	28.0	280	2	BB566632	BB566632	BB566632	c 382	14	28.0	420	9	AZ897669	AZ897669	RPCT-24-2
C 309	14	28.0	284	2	BB235980	BB235980	BB235980	c 383	14	28.0	423	3	BP645504	BP645504	BP645504
C 310	14	28.0	289	2	BB281968	BB281968	BB281968	c 384	14	28.0	423	9	CC866157	CC866157	NDL.82K22
C 311	14	28.0	289	8	DN361665	DN361665	LI83628-0	c 385	14	28.0	424	1	AV540259	AV540259	AV540259
C 312	14	28.0	292	1	AW346358	AW346358	27814 MAR	c 386	14	28.0	425	1	AW522730	AW522730	UT-R-B00-
C 313	14	28.0	294	1	BB111136	BB111136	BB111136	c 387	14	28.0	425	5	BM510541	BM510541	BM510541
C 314	14	28.0	294	10	CE481662	CE481662	tigr-g88-								



388	14	28.0	425	9	BH186578	BH186578 029 L 20-	C 461	14	28.0	500	9	CE041368	CE041368 L1gr-g88-
389	14	28.0	425	11	CNS07R02	AI623525 T7 end of	C 462	14	28.0	501	10	CM837487	CM837487 ET9892.Ds
390	14	28.0	426	8	DN161815	DN161815 Nabhd2.E	C 463	14	28.0	503	13	BJ195133	BJ195133 BJ195133
391	14	28.0	427	5	BE059336	BE059336 bn31d12.Y	C 464	14	28.0	503	10	CZ670205	CZ670205 OM_BA022
392	14	28.0	427	5	BW577295	BW577295	C 465	14	28.0	503	10	BM123332	BM123332 DANTO rer
393	14	28.0	428	3	BP659755	BP659755 BP659755	C 466	14	28.0	504	1	AV436887	AV436887 AV436887
394	14	28.0	428	10	BX210744	BX210744 Dantio rer	C 467	14	28.0	505	3	BP672876	BP672876 BP672876
395	14	28.0	429	4	CNS06GLX	CR709769 Tetradon	C 468	14	28.0	505	9	CC023863	CC023863 3591_1.36
396	14	28.0	430	4	AK181840	AK181840 Mus muscu	C 469	14	28.0	506	9	AQ522919	AQ522919 HS_5214.B
397	14	28.0	431	9	CC143690	CC143690 ND.L.12H15	C 470	14	28.0	507	3	BT516826	BT516826 BT160023B
398	14	28.0	432	1	AV646304	AV646304 AV646304	C 471	14	28.0	507	10	CL914380	CL914380 OA_ABA001
399	14	28.0	434	2	BP050441	BP050441 EST435599	C 472	14	28.0	509	1	AI1856992	AI1856992 MBNAD-.07
400	14	28.0	434	3	BP624318	BP624318 BP624318	C 473	14	28.0	509	3	BI417036	BI417036 949052C02
401	14	28.0	439	5	AK188208	AK188208 Mus muscu	C 474	14	28.0	509	3	BI674068	BI674068 949052C02
402	14	28.0	439	5	BW527718	BW527718	C 475	14	28.0	509	7	CO340734	CO340734 EP11234.3
403	14	28.0	440	10	CL271859	CL271859 Gga1_75c	C 476	14	28.0	510	1	AI508150	AI508150 BSBML3520
404	14	28.0	441	10	CM031773	CM031773 104_260_1	C 477	14	28.0	511	1	AM100486	AM100486 BGD5907.Y
405	14	28.0	442	10	AG977039	AG977039 Drosophi1	C 478	14	28.0	511	7	CV124243	CV124243 OSTF30026
406	14	28.0	443	8	DN388503	DN388503 LIB3893-0	C 479	14	28.0	512	7	CV124244	CV124244 AQ358649
407	14	28.0	448	4	CNS06DVO	CR714008 Tetradon	C 480	14	28.0	512	9	AQ358649	AQ358649 HS_5030.A
408	14	28.0	449	5	BW557933	BW557933	C 481	14	28.0	512	10	CL321919	CL321919 CH242_15F
409	14	28.0	454	9	B96681	B96681 T3001TR TAM	C 482	14	28.0	514	3	BT325981	BT325981 fph3e10.Y
410	14	28.0	454	11	TA203E09P	AI759710 sb63b07.Y	C 483	14	28.0	514	3	BH071262	BH071262 RPTC-24-2
411	14	28.0	455	10	AI759710	AI759710 RPTC144_24	C 484	14	28.0	515	10	CM025801	CM025801 104_227_1
412	14	28.0	455	10	CL325787	CL325787 n015f10.s	C 485	14	28.0	516	1	AI527520	AI527520 uE12F01.Y
413	14	28.0	457	2	AA601318	AA601318	C 486	14	28.0	516	3	BT205254	BT205254 BJ205476
414	14	28.0	457	2	BG543824	BG543824 E1540 Chi	C 487	14	28.0	516	3	BT205476	BT205476 BJ205524
415	14	28.0	459	11	FR0026049	AL018884 F.fubrtipe	C 488	14	28.0	516	3	BT205682	BT205682 BJ205682
416	14	28.0	461	5	BW557657	BW557657	C 489	14	28.0	517	3	BT206240	BT206240 BJ206240
417	14	28.0	461	1	AI546766	AI546766 BSBML3521	C 490	14	28.0	517	3	BP728879	BP728879 BP728879
418	14	28.0	462	1	AM459792	AM459792 sh95c08.Y	C 491	14	28.0	518	5	BY471833	BY471833 BY471833
419	14	28.0	463	1	AL383326	AL383326 MCB13D11	C 492	14	28.0	519	6	CA539156	CA539156 C0275F05-
420	14	28.0	463	1	AA497810	AA497810 v174a06.T	C 493	14	28.0	519	9	BH539492	BH539492 BOCPH40TR
421	14	28.0	463	6	CA329683	CA329683 hab30c07.	C 494	14	28.0	521	1	AM635119	AM635119 b129609.W
422	14	28.0	464	6	BI270353	BI270353 NF006H07F	C 495	14	28.0	521	1	AM032080	AM032080 EST775534
423	14	28.0	464	6	CA663742	CA663742 w1mk1.pko	C 496	14	28.0	524	5	BX554251	BX554251 BX554251
424	14	28.0	464	7	CK322136	CK322136 A1CMA.CNS.N	C 497	14	28.0	524	9	AZ761493	AZ761493 1M0555A22
425	14	28.0	466	9	BH200178	BH200178 Sml--47B2.	C 498	14	28.0	526	1	AV436474	AV436474 AV436474
426	14	28.0	467	9	AZ259688	AZ259688 RPTC-23-1	C 499	14	28.0	526	1	AM684639	AM684639 NF019C04N
427	14	28.0	469	1	AL387171	AL387171 MCB40G10	C 500	14	28.0	526	2	BG447784	BG447784 NF093G01E
428	14	28.0	470	1	AM756897	AM756897 sk82e08.Y	C 501	14	28.0	526	7	CV722289	CV722289 YDARK-.01
429	14	28.0	472	1	AM200430	AM200430 da21d06.Y	C 502	14	28.0	527	9	AQ624696	AQ624696 CITB1-E1-
430	14	28.0	472	1	AM733864	AM733864 sk78d10.Y	C 503	14	28.0	528	1	AL373551	AL373551 MCB01B01
431	14	28.0	473	1	AU722648	AU722648	C 504	14	28.0	528	1	AL383327	AL383327 MCB13D11
432	14	28.0	475	2	BE132335	BE132335 db45a07.Y	C 505	14	28.0	528	7	CH150752	CH150752 WOUND1_71
433	14	28.0	476	1	AL816373	AL816373	C 506	14	28.0	528	7	CV006817	CV006817 zE101_Lime
434	14	28.0	477	7	CK928829	CK928829 p5imgcr.1	C 507	14	28.0	528	7	CV006817	CV006817 zE101_Lime
435	14	28.0	478	3	BW540296	BW540296 hb20d06.G	C 508	14	28.0	529	3	BM666027	BM666027 BM666027
436	14	28.0	478	10	CM714494	CM714494 A1AA-aab6	C 509	14	28.0	530	1	AV432420	AV432420 AV432420
437	14	28.0	479	5	BM581825	BM581825	C 510	14	28.0	531	6	CA280981	CA280981 SCRFSD102
438	14	28.0	479	6	CF656508	CF656508 tacs5e01.	C 511	14	28.0	531	8	CX187817	CX187817 93-R01936
439	14	28.0	481	1	AA000468	AA000468 mg36d04.Y	C 512	14	28.0	531	9	AQ494166	AQ494166 HS_5145.B
440	14	28.0	482	1	AU179991	AU179991	C 513	14	28.0	532	1	AU289923	AU289923 AU289923
441	14	28.0	482	1	B58890	B58890 CIT-HSP-201	C 514	14	28.0	532	1	AV434341	AV434341 AV434341
442	14	28.0	483	5	BW545414	BW545414	C 515	14	28.0	532	3	BJ665761	BJ665761 BJ665761
443	14	28.0	483	7	CO263845	CO263845 EK136632.	C 516	14	28.0	533	1	AL926787	AL926787 AL926787
444	14	28.0	485	3	BT388757	BT388757 949045B09	C 517	14	28.0	533	9	AO603476	AO603476 HS_2132.B
445	14	28.0	485	8	NQ6425	NQ6425 21004 CD4-1	C 518	14	28.0	535	1	AM635341	AM635341 b133d09.W
446	14	28.0	485	9	AQ476432	AQ476432 CITB1-E1-	C 519	14	28.0	535	3	BU648522	BU648522 BU648522
447	14	28.0	486	1	AU188525	AU188525	C 520	14	28.0	535	5	BW521347	BW521347 BW521347
448	14	28.0	486	1	AM286856	AM286856 LG1_222.C	C 521	14	28.0	535	5	BX516662	BX516662 BX516662
449	14	28.0	488	5	BM564480	BM564480	C 522	14	28.0	535	5	AZ252739	AZ252739 RPTC-23-9
450	14	28.0	488	6	CA585134	CA585134 LBD01707.	C 523	14	28.0	536	1	AI488469	AI488469 EST246808
451	14	28.0	489	11	DR22M4T	ALU41139 Dantio rer	C 524	14	28.0	536	8	DN256576	DN256576 M0902376
452	14	28.0	492	3	BU656905	BU656905	C 525	14	28.0	537	11	TA335F01P	TA335F01P
453	14	28.0	493	6	CD411463	CD411463 Gm_CK4146	C 526	14	28.0	539	8	BM591220	BM591220 BM591220
454	14	28.0	493	7	CV513692	CV513692 TgESTYg9	C 527	14	28.0	539	8	DN161754	DN161754 NARod1.G
455	14	28.0	496	6	CF495846	CF495846 MS1-0007U	C 528	14	28.0	539	8	CA537426	CA537426 C0253B09-
456	14	28.0	496	8	DN185428	DN185428 HO32M21w	C 529	14	28.0	540	6	BF518714	BF518714 EST46165
457	14	28.0	497	7	AV437659	AV437659	C 530	14	28.0	542	2	AQ293105	AQ293105 HS_2245_A
458	14	28.0	497	7	CN621016	CN621016 TgESTZym1	C 531	14	28.0	542	1	AV437282	AV437282 AV437282
459	14	28.0	499	9	AQ732243	AQ732243 HS_5533.B	C 532	14	28.0	543	1	AV437282	AV437282 AV437282
460	14	28.0	500	5	BX549451	BX549451	C 533	14	28.0	543	5	BX564649	BX564649 BX564649



C 534	14	28.0	544	7	CK875853	CK875853	SGP137108	607	14	28.0	593	11	FR0031807	AL028176	Fugu rubr
C 535	14	28.0	545	6	CA825708	CA825708	R65B04.tw	608	14	28.0	594	6	CA605922	C605922	wrl.pk007
C 536	14	28.0	546	11	AV438757	AV438757	AV438757	609	14	28.0	594	7	CY015738	CY015738	ONA-RHOD4
C 537	14	28.0	546	11	TA113G01Q	TA113G01Q	TA113G01Q	610	14	28.0	594	10	CZ074840	CZ074840	OM_Ba007
C 538	14	28.0	547	10	BX147265	BX147265	Danilo rer	611	14	28.0	595	7	CN724934	CN724934	E0888F09-
C 539	14	28.0	548	5	BM526164	BM526164	rsmhb0.00	612	14	28.0	595	7	CY067505	CY067505	Le.mxo.38
C 540	14	28.0	548	7	CK542540	CK542540	rsmhb0.00	613	14	28.0	596	9	AQ054466	AQ054466	CIT-HSP-2
C 541	14	28.0	549	1	AI977867	AI977867	496034E08	614	14	28.0	597	8	CK539184	CK539184	B13dNPF2B
C 542	14	28.0	551	1	AM935304	AM935304	BH46d10.Y	615	14	28.0	597	10	CZ612761	CZ612761	OM_Ba014
C 543	14	28.0	553	11	AG233574	AG233574	Locus cor	616	14	28.0	597	10	CG128900	CG128900	PUIEM03TB
C 544	14	28.0	553	10	TA133B08P	TA133B08P	AL465902.T.brucel	617	14	28.0	597	11	CR324955	CR324955	mei-5.2E2
C 545	14	28.0	556	2	BR290903	BR290903	601084207	618	14	28.0	598	6	CB864402	CB864402	H06A03W-
C 546	14	28.0	556	2	CP882132	CP882132	tric029xa	619	14	28.0	598	6	CP908451	CP908451	AD0523G08-
C 547	14	28.0	557	9	CC132167	CC132167	NDL.12H20	620	14	28.0	600	3	BI991511	BI991511	4101-86.M
C 548	14	28.0	557	10	CU171961	CU171961	104_374_1	621	14	28.0	600	3	BI9924016	BI9924016	7074-18.M
C 549	14	28.0	558	3	BU654416	BU654416	BO544723	622	14	28.0	600	7	CN781940	CN781940	EST00035
C 550	14	28.0	558	5	BO544723	BO544723	EST628350	623	14	28.0	601	2	BR384570	BR384570	601277987
C 551	14	28.0	558	10	CM472261	CM472261	f8db001f2	624	14	28.0	601	7	CO034883	CO034883	3530.1.23
C 552	14	28.0	560	6	CB398925	CB398925	OSTR212C6	625	14	28.0	602	1	AM519778	AM519778	up39a04.Y
C 553	14	28.0	561	7	CK992147	CK992147	007C05R1.	626	14	28.0	602	3	BU654005	BU654005	TNE..003A0
C 554	14	28.0	561	11	TA381A02P	TA381A02P	AL498033.T.brucel	627	14	28.0	602	6	CB860780	CB860780	OM_Ba006
C 555	14	28.0	564	3	BI396175	BI396175	949045B09	628	14	28.0	603	3	BU660459	BU660459	OM_Ba006
C 556	14	28.0	565	9	BH001965	BH001965	BMBAC01N1	629	14	28.0	604	8	CK715234	CK715234	RTPO1.32
C 557	14	28.0	566	7	CV173443	CV173443	db339a11.	630	14	28.0	604	10	CM892379	CM892379	RTPO1.32
C 558	14	28.0	567	11	TA11B04Q	TA11B04Q	AL460669.T.brucel	631	14	28.0	604	10	AM299207	AM299207	EST106036
C 559	14	28.0	568	5	BM586806	BM586806	BW586906	632	14	28.0	605	1	AM299207	AM299207	EST106036
C 560	14	28.0	569	3	BU106877	BU106877	BU106877	633	14	28.0	605	3	BU318788	BU318788	BU318788
C 561	14	28.0	569	6	CA918830	CA918830	EST63648	634	14	28.0	605	3	BU660716	BU660716	BM660716
C 562	14	28.0	569	8	DN259143	DN259143	Me8002453	635	14	28.0	606	1	AA497914	AA497914	v174b03.X
C 563	14	28.0	571	3	BI478412	BI478412	949065R12	636	14	28.0	606	9	BH861072	BH861072	S3B5SP6.W
C 564	14	28.0	571	5	BU637182	BU637182	mgcw002xb	637	14	28.0	606	9	BZ781929	BZ781929	AIAP1C10
C 565	14	28.0	571	7	CP980196	CP980196	tg66a10.Y	638	14	28.0	607	10	CM202554	CM202554	104_628_1
C 566	14	28.0	572	6	CD430982	CD430982	ETH1_6.GO	639	14	28.0	607	5	CA051389	CA051389	sealTga50
C 567	14	28.0	573	3	BM079832	BM079832	NE067H01E	640	14	28.0	607	11	DR9P7T	DR9P7T	Danilo rer
C 568	14	28.0	573	2	BM079832	BM079832	MEST100-C	641	14	28.0	608	3	BU337912	BU337912	BU337912
C 569	14	28.0	575	1	AM635349	AM635349	h132e09.W	642	14	28.0	608	8	CK531223	CK531223	g13dNPF1F
C 570	14	28.0	575	10	CZ267162	CZ267162	dbes10.CH2	643	14	28.0	608	8	DN905215	DN905215	g13dNPF1F
C 571	14	28.0	576	7	CK875728	CK875728	SGP136980	644	14	28.0	609	1	AL485512	AL485512	EST143833
C 572	14	28.0	576	8	CV986854	CV986854	Md6r6021c	645	14	28.0	609	8	CK177399	CK177399	F12_45-35
C 573	14	28.0	577	8	BJ421093	BJ421093	BJ421093	646	14	28.0	611	1	AI486846	AI486846	EST245168
C 574	14	28.0	577	8	CK177870	CK177870	H01_45-92	647	14	28.0	611	7	CN250186	CN250186	EST016108
C 575	14	28.0	578	9	BZ250576	BZ250576	CH23T0-262	648	14	28.0	612	8	CK531368	CK531368	g13dNPF30A
C 576	14	28.0	579	1	AM586517	AM586517	EST1318212	649	14	28.0	612	10	CU791125	CU791125	OR_BBa011
C 577	14	28.0	579	6	CF200080	CF200080	EST1695.T	650	14	28.0	613	10	AG919030	AG919030	Dicoph11
C 578	14	28.0	580	8	CK598313	CK598313	CT020020B	651	14	28.0	614	11	FR0035546	FR0035546	Fugu rubr
C 580	14	28.0	581	10	CM881908	CM881908	shS2Kd52-	653	14	28.0	615	6	CB445023	CB445023	696261.MA
C 581	14	28.0	582	2	BF266639	BF266639	HV.CBA001	654	14	28.0	615	9	BZ890876	BZ890876	CH240.244
C 582	14	28.0	582	4	CNS0GKM	CR222698	TelTraodon	655	14	28.0	616	11	CR491113	CR491113	mtH2-175F
C 583	14	28.0	583	2	BG131634	BG131634	EST164526	656	14	28.0	617	6	CF068105	CF068105	EST1668826
C 584	14	28.0	584	8	CK519784	CK519784	B13dNPF2F	657	14	28.0	618	2	BF645632	BF645632	NF018B04E
C 585	14	28.0	585	3	BJ660858	BJ660858	BJ660858	658	14	28.0	618	3	BU668201	BU668201	BF668201
C 586	14	28.0	585	9	AOT03224	AOT03224	HS.5468.A	659	14	28.0	618	7	CP959291	CP959291	6679r9ice
C 587	14	28.0	586	9	CC023686	CC023686	3591_1_36	660	14	28.0	618	8	CK179028	CK179028	D11_45-31
C 588	14	28.0	586	9	CE148304	CE148304	C19r_-988-	661	14	28.0	618	9	CE187260	CE187260	C19r_-988-
C 589	14	28.0	586	10	CM005090	CM005090	ZMMBLA000	662	14	28.0	620	3	BU651022	BU651022	BM295778
C 590	14	28.0	587	3	BU660440	BU660440	Q06GA05.P	663	14	28.0	620	5	BM295778	BM295778	EST266892
C 591	14	28.0	587	7	BU874251	BU874251	Q06GA05.P	664	14	28.0	622	1	AI897449	AI897449	EST266892
C 592	14	28.0	587	5	CO512615	CO512615	g13dSG13D	665	14	28.0	622	10	BU191818	BU191818	Danilo rer
C 593	14	28.0	587	9	AO967772	AO967772	LERTU90TF	666	14	28.0	622	10	CU823387	CU823387	OR_CBA004
C 594	14	28.0	587	10	CU844994	CU844994	OR_CBA006	667	14	28.0	623	6	BM706292	BM706292	BM706292
C 595	14	28.0	588	5	BO916724	BO916724	QHB18N08.	668	14	28.0	623	6	CA754029	CA754029	BR0400070
C 596	14	28.0	588	8	CK539486	CK539486	g13dNPF1E	669	14	28.0	623	9	CU431024	CU431024	ETH1_6.GO
C 597	14	28.0	588	8	AZ143338	AZ143338	SP.0007.B	670	14	28.0	623	6	AQ041521	AQ041521	RPCT-11-1
C 598	14	28.0	589	10	CM139323	CM139323	104_529_1	671	14	28.0	624	3	BU649183	BU649183	g13dNPF5C
C 599	14	28.0	589	3	BU655004	BU655004	BU655004	672	14	28.0	624	8	CK529883	CK529883	g13dNPF5C
C 600	14	28.0	590	3	BU666387	BU666387	BU666387	673	14	28.0	625	3	BU646385	BU646385	BU646385
C 601	14	28.0	591	2	BI263489	BI263489	NF091B01P	674	14	28.0	626	8	CK532922	CK532922	g13dNPF4C
C 602	14	28.0	591	7	CN919713	CN919713	030213ABQ	675	14	28.0	627	5	BU799042	BU799042	SJF2BUC06
C 603	14	28.0	591	8	CK185934	CK185934	C05_45-98	676	14	28.0	627	8	CK539056	CK539056	g13dNPF47F
C 604	14	28.0	593	8	BU333281	BU333281	BU333281	677	14	28.0	627	9	AO952529	AO952529	Sheared.D
C 605	14	28.0	593	8	DN161969	DN161969	NARhodA.C	678	14	28.0	628	5	BM304904	BM304904	BM304904
C 606	14	28.0	593	10	CE832851	CE832851	C19r_-988-	679	14	28.0	628	7	CU129035	CU129035	MdEtc3091



C 680	14	28.0	628	7	CV296054	CV296054	EST884431	C 753	14	28.0	657	5	BQ620624	BQ620624	TaLr1138F
681	14	28.0	628	8	DN161948	DN161948	NaRhod4.A	C 754	14	28.0	657	7	CO222499	CO222499	WS01016-B
682	14	28.0	628	10	CN115208	CN115208	104_4901	C 755	14	28.0	657	9	AO653241	AO653241	Sheared.D
683	14	28.0	629	1	A1488800	A1488800	EST247139	C 756	14	28.0	658	3	BQ491974	BQ491974	BQ491974
C 684	14	28.0	629	5	BQ632039	BQ632039		C 757	14	28.0	658	8	CX531214	CX531214	B130NF31E
C 685	14	28.0	629	5	BQ387474	BQ387474	NISC_mm24	C 758	14	28.0	659	1	AU294243	AU294243	AU294243
C 686	14	28.0	630	5	BQ387291	BQ387291	NISC_mm23	C 759	14	28.0	659	2	BQ657772	BQ657772	BQ657772
C 687	14	28.0	630	8	DE677186	DE677186	EST106730	C 760	14	28.0	659	5	BW566300	BW566300	BW566300
C 688	14	28.0	631	10	CM485858	CM485858	FabD001f2	C 761	14	28.0	659	5	BX411305	BX411305	BX411305
C 689	14	28.0	631	10	CM631231	CM631231	OM_Ba017	C 762	14	28.0	660	10	CG043389	CG043389	PURK023TB
C 690	14	28.0	632	3	BQ645910	BQ645910		C 763	14	28.0	661	1	A1487331	A1487331	EST245653
C 691	14	28.0	632	7	CV168347	CV168347	rsmex1_00	C 764	14	28.0	661	8	CV998124	CV998124	LI23405.9
C 692	14	28.0	632	8	CX180694	CX180694	F11_45-39	C 765	14	28.0	661	9	BH579832	BH579832	BQGM277E
C 693	14	28.0	633	10	BX549450	BX549450	BX549450	C 766	14	28.0	662	3	BQ328762	BQ328762	BQ328762
C 694	14	28.0	633	10	CV2633971	CV2633971	OM_Ba017	C 767	14	28.0	662	8	CX179108	CX179108	D02_45--59
C 695	14	28.0	634	3	B1935226	B1935226	EST55515	C 768	14	28.0	662	8	DN161880	DN161880	NaRhod3.C
C 696	14	28.0	634	5	BQ400945	BQ400945	NISC_mpl2	C 769	14	28.0	663	9	BH930068	BH930068	odh69a03.
C 697	14	28.0	634	5	CA031753	CA031753	HX1A14r	C 770	14	28.0	663	9	BH930077	BH930077	odh69a03.
C 698	14	28.0	634	9	AZ065869	AZ065869	RPCI-23-4	C 771	14	28.0	663	10	CZ267129	CZ267129	odh69a02.
C 699	14	28.0	634	10	AG980701	AG980701	DroGoph11	C 772	14	28.0	664	3	BQ393097	BQ393097	BQ393097
C 700	14	28.0	635	3	B1904295	B1904295	603167030	C 773	14	28.0	664	7	CV177695	CV177695	LEP1SMA55
C 701	14	28.0	635	7	CV015443	CV015443	ONaRhOD_	C 774	14	28.0	664	7	CV249731	CV249731	WS01125.B
C 702	14	28.0	636	1	AM687648	AM687648	NFO11F11R	C 775	14	28.0	665	2	BE491133	BE491133	db45a07.x
C 703	14	28.0	636	3	BN649010	BN649010		C 776	14	28.0	665	8	DR171688	DR171688	HF0001.R1
C 704	14	28.0	636	7	CN724023	CN724023	E0871F02-	C 777	14	28.0	665	8	DR663899	DR663899	ST105401
C 705	14	28.0	636	9	AO991537	AO991537	RfC02517	C 778	14	28.0	665	9	CC389287	CC389287	PURHB03TD
C 706	14	28.0	636	9	AZ629757	AZ629757	1M0482023	C 779	14	28.0	666	2	B1267430	B1267430	NF104F11I
C 707	14	28.0	636	9	CC602570	CC602570	OGMBV47TV	C 780	14	28.0	666	5	CA050425	CA050425	aaalrpb53
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C 710	14	28.0	637	7	CV633256	CV633256	E5T912009	C 783	14	28.0	667	3	BQ666991	BQ666991	BQ666991
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ACCESSION AV590963  
 VERSION AV590963.1 GI:9701956  
 KEYWORDS  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 426)  
 Takasuga,A., Hirotsune,S., Itoh,R., Jitchazono,A., Suzuki,H., Aso,H. and Sugimoto,Y.  
 Establishment of a high throughput EST sequencing system using poly(A) tail-removed cDNA libraries and determination of 36,000 bovine ESTs  
 Nucleic Acids Res. 29 (22), E108 (2001)  
 11713328  
 Contact: Yoshikazu Sugimoto  
 Animal Genetics Division  
 Shikakawa Institute of Animal Genetics  
 Odakura, Nishigo, Nishi-shirakawa, Fukushima 961-8061, Japan  
 Tel: 81-248-25-5641  
 Fax: 81-248-25-5725  
 Email: kazusugi@sig.or.jp  
 Single pass sequencing.  
 This clone was obtained from a polyA-deleted cDNA library.  
 Location/Qualifiers  
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 413 GACGGCTCCATCTACA 397

RESULT 6  
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 VERSION BG689655.1 GI:13931456  
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 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 459)  
 Sonstegard,T., Capuco,A.V., White,J., Van Tassel,C.P., and Quackenbush,U.  
 Connors,B.E., Cho,J., Sultana,R., Shade,L., Wray,J.E., Wells,K.D. and Quackenbush,U.  
 Analysis of bovine mammary gland EST and functional annotation of the Bos taurus gene index  
 Mamm. Genome 13 (7), 373-379 (2002)  
 12140684  
 Contact: Sonstegard TS  
 USDA, ARS, Beltsville Agricultural Research Center  
 Bldg. 200 Rm 2A, Beltsville, MD 20705, USA  
 Tel: 301 504 8416  
 Fax: 301 504 8414

JOURNAL  
 PUBMED  
 COMMENT

Email: tad@ipsi.barc.usda.gov  
 Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross\_match with the -minscore 18 and -mismatch 12 options.  
 PCR Primers  
 FORWARD: AGGAACAGCTATGACCAT  
 BACKWARD: GTTTCCTCAGTCACGACG  
 Plate: 102 row: J column: 18  
 Seq primer: ATTGAGGACACTATAG.  
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RESULT 7  
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 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Stolidobranchia; Molgulidae; Molgula.  
 1 (bases 1 to 593)  
 Gyoja,F., Satou,Y. and Satoh,N.  
 Expressed genes in Molgula tectiformis  
 Unpublished (2005)  
 Contact: Tadasu Shin-I  
 National Institute of Genetics  
 Center For Genetic Resource Information  
 1111 Yata, Mishima, Shizuoka 411-8540, Japan  
 Tel: 81-559-81-6856  
 Fax: 81-559-81-6855  
 Email: tshini@genes.nig.ac.jp  
 When you want to obtain this EST clone, please send an e-mail to Nori Satoh (satoh@acidian.zool.kyoto-u.ac.jp) and its cc to Yutaka Satou (yutaka@acidian.zool.kyoto-u.ac.jp).  
 Location/Qualifiers  
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 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Qy 12 AATCTACAAGTGTAC 28  
 |||||  
 Db 93 AATCTACAAGTGTAC 109

RESULT 8  
 LOCUS AW289342 630 bp mRNA linear EST 29-SEP-2000  
 DEFINITION 1594 Lewin Cattle Spleen Bos taurus cDNA, mRNA sequence.  
 ACCESSION AW289342  
 VERSION AW289342.1 GI:9257814  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 630)  
 Band,M.R., Larson,J.H., Rebeiz,M., Green,C.A., Heyen,D.W.,  
 Donovan,J., Windish,R., Steining,C., Mahyuddin,P., Womack,J. and  
 Lewin,H.A.  
 An ordered comparative map of the cattle and human genomes  
 Genome Res. 10 (9), 1359-1368 (2000)  
 COMMENT 10984454  
 Contact: Lewin, H. A.  
 M. M. Keck Center for Comparative and Functional Genomics  
 University of Illinois at Urbana-Champaign  
 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
 61801, USA  
 Tel: 217 333 5998  
 Fax: 217 244 5617  
 Email: h-lewin@uiuc.edu

FEATURES  
 source location/Qualifiers  
 1..630  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /strain="Angus"  
 /db\_xref="taxon:9913"  
 /sex="Female"  
 /dev\_stage="Adult"  
 /clone\_lib="Lewin Cattle Spleen"  
 /note="Organ: Spleen; Vector: pBluescript SK(+/-)"

ORIGIN  
 Query Match 34.0%; Score 17; DB 1; Length 630;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGGCTCCATCTACA 19  
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 Db 185 GACGGCTCCATCTACA 201

RESULT 9  
 LOCUS CK773609/c 781 bp mRNA linear EST 20-FEB-2004  
 DEFINITION 9626267 MARC 2BOV Bos taurus cDNA 3', mRNA sequence.  
 ACCESSION CK773609  
 VERSION CK773609.1 GI:42727752  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 781)  
 Smith,T.P.L., Grosee,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,  
 Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
 Chitko-McKown,C.G., Perteau,G., Holt,I., Karaymcheva,S., Liang,F.,  
 Quackenbush,J. and Keefe,J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle

JOURNAL  
 PUBMED  
 COMMENT 11282978  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross\_match v0.990329.  
 Plate: 71 row: F column: 17  
 Seq primer: GTAATACGATCCTCATATGGG.

FEATURES  
 source location/Qualifiers  
 1..781  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="RDH10B"  
 /clone\_lib="MARC 2BOV"  
 /note="Vector: pCMV SPORT6; Site\_1: NotI; Site\_2: SalI;  
 Library made from pooled tissue from testis, thymus,  
 semitendinosus muscle, longissimus muscle, pancreas,  
 adrenal, and endometrium."

ORIGIN  
 Query Match 34.0%; Score 17; DB 7; Length 781;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 GACGGCTCCATCTACA 19  
 |||||  
 Db 441 GACGGCTCCATCTACA 425

RESULT 10  
 LOCUS CK776895/c 787 bp mRNA linear EST 20-FEB-2004  
 DEFINITION 966180 MARC 3BOV Bos taurus cDNA 3', mRNA sequence.  
 ACCESSION CK776895  
 VERSION CK776895.1 GI:42731315  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 REFERENCE 1 (bases 1 to 787)  
 Smith,T.P.L., Grosee,W.M., Freking,B.A., Roberts,A.J., Stone,R.T.,  
 Casas,E., Wray,J.E., White,J., Cho,J., Fahrenkrug,S.C.,  
 Bennett,G.L., Heaton,M.P., Laegreid,W.W., Rohrer,G.A.,  
 Chitko-McKown,C.G., Perteau,G., Holt,I., Karaymcheva,S., Liang,F.,  
 Quackenbush,J. and Keefe,J.W.  
 Sequence evaluation of four pooled-tissue normalized bovine cDNA  
 libraries and construction of a gene index for cattle

JOURNAL  
 PUBMED  
 COMMENT 11282978  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smith@email.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross\_match v0.990329.  
 Plate: 90 row: D column: 12  
 Seq primer: GTAATACGATCCTCATATGGG.

FEATURES  
 source location/Qualifiers  
 1..787  
 /organism="Bos taurus"  
 /mol\_type="mRNA"



/db\_xref="taxon:9913"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;  
Library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

ORIGIN

Query Match 34.0%; Score 17; DB 7; Length 787;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GACGGCTCCAACTTACA 19  
|||||  
Db 673 GACGGCTCCAACTTACA 657

RESULT 11  
CG749587 1133 bp DNA linear GSS 24-OCT-2003  
LOCUS P043-4-B12.ya Ppa ECoRI BAC Library Pristionchus pacificus genomic,  
DEFINITION genomic survey sequence.  
ACCESSION CG749587  
VERSION CG749587.1 GI:37970529  
KEYWORDS GSS.  
SOURCE Pristionchus pacificus  
ORGANISM Pristionchus pacificus  
Bukariyota; Metazoa; Nematoda; Chromadorea; Diplogasterida;  
Neodiplogasteridae; Pristionchus.  
1 (bases 1 to 1133)  
Srinivasan,J., Sinz,W., Jeease,T., Wiggers-Perebolte,L., Jansen,K.,  
Buntjer,J., van der Meulen,M. and Sommer,R.V.  
An integrated physical and genetic map of the nematode Pristionchus  
pacificus  
Mol. Genet. Genomics 269 (5), 715-722 (2003)  
JOURNAL 12884007  
COMMENT Contact: Sommer RJ  
Evolutionary Biology  
Max-Planck-Institute for Developmental Biology  
Spemannstr. 37-39, Tuebingen D-72076, Germany  
Tel: 00497071601371  
Fax: 00497071601498  
Email: ralf.sommer@tuebingen.mpg.de  
Classes: BAC ends.  
Location/Qualifiers  
1. 1133  
/organism="Pristionchus pacificus"  
/mol\_type="genomic DNA"  
/strain="California"  
/db\_xref="taxon:54126"  
/clone\_lib="Ppa ECoRI BAC Library"  
/note="The library was generated by a partial digest of  
the genomic DNA with EcoRI and cloning into the BAC  
vector."

ORIGIN

Query Match 34.0%; Score 17; DB 10; Length 1133;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 CGGCTCCAACTTACAAC 21  
|||||  
Db 432 CGGCTCCAACTTACAAC 448

RESULT 12  
BP719333 187 bp mRNA linear EST 19-JUL-2004  
LOCUS BP719333 Osada Taira anterior neuroectoderm (ANE) PCS105 cDNA  
DEFINITION library Xenopus laevis cDNA clone Xl442b1lex 3', mRNA sequence.  
ACCESSION BP719333

VERSION BP719333.1 GI:46067926  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 187)  
Osada,S., Kitayama,A., Ueno,N. and Taira,M.  
Expression analysis of genes which are expressed in the anterior  
neuroectoderm of Xenopus embryos  
Unpublished (2004)  
JOURNAL Contact: Masanori Taira  
Department of Biological Sciences  
Graduate School of Science, University of Tokyo; CREST, Japan  
Science and Technology Corporation, Japan  
7-3-1 Hongo, Bunkyo-ku, Tokyo 113-0033, Japan  
Tel: 81-03-5641-4434  
Fax: 81-03-5641-4434  
Email: m.taira@biol.s.u-tokyo.ac.jp,  
URL: http://www.shigen.nig.ac.jp/db/np/xenopus/est/  
Location/Qualifiers  
1. 187  
/organism="Xenopus laevis"  
/mol\_type="mRNA"  
/db\_xref="taxon:8355"  
/clone="Xl442b1lex"  
/issue\_type="anterior neuroectoderm"  
/dev\_stage="late gastrula (stage 12.5)"  
/clone\_lib="Osada Taira anterior neuroectoderm (ANE)  
PCS105 cDNA library"

ORIGIN

Query Match 32.0%; Score 16; DB 3; Length 187;  
Best Local Similarity 100.0%; Pred. No. 1.2e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGACGGCTCCAACTCTA 17  
|||||  
Db 57 GGACGGCTCCAACTCTA 72

RESULT 13  
BG234864 318 bp mRNA linear EST 12-FEB-2001  
LOCUS dab66a05.y1 NICHD\_XGC\_Emb4 Xenopus laevis cDNA clone IMAGE:420200  
DEFINITION 5', mRNA sequence.  
ACCESSION BG234864  
VERSION BG234864.1 GI:12748790  
KEYWORDS EST.  
SOURCE Xenopus laevis (African clawed frog)  
ORGANISM Xenopus laevis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;  
Xenopodinae; Xenopus; Xenopus.  
1 (bases 1 to 318)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
Email: cgaabs-r@mail.nih.gov  
Tissue Procurement: Marsha Rebber, Steven L. Klein, Ph.D.  
cDNA Library Preparation: Life Technologies, Inc.  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: Xenopus clones from this library are available  
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov  
Seq primer: -40RP from Gibco  
High quality sequence stop: 307.  
Location/Qualifiers  
1. 318  
/organism="Xenopus laevis"



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/mol_type="mRNA"
/db_xref="taxon:8355"
/clone="IMAGE:4202000"
/dev_stage="embryo, stage 31-32"
/lab_host="DH10B (phage-resistant)"
/clone_1ib="NICHD XGC Emb4"
/note="Organ: whole embryo; Vector: pCMV-SPORT6; Site 1:
NotI; Site 2: SalI; Cloned unidirectionally. Primer: Oligo
dT. Average insert size 2.1 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

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## ORIGIN

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Query Match      32.0%; Score 16; DB 2; length 318;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      2 GAGCGCTCCATCTTA 17
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Db      184 GAGCGCTCCATCTTA 199

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RESULT 14      330 bp      mRNA      linear      EST 01-AUG-2000
BB559488      BB559488 RIKEN full-length enriched, 2 days pregnant adult female
LOCUS          ovary Mus musculus cDNA clone E330039C08 3, mRNA sequence.
ACCESSION      BB559488
VERSION        BB559488.1 GI:9645854
KEYWORDS       EST.
SOURCE         Mus musculus
ORGANISM       Mus musculus (house mouse)

```

```

REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                Sciurognathi; Muridae; Murinae; Mus.
                1 (bases 1 to 330)
                Komno, H., Aizawa, K., Akahira, S., Akiyama, J., Arakawa, T.,
                Carninci, P., Endo, T., Fukuda, S., Fukunishi, Y., Hara, A., Hayatsu, N.,
                Hirozane, T., Hori, F., Ishii, Y., Ishikawa, J., Ishikawa, T., Itoh, M.,
                Izawa, M., Kadota, K., Kagawa, I., Kai, C., Kawai, J., Kikuchi, N.,
                Kiyosawa, H., Kojima, K., Kondo, S., Koya, S., Kurihara, C.,
                Kusakabe, M., Matsuyama, T., Miki, R., Mizuno, Y., Nakamura, M., Oda, H.,
                Okazaki, Y., Ono, T., Owa, C., Saito, H., Sakai, C., Sato, K.,
                Shibata, K., Shibata, Y., Shigemoto, Y., Shingawa, A., Shiraki, T.,
                Sogabe, Y., Sugahara, Y., Suzuki, H., Suzuki, H., Tagawa, A.,
                Takahashi, F., Tomimaga, N., Toya, T., Tsunoda, Y., Watabiki, A.,
                Watanabe, S., Yamamura, T., Yamanaka, I., Yano, R., Yasunishi, A.,
                Yokota, T., Yoshida, K., Yoshiki, A., Yoshino, M., Muramatsu, M. and
                Hayashizaki, Y.

```

```

TITLE          RIKEN Mouse ESTs (Komno, H., et al.)
JOURNAL        Unpublished (2000)
COMMENT        Contact: Yoshihide Hayashizaki
                Laboratory for Genome Exploration Research Group, RIKEN Genomic
                Sciences Center (GSC), Yokohama Institute
                The Institute of Physical and Chemical Research (RIKEN)
                1-7-22 Suicho-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
                Tel.: 81-45-503-9222
                Fax: 81-45-503-9216
                Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/
                Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagoka, S.,
                Saeki, N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
                Thermostabilization and thermoinactivation of thermolabile enzymes by
                trehalose and its application for the synthesis of full length
                cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
                Itoh, M., Katsunai, T., Akiyama, J., Shibata, K., Izawa, M., Kawai, J.,
                Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M.,
                Okazaki, Y. and Hayashizaki, Y.
                Automated filtration-based high-throughput plasmid preparation
                system. Genome Res. 9 (5), 465-470 (1999)
                Carninci, P. and Hayashizaki, Y.
                High-efficiency full-length cDNA cloning. Methode Enzymol. 303,
                19-44 (1999)

```

Please visit our web site (<http://genome.rtc.riken.go.jp>) for

```

FEATURES
SOURCE

```

## further details.

```

location/Qualifiers
1..330
organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
/clone="E330039C08"
/sex="female"
/tissue_type="ovary"
/dev_stage="2 days pregnant adult"
/lab_host="DH10B"
/clone_1ib="RIKEN full-length enriched, 2 days pregnant
adult female ovary"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5'
GAGGAGAGAGCGCGCGCACTCGAGTTTCTTTTCTTTTCTTTN 3'], cDNA was
transcribed by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5'
GAGGAGAGAGTTCTCGAGTTTAAATTAATTAATTCCTCCCTCCCTCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from lambdaFLC 1."

```

## ORIGIN

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Query Match      32.0%; Score 16; DB 2; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      33 GACTTCGTAGTGTTA 48
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Db      232 GACTTCGTAGTGTTA 247

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```

RESULT 15      356 bp      mRNA      linear      EST 11-JUL-2001
BI214804/c      RE20932 5prime RE Drosophila melanogaster normalized Embryo pf1c-1
LOCUS          Drosophila melanogaster cDNA clone RE20932 5 similar to Shg:
                Fban003722, 'cell adhesion' located on: 2R 57B16-57B16;:
                04/12/2001, mRNA sequence.

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ACCESSION      BI214804
VERSION        BI214804.1 GI:14692528
KEYWORDS       EST.
SOURCE         Drosophila melanogaster (fruit fly)
ORGANISM       Drosophila melanogaster
                Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
                Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                Ephydroidea; Drosophilidae; Drosophila.
                1 (bases 1 to 356)
                Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,
                Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Friese, E.,
                George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,
                Misra, S., Mungall, C.J., Nunoo, J., Pacלב, J., Pargias, V., Park, S.,
                Pounanavong, S., Wan, K., Yu, C., Lewis, S.E., Celniker, S. and
                Rubin, G.M.
                BDGP/HMT RE Drosophila EST Project
                Unpublished (2001)
                Contact: Stapleton, M.

```

```

TITLE          Lawrence Berkeley National Lab
JOURNAL        One Cyclotron Rd, Berkeley, CA 94720, USA
COMMENT        Fax: 510 486 6798
                Email: http://www.fruitfly.org/EST, est@fruitfly.berkeley.edu
                hlt genomic AEO003452: arm:2R [15705280,16010299]
                estimated-cyto:57B3-57B20: 04/12/2001
                Plate: RE.209 row: C column: 8
                High quality sequence stop: 225.

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FEATURES  
source

Location/Qualifiers  
1. 356  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="R20932"  
/sex="male and female"  
/dev\_stage="0-24 hours mixed stage embryonic"  
/lab\_host="DHS-alpha Tona"  
/clone\_lib="RE Drosophila melanogaster normalized Embryo p1C-1"  
/note="Organ: embryo; Vector: p1C1; Site 1: XhoI; Site 2: BamHI; Library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

ORIGIN

Query Match 32.0%; Score 16; DB 2; Length 356;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTTTACCAAGACTT 37  
|||||  
Db 222 GTTTACCAAGACTT 207

RESULT 16 356 bp mRNA linear EST 03-NOV-2002  
BM165338  
LOCUS BM165338 Nori Satoh unpublished cDNA library, gonad Ciona  
DEFINITION intestinalis cDNA clone rc1gd008j11 3', mRNA sequence.  
ACCESSION BM165338  
VERSION BM165338.1 GI:24522563  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
1 (bases 1 to 356)  
Saton, Y., Shin-I, T., Kohara, Y. and Satoh, N.  
Expressed genes in Ciona intestinalis (2002c)  
Unpublished (2002)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1. 356  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="rc1gd008j11"  
/isue\_type="gonad"  
/clone\_lib="Nori Satoh unpublished cDNA library, gonad"

ORIGIN

Query Match 32.0%; Score 16; DB 5; Length 356;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TGTTACCAAGACTT 38  
|||||  
Db 60 TGTTACCAAGACTT 75

RESULT 17 387 bp mRNA linear EST 12-DEC-2002  
BY403337  
LOCUS BY403337 RIKEN full-length enriched, CRL-1722 L5178Y-R Mus musculus  
DEFINITION cDNA clone I730044L20 3', mRNA sequence.

ACCESSION BY403337  
VERSION BY403337.1 GI:26632905  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murine; Mus.  
REFERENCE 1 (bases 1 to 387)  
Oikazaki, Y., Furuno, M., Kasukawa, T., Adachi, J., Bono, H., Kondo, S., Mikado, I., Oshio, N., Satoh, R., Suzuki, H., Yamamoto, I., Kiyosawa, H., Yagi, K., Tomaru, Y., Hasegawa, Y., Nogami, A., Schomach, C., Gotohori, T., Baldarelli, R., Hill, D. P., Bull, C., Hume, D. A., Quackenbush, J., Schiraldi, L. M., Kanapin, A., Matsuda, H., Batalov, S., Beisel, K. W., Blake, J. A., Brady, D., Brasic, V., Chochia, C., Corbani, L. E., Cousins, S., Dalia, E., Dragani, T. A., Fletcher, C. F., Forrest, A., Frazer, K. S., Gaasterland, T., Gariboldi, C. F., Gissi, C., Godzik, A., Gough, J., Grimmond, T., Gustincich, S., Hirokawa, N., Jackson, I. D., Jarvis, E. D., Kanai, A., Kawai, H., Kawasawa, Y., Kedzierski, R. M., King, B. L., Kongaya, A., Kurochkin, I. V., Lee, Y., Lenhard, B., Lyons, P. A., Maglott, D. R., Maltais, L., Marchionni, L., McKenzie, L., Miki, H., Nagashima, T., Numata, K., Okido, T., Pavan, W. J., Petrea, G., Pezole, G., Wells, C., Wilming, L. G., Wynshaw-Boris, A., Yangisawa, M., Yang, I., Yang, L., Yuan, Z., Zavolan, M., Zhu, Y., Zimmer, A., Carninci, P., Hayatsu, N., Hirozane-Kishikawa, T., Konno, H., Nakamura, M., Sakazume, N., Sato, K., Shiraki, T., Waki, K., Waki, K., Aizawa, T., Fukuda, S., Hara, A., Hashizume, M., Imocani, K., Ishii, Y., Itoh, M., Kagawa, I., Miyazaki, A., Sakai, K., Saeki, D., Shibata, K., Shinagawa, A., Yasunishi, A., Yoshino, M., Waterston, R., Lander, E. S., Rogers, J., Birney, E. and Hayashizaki, Y.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)  
12466851  
JOURNAL PUBLISHED  
COMMENT Contact: Yoshihide Hayashizaki  
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute  
The Institute of Physical and Chemical Research (RIKEN)  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
Tel: 81-45-503-9222  
Fax: 81-45-503-9216  
Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
Aizawa, K., Akimura, T., Arakawa, T., Carninci, P., Fukuda, S., Hirozane, T., Imocani, K., Ishii, Y., Itoh, M., Kawai, J., Konno, H., Miyazaki, A., Murata, M., Nakamura, M., Nomura, K., Numazaki, R., Ohno, M., Sakai, K., Sakazume, N., Saeki, D., Sato, K., Shibata, K., Shiraki, T., Tagami, M., Waki, K., Wataniki, A., Watanabe, M. and Hayashizaki, Y. Direct Submission  
Computational Analysis of Full-length Mouse cDNAs Compared with Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)  
RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multichannel sequencer. Genome Res. 10 (11), 1757-1771 (2000)  
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in RIKEN Genomic Sciences Center and Genome Science Laboratory in RIKEN Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site (http://genome.gsc.riken.go.jp) for further details.  
Location/Qualifiers



```

source
1..387
/organism="Mus musculus"
/mol_type="mRNA"
/strain="DBA/2"
/db_xref="taxon:10090"
/clone_lib="I730044L20"
/cell_line="CRL-1722 L5178Y-R"
/clone_lib="RIKEN full-length enriched, CRL-1722 L5178Y-R"

ORIGIN

Query Match          32.0%; Score 16; DB 5; Length 387;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 5 CGGCTCCATCTACAA 20
Db 181 CGGCTCCATCTACAA 196

RESULT 18
LOCUS CB398775 446 bp mRNA linear EST 15-MAY-2003
DEFINITION OSTR209B1_1 AD-wtmcDNA Caenorhabditis elegans cDNA, mRNA sequence.
ACCESSION CB398775
VERSION CB398775.1 GI:30740502
KEYWORDS EST.
ORGANISM Caenorhabditis elegans
           Caenorhabditis elegans
           Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilitida;
           Rhabdilitida; Peloderinae; Caenorhabditis.
REFERENCE 1 (bases 1 to 446)
AUTHORS Reboul,J., Vaglio,P., Rual,J.F., Lamesch,P., Martinez,M.,
          Armstrong,C.M., Li,S., Jacotot,L., Bertin,N., Janky,R., Moore,T.,
          Hudson,J.R., Hartley,J.L., Brasch,M.A., Vandenhaute,J., Boulton,S.,
          Endress,G.A., Jemna,S., Chevet,E., Papasotiropoulos,V.,
          Tollas,P.P., Placek,J., Snyder,M., Huang,R., Chance,M.R., Lee,H.,
          Doucette-Stamm,L., Hill,D.E. and Vidal,M.
          C. elegans ORFome version 1.1: experimental verification of the
          genome annotation and resource for proteome-scale protein
          expression
JOURNAL Nat. Genet. (2003) In press
COMMENT Contact: Vidal M
          Marc Vidal laboratory
          Dana Farber Cancer Institute
          1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA
          Tel: 617 632 5180
          Fax: 617 632 5739
          Email: Marc.Vidal@dfci.harvard.edu
          Sequence tag of Gateway entry clones. The primers used were
          designed on the predicted protein encoding ORF. C. elegans ORFome
          cloning project : Contact david_hill@dfci.harvard.edu or
          marc_vidal@dfci.harvard.edu
          POLYA=No.

FEATURES
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1..446
Location/Qualifiers
/organism="Caenorhabditis elegans"
/mol_type="mRNA"
/strain="N2"
/db_xref="taxon:6239"
/seq="Hermaphrodite and male"
/risue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wtmcDNA"
/note="The AD-wtmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pPC86"

ORIGIN

Query Match          32.0%; Score 16; DB 6; Length 446;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Cy 18 CAACGTGTACCAACG 33
Db 263 CAACGTGTACCAACG 248

RESULT 19
LOCUS CG993295 460 bp DNA linear GSS 16-DEC-2003
DEFINITION ZMWB0375G11.f ZMWB0375G11 f ZMWB0375G11 5',
          genomic survey sequence.
ACCESSION CG993295
VERSION CG993295.1 GI:39947162
KEYWORDS GSS.
SOURCE Zea mays
ORGANISM Zea mays
          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
          clade; Panicoideae; Andropogoneae; Zea.
REFERENCE 1 (bases 1 to 460)
AUTHORS Yu,Y., Kim,H.R., Hatfield,J., Soderlund,C., Bharti,A.K., Messing,J.
          and Wang,R.
          Sequencing of the maize genome
          Unpublished (2003)
COMMENT Contact: Rod Wing
          Arizona Genomics Institute
          University of Arizona
          Biological Sciences West, 449A, P.O. Box 210088, Tucson, AZ
          85721-0088, USA
          Tel: 520 626 3967
          Fax: 520 621 9288
          Email: twing@genome.arizona.edu
          PCR Primers
          FORWARD: T7
          BACKWARD: M13r
          Plate: 0375 row: G column: 11
          Seq primer: T7
          Class: BAC ends.

FEATURES
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1..460
Location/Qualifiers
/organism="Zea mays"
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/cultivar="B73"
/db_xref="taxon:4577"
/clone="ZMWB0375G11"
/lab_host="DH10B"
/clone_lib="ZMWB03"
/note="Vector: pBeloBAC11; Site_1: HindIII; Site_2:
HindIII; Zea mays L. ssp. mays"

ORIGIN

Query Match          32.0%; Score 16; DB 10; Length 460;
Best Local Similarity 100.0%; Pred. No. 1,1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 13 ATCTACAACGTGTAC 28
Db 243 ATCTACAACGTGTAC 258

RESULT 20
LOCUS B1229863 463 bp mRNA linear EST 11-JUN-2001
DEFINITION RE27736.pprime RE Drosophila melanogaster normalized Embryo pfic-1
          P8an0003722 'cell adhesion' located on: 2R 57B16-57B16;:
          04/12/2001, mRNA sequence.
ACCESSION B1229863
VERSION B1229863.1 GI:14697127
KEYWORDS EST.
ORGANISM Drosophila melanogaster (fruit fly)
          Drosophila melanogaster
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

```



Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydriidae; Drosophilidae; Drosophila.  
1 (bases 1 to 463)

Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,  
Carlson, J., Champe, M., Chavez, C., Dorsett, V., Farfan, D., Friese, E.,  
George, R., Gonzalez, M., Guarin, H., Harris, N., Li, P., Liao, G.,  
Miera, S., Mungall, C. J., Nunoo, J., Pacleb, J., Paragas, V., Park, S.,  
Phouanavong, S., Wan, K., Yu, C., Lewis, S. E., Celniker, S. and  
Rubin, G. M.

TITLE BDGP/HMT RE Drosophila EST Project  
JOURNAL Unpublished (2001)  
COMMENT Contact: Stapleton, M.  
BDGP

Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: [http://www.fruitfly.org/EST\\_est@fruitfly.berkeley.edu](http://www.fruitfly.org/EST_est@fruitfly.berkeley.edu)  
hit genomic AE003452; arm:2R [15705280,16010299]  
estimated-cyto:57B3-57B20: 04/12/2001  
Plate: RE:277 row: C column: 12  
High quality sequence stop: 325.  
Location/Qualifiers

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/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="RE27736"  
/sex="male and female"  
/dev\_stage="0-24 hours mixed stage embryonic"  
/lab\_host="DHS-alpha Tona"  
/clone\_lib="RE Drosophila melanogaster normalized Embryo  
p1C-1"

/note="Organ: embryo; Vector: p1C1; Site 1: XhoI; Site 2:  
BamHI; Library was kindly generated by Piero Carninci at  
the RIKEN. The library was normalized and excised using  
Cre recombinase. Plasmid cDNA library."

## ORIGIN

Query Match 32.0%; Score 16; DB 2; Length 463;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GTGTTACCAAGCACTT 37  
DB 228 GTGTTACCAAGCACTT 213

RESULT 21  
DRI3P12T 498 bp DNA linear GSS 26-NOV-2002  
DEFINITION Danio rerio genomic clone DKRY-13P12, genomic survey sequence.  
ACCESSION AL733894  
VERSION AL733894.1 GI:21339372  
KEYWORDS GSS.  
SOURCE Danio rerio (zebrafish)  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 498)

REFERENCE Humphray, S. J., Huckle, E. and Hunt, S. E.  
AUTHORS Direct SubMISSION  
JOURNAL Submitted (06-JUN-2002) The Sanger Institute, Wellcome Trust Genome  
Campus, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail contact:  
humquerry@sanger.ac.uk Unpublished

COMMENT This sequence was generated from the T7 end of BAC 13P12. 13P12 is  
part of the Daniokey BAC library created by R. Plaetker and N.V.  
Keygene.  
Further details: [http://www.sanger.ac.uk/Projects/D\\_rerio/](http://www.sanger.ac.uk/Projects/D_rerio/).

FEATURES  
source 1..498  
Location/Qualifiers  
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/mol\_type="genomic DNA"

/db\_xref="taxon:7955"  
/clone="DKRY-13P12"  
/tissue\_type="testis"  
/note="Vector pIndigoBAC-536"

ORIGIN  
Query Match 32.0%; Score 16; DB 11; Length 498;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 ACGACTTGTTAGTGT 46  
DB 269 ACGACTTGTTAGTGT 284

RESULT 22  
CK545847 500 bp mRNA linear EST 05-OCT-2004  
LOCUS rswb0.017116.y1 swb Bombyx mori cDNA, mRNA sequence.  
DEFINITION CK545847  
ACCESSION CK545847  
VERSION CK545847.1 GI:40930301  
KEYWORDS EST.  
SOURCE Bombyx mori (domestic silkworm)  
ORGANISM Bombyx mori  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;  
Neoptera; Endopterygota; Lepidoptera; Glossata; Ditryala;  
Bombycoidea; Bombycidae; Bombyx.  
1 (bases 1 to 500)

REFERENCE Xia, Q., Zhou, Z., Lu, C., Cheng, D., Dai, F., Li, B., Zhao, P., Zha, X.,  
Cheng, T., Chai, C., Pan, G., Xu, J., Liu, C., Lin, Y., Qian, J., Hou, Y.,  
Wu, Z., Li, G., Pan, M., Li, C., Shen, Y., Lan, X., Yuan, L., Li, T.,  
Xu, H., Yang, G., Yan, Y., Zhu, Y., Yu, M., Shen, W., Wu, D., Xiang, Z.,  
Yu, J., Wang, J., Li, R., Shi, J. P., Li, H., Li, G. Y., Su, J. N.,  
Wang, X. L., Li, G. Q., Zhang, Z. J., Wu, Q. F., Li, J., Zhang, Q. P., Wei, N.,  
Xu, J. Z., Sun, H. B., Dong, L., Liu, D. Y., Zhao, S. L., Zhao, X. L.,  
Meng, Q. S., Lan, F. D., Huang, X. G., Li, Y. Z., Pang, F., Li, C. F.,  
Li, D. W., Sun, Y. Q., Zhang, Z. P., Yang, Z., Huang, Y. Q., Xi, Y., Qi, Q. H.,  
He, D. D., Huang, H. Y., Zhang, X. W., Wang, Z. Q., Li, W. J., Cao, Y. Z.,  
Yu, J., Yu, H., Ji, H., Ye, J., Chen, H., Zhou, Y., Liu, B., Wang, J.,  
Ye, J., Ji, H., Li, S., Ni, P., Zhang, J., Zhang, Y., Zheng, H., Mao, B.,  
Mao, B., Ye, C., Li, S., Wang, J., Wong, G. K. and Yang, H.  
A draft sequence for the genome of the domesticated silkworm  
(Bombyx mori)  
Science 306 (5703), 1937-1940 (2004)

JOURNAL 15591204  
PUBMED  
COMMENT Contract: Zhonghua Xiang  
Southwest Agricultural University  
Chongqing Beibei  
Tel: 86-23-68251123  
Fax: 86-23-68251128  
Email: xzh@swu.cq.cn.  
Location/Qualifiers

FEATURES  
source 1..500  
/organism="Bombyx mori"  
/mol\_type="mRNA"  
/strain="Dazhao (P50)"  
/db\_xref="taxon:7091"  
/sex="female"  
/tissue\_type="ovary"  
/dev\_stage="5th-instar day-3 larva"  
/clone\_lib="swb"  
/note="Vector: pBluescript II SK(+)"

## ORIGIN

Query Match 32.0%; Score 16; DB 7; Length 500;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 GCTCCATCTACACG 22  
DB 69 GCTCCATCTACACG 84



**RESULT 23**  
**CEI23069**  
**LOCUS** tigr-gss-dog-17000325962242 Dog Library Canis familiaris genomic,  
**DEFINITION** genomic survey sequence.  
**ACCESSION** CEI23069  
**VERSION** CEI23069.1 GI:35218470  
**KEYWORDS** GSS.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
**REFERENCE** 1 (bases 1 to 507)  
**AUTHORS** Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,  
Rusch D.B., Delcher A.L., Pop M., Wang W., Fraser C.W. and  
Venter J.C.  
**TITLE** The dog genome: survey sequencing and comparative analysis  
**JOURNAL** Science 301 (5641), 1898-1903 (2003)  
**PUBMED** 14512627  
**COMMENT** Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.  
**FEATURES**  
**source**  
1..507  
location/Qualifiers  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"  
**ORIGIN**  
Query Match 32.0%; Score 16; DB 9; Length 507;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**Oy** 16 TACAACGCGTTACCAA 31  
|||||  
**Db** 144 TACAACGCGTTACCAA 159  
|||||

**RESULT 24**  
**AZ156816**  
**LOCUS** SP\_0049\_B2\_P10\_T7 Strongylocentrotus purpuratus, purple sea urchin,  
**DEFINITION** sperm genomic BAC library Strongylocentrotus purpuratus genomic  
clone Plate=49 Col=20 Row=L, genomic survey sequence.  
**ACCESSION** AZ156816  
**VERSION** AZ156816.1 GI:8309416  
**KEYWORDS** GSS.  
**SOURCE** Strongylocentrotus purpuratus  
**ORGANISM** Strongylocentrotus purpuratus  
**REFERENCE** 1 (bases 1 to 509)  
**AUTHORS** Cameron R.A., Mahairas G., Raetz J.P., Martinez P., Biondi T.R.,  
Wray G.A., Wallace J.C., Poustka A.J., Livingston B.T.,  
Swartzell S., Britten R.J., Davidson E.H.  
**TITLE** A sea urchin genome project: Sequence scan, virtual map, and  
additional resources  
**JOURNAL** Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
**PUBMED** 10920195  
**COMMENT** Contact: Cameron, RA, Davidson, EH, Hood, L  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-3047  
Email: acameron@caltech.edu  
Plate: 49 row: L column: 20  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 509.  
**FEATURES**  
**source**  
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location/Qualifiers  
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/mol\_type="genomic DNA"  
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/clone\_lib="Strongylocentrotus purpuratus, purple sea  
urchin, sperm genomic BAC library"  
/note="Organ: sperm; Vector: BAC63.6; BAC clones in E-Coli  
DH10B"  
**ORIGIN**  
Query Match 32.0%; Score 16; DB 9; Length 509;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**Oy** 27 ACCAAGCACTTCGTTA 42  
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**Db** 174 ACCAAGCACTTCGTTA 159  
|||||

**RESULT 25**  
**CX856756**  
**LOCUS** CX856756 533 bp mRNA  
**DEFINITION** SJPART109.T3##seg1 SJA Schistosoma japonicum cDNA, mRNA sequence.  
**ACCESSION** CX856756  
**VERSION** CX856756.1 GI:5857176  
**KEYWORDS** EST.  
**SOURCE** Schistosoma japonicum  
**ORGANISM** Schistosoma japonicum  
**REFERENCE** 1 (bases 1 to 533)  
**AUTHORS** Han Z.  
**TITLE** Schistosoma japonicum SJA EST sequences  
**JOURNAL** Unpublished (2005)  
**COMMENT** Contact: Zeguang Han  
Chinese National Human Genome Center at Shanghai  
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
201203, P. R. China  
Tel: 86-21-50801919 (ex.45)  
Fax: 86-21-50801922  
Email: hanzg@chgc.sh.cn.  
**FEATURES**  
**source**  
1..533  
location/Qualifiers  
/organism="Schistosoma japonicum"  
/mol\_type="mRNA"  
/db\_xref="taxon:6182"  
/clone\_lib="SJA"  
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Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
**Oy** 8 CTCGATCTCAACGT 23  
|||||  
**Db** 472 CTCGATCTCAACGT 487  
|||||

**RESULT 26**  
**AI294195**  
**LOCUS** AI294195 540 bp mRNA  
**DEFINITION** LP07515.5prlme LP Drosophila melanogaster larval-early pupal P0T2



Drosophila melanogaster cDNA clone LP07515 5prime similar to D28749: Fruitfly mRNA for DE-cadherin, complete cds, mRNA sequence.

ACCESSION AI294195  
VERSION AI294195.1 GI:3943602  
KEYWORDS EST.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 540)  
AUTHORS Harvey,D., Brokstein,P., Hong,L., Evans-Holm,M., Su,C., Tsang,G., Lewis,S. and Rubin,G.M.  
TITLE BDGP/HMI Drosophila EST Project  
JOURNAL Unpublished (2001)  
COMMENT Contact: Stapleton, M.  
BDGP Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: <http://www.fruitfly.org/EST/estefruitfly.berkeley.edu>  
hit genomic sequence DS02397; hit genomic sequence DS03550; hit P element sequence 1(2)10469  
plate: 75 row: B column: 3  
High quality sequence scrop: 343.  
Location/Qualifiers  
1..540  
/organism="Drosophila melanogaster"  
/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="LP07515"  
/sex="male and female"  
/dev\_stage="larvae-pupae"  
/lab\_host="DH5-alpha"  
/clone\_lib="LP Drosophila melanogaster larval-early pupal POT2"  
/note="Organ: whole body; Vector: POT2; Site 1: EcoRI; Site 2: XhoI; Sized fractionated cDNAs were directly ligated into POT2. Plasmid cDNA library."

ORIGIN  
Query Match 32.0%; Score 16; DB 1; Length 540;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 22 GTGTACCAACGACTT 37  
DB 195 GTGTACCAACGACTT 180

RESULT 27  
AV677273 550 bp mRNA linear EST 26-MAY-2005  
LOCUS AV677273 Nori Satoh unpublished cDNA library Ciona intestinalis  
DEFINITION AV677273 Nori Satoh unpublished cDNA library Ciona intestinalis  
ACCESSION AV677273  
VERSION AV677273.1 GI:10115272  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 550)  
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-I,T.  
TITLE Expressed genes in Ciona intestinalis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113

Email: [satoh@ascidian.zool.kyoto-u.ac.jp](mailto:satoh@ascidian.zool.kyoto-u.ac.jp).

FEATURES  
source  
1..550  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="rcitb5k1"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud embryo"  
/clone\_lib="Nori Satoh unpublished cDNA library"

ORIGIN  
Query Match 32.0%; Score 16; DB 1; Length 550;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 23 TGTACCAACGACTTC 38  
DB 277 TGTACCAACGACTTC 292

RESULT 28  
CA697847 552 bp mRNA linear EST 26-NOV-2002  
LOCUS CA697847  
DEFINITION wtk4.pk0024.fl wtk4 Triticum aestivum cDNA clone wtk4.pk0024.fl 5'  
end, mRNA sequence.  
ACCESSION CA697847 GI:25419639  
VERSION CA697847  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 552)  
AUTHORS Tingey,S.V., Powell,W., Wolters,P., Dolan,M., Hainey,C., Yuan,Z., Miao,G., Caraher,N. and Hanafey,M.K.  
TITLE Dupont Wheat cDNA Sequence  
JOURNAL Unpublished (2002)  
COMMENT Contact: Scott V. Tingey  
Crop Genetics  
B. I. Dupont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: [Scott.V.Tingey@USA.dupont.com](mailto:Scott.V.Tingey@USA.dupont.com)  
Seq primer: M13.  
Location/Qualifiers  
1..552  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Stephens"  
/db\_xref="taxon:4565"  
/clone="wtk4.pk0024.fl"  
/tissue\_type="leaf"  
/clone\_lib="wtk4"  
/note="Vector: pBluescript SK+; Site 1: EcoRI; Site 2: XhoI; Wheat (Triticum aestivum L.) seedlings 4 hr after treatment with 6-iodo-3-propyl-2-propyl-4(3H)-quinazolinone"

ORIGIN  
Query Match 32.0%; Score 16; DB 6; Length 552;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 16 TACAACGTGTACCA 31  
DB 482 TACAACGTGTACCA 497

RESULT 29  
BU803375



LOCUS BU803375 577 bp mRNA linear EST 23-OCT-2003  
 DEFINITION SJF Schistosoma japonicum cDNA, mRNA sequence.  
 ACCESSION BU803375  
 VERSION BU803375.1 GI:28360382  
 KEYWORDS EST  
 SOURCE Schistosoma japonicum  
 ORGANISM Schistosoma japonicum  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida; Schistosomatidae; Schistosomidae.  
 1 (bases 1 to 577)  
 Hu, M., Yan, Q., Shen, D.K., Liu, F., Zhu, Z.D., Song, H.D., Xu, X.R., Wang, Z.J., Kong, Y.P., Zeng, L.C., Wu, J., Zhang, X., Wang, J.J., Xu, X.N., Wang, S.Y., Fu, G., Zhang, X.L., Wang, Z.Q., Brindley, P.J., McManus, D.P., Xue, C.L., Feng, Z., Chen, Z., and Han, Z.G. Evolutionary and biomedical implications of a Schistosoma japonicum complementary DNA resource  
 Nat. Genet. 35 (2), 139-147 (2003)  
 1297349  
 JOURNAL PUBMED  
 COMMENT Contact: Zeguang Han  
 Chinese National Human Genome Center at Shanghai  
 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai  
 201203, P. R. China  
 Tel: 86-21-50801919 (ex. 45)  
 Fax: 86-21-50801922  
 Email: hanzg@chgc.sh.cn.  
 Location/Qualifiers  
 1..577  
 /organism="Schistosoma japonicum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6182"  
 /sex="female"  
 /tissue\_type="whole body"  
 /dev\_stage="adult"  
 /lab\_host="rabbit"  
 /clone\_lib="SJF"  
 ORIGIN  
 Query Match 32.0%; Score 16; DB 5; Length 577;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 8 CTCGATCTACACGT 23  
 Db 473 CTCGATCTACACGT 488  
 RESULT 30 585 bp mRNA linear EST 15-MAY-2003  
 CB402237  
 LOCUS OSTRF209B1\_1 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.  
 DEFINITION CB402237  
 ACCESSION CB402237.1 GI:30743964  
 VERSION CB402237.1 GI:30743964  
 KEYWORDS EST  
 SOURCE Caenorhabditis elegans  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
 1 (bases 1 to 585)  
 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression  
 Nat. Genet. (2003) In press  
 JOURNAL COMMENT Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180

Fax: 617 632 5739  
 Email: Marc.Vidal@fci.harvard.edu  
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david\_hill@fci.harvard.edu or marc\_vidal@fci.harvard.edu  
 POLY=A=No.  
 Location/Qualifiers  
 1..585  
 /organism="Caenorhabditis elegans"  
 /mol\_type="mRNA"  
 /strain="N2"  
 /db\_xref="taxon:6239"  
 /sex="Hermaphrodite and male"  
 /tissue\_type="whole animal"  
 /dev\_stage="mixed stage"  
 /clone\_lib="AD-wrmcDNA"  
 /note="The AD-wrmcDNA library was generated with poly(A)+ RNA isolated from both hermaphrodite and male N2 worms of all larval stages, embryos, adults and dauers and the subsequent generation of cDNAs by poly(A) priming. The cDNAs were cloned into pPC86"  
 ORIGIN  
 Query Match 32.0%; Score 16; DB 6; Length 585;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 18 CACGCTTACCAACG 33  
 Db 514 CACGCTTACCAACG 529  
 RESULT 31 585 bp mRNA linear EST 15-MAY-2003  
 CB402242  
 LOCUS OSTRF209B1\_2 AD-wrmcDNA Caenorhabditis elegans CDNA, mRNA sequence.  
 DEFINITION CB402242  
 ACCESSION CB402242.1 GI:30743969  
 VERSION CB402242.1 GI:30743969  
 KEYWORDS EST  
 SOURCE Caenorhabditis elegans  
 ORGANISM Caenorhabditis elegans  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
 1 (bases 1 to 585)  
 Reboul, J., Vaglio, P., Rual, J.F., Lamesch, P., Martinez, M., Armstrong, C.M., Li, S., Jacotot, L., Bertin, N., Janky, R., Moore, T., Hudson, J.R., Hartley, J.L., Brasch, M.A., Vandenhaute, J., Boulton, S., Endress, G.A., Jenna, S., Chevet, E., Papasotiropoulos, V., Tolia, P.P., Placek, J., Snyder, M., Huang, R., Chance, M.R., Lee, H., Doucette-Stamm, L., Hill, D.E. and Vidal, M. C. elegans ORFome version 1.1: experimental verification of the genome annotation and resource for proteome-scale protein expression  
 Nat. Genet. (2003) In press  
 JOURNAL COMMENT Contact: Vidal M  
 Marc Vidal Laboratory  
 Dana Farber Cancer Institute  
 1 Jimmy Fund Way Smith 858, BOSTON, MA 02115, USA  
 Tel: 617 632 5180  
 Fax: 617 632 5739  
 Email: Marc.Vidal@fci.harvard.edu  
 Sequence tag of Gateway entry clones. The primers used were designed on the predicted protein encoding ORF. C. elegans ORFome cloning project : Contact david\_hill@fci.harvard.edu or marc\_vidal@fci.harvard.edu  
 POLY=A=No.  
 Location/Qualifiers  
 1..585  
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 /mol\_type="mRNA"  
 /strain="N2"  
 /db\_xref="taxon:6239"

FEATURES  
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 1..585  
 /organism="Caenorhabditis elegans"  
 /mol\_type="mRNA"  
 /strain="N2"  
 /db\_xref="taxon:6239"



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/ssex="Hermaphrodite and male"
/tissue_type="whole animal"
/dev_stage="mixed stage"
/clone_lib="AD-wrmcDNA"
/notes="The AD-wrmcDNA library was generated with poly(A)+
RNA isolated from both hermaphrodite and male N2 worms of
all larval stages, embryos, adults and dauers and the
subsequent generation of cDNAs by poly(A) priming. The
cDNAs were cloned into pC86"

ORIGIN
Query Match      32.0%; Score 16; DB 6; Length 585;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      18 CAACGTGTACCAACG 33
      |||||
      514 CAACGTGTACCAACG 529

RESULT 32
CK103491      586 bp      mRNA      linear      EST 01-DEC-2003
LOCUS      G120P06.5BR Populus tremula wood cDNA library Populus tremula x
DEFINITION Populus tremuloides cDNA clone G120P06 5', mRNA sequence.
ACCESSION CK103491 GI:38587816
VERSION CK103491.1 GI:38587816
KEYWORDS EST.
SOURCE Populus tremula x Populus tremuloides
ORGANISM Populus tremula x Populus tremuloides
          Buxaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
          Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
          rosids; eurosids I; Malpighiales; Salicaceae; Saliceae; Populus.
          1 (bases 1 to 586)
REFERENCE Sterky,F., Bhaleao,R.R., Umeberg,P., Segerman,B., Nilsson,P.,
          Brunner,A.M., Charbonnel-Campas,L., Lindvall,J.J., Tandere,K.,
          Strauss,S.H., Sundberg,B., Gustafsson,P., Uhlen,M., Bhaleao,R.P.,
          Nilsson,O., Sandberg,G., Karlsson,J., Lundberg,J. and Jansson,S.
          A Populus EST resource for plant functional genomics
          Proc. Natl. Acad. Sci. U.S.A. 101 (38), 13951-13956 (2004)
PUBMED 15353603
COMMENT Other ESTs: G120P06Y, G120P06.3PR
          Contact: Bo Segerman
          Umea Plant Science Center, Department of Plant Physiology
          Umea University
          901 87 Umea, Sweden
          Tel: +46 90 786 5279
          Fax: +46 90 786 6676
          Email: bo.segerman@planphys.umu.se.

FEATURES
          source
          1..586
          /organism="Populus tremula x Populus tremuloides"
          /mol_type="mRNA"
          /db_xref="taxon:47664"
          /clone_lib="G120P06"
          /tissue_type="tension wood"
          /clone_lib="Populus tension wood cDNA library"

ORIGIN
Query Match      32.0%; Score 16; DB 7; Length 586;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      6 GGCTCCATCTACAC 21
      |||||
      535 GGCTCCATCTACAC 550

RESULT 33
CK533266      588 bp      mRNA      linear      EST 05-OCT-2004
LOCUS      rwmB0.001220.y1 Bwg Bombyx mori cDNA, mRNA sequence.
DEFINITION
ACCESSION CK533266
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VERSION CK533266.1 GI:40917719
KEYWORDS EST.
SOURCE Bombyx mori (domestic silkworm)
ORGANISM Bombyx mori
          Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
          Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
          Bombycoidea; Bombycidae; Bombyx.
          1 (bases 1 to 588)
REFERENCE Xia,Q., Zhou,Z., Lu,C., Cheng,D., Dai,F., Li,B., Zhao,P., Zha,X.,
          Cheng,T., Chai,C., Pan,G., Xu,J., Liu,C., Lin,Y., Qian,J., Hou,Y.,
          Wu,Z., Li,G., Pan,W., Li,C., Shen,Y., Lan,X., Yuan,L., Li,T.,
          Xu,H., Yang,G., Wan,Y., Zhu,Y., Yu,M., Shen,W., Wu,D., Xiang,Z.,
          Yu,J., Wang,J., Li,R.Q., Shi,J.P., Li,H., Li,G.Y., Su,D.N.,
          Wang,X.L., Li,G.Q., Zhang,Z.J., Wu,Q.F., Li,J., Zhang,Q.P., Wei,N.,
          Xu,J.Z., Sun,H.B., Dong,L., Liu,D.Y., Zhao,S.L., Zhang,X.L.,
          Meng,Q.S., Lan,P.D., Huang,X.G., Li,Y.Z., Fang,F., Li,C.F.,
          Li,D.W., Sun,Y.Q., Zhang,Z.P., Yang,Z., Huang,Y.Q., Xi,Y., Qi,Q.H.,
          He,D.D., Huang,H.Y., Zhang,X.W., Wang,Z.Q., Li,W.J., Cao,Y.Z.,
          Yu,Y., Yu,H., Ji,H., Ye,J., Chen,H., Zhou,Y., Liu,B., Wang,J.,
          Ye,J., Ji,H., Li,S., Ni,P., Zhang,J., Zhang,Y., Zheng,H., Mao,B.,
          Mao,B., Ye,C., Li,S., Wang,J., Wong,G.K. and Yang,H.
          A draft sequence for the genome of the domesticated silkworm
          (Bombyx mori)
          Science 306 (5703), 1937-1940 (2004)
          15591204
          Contact: Zhonghui Xiang
          Southwest Agricultural University
          Chongqing, Beibei
          Tel: 86-23-68251123
          Fax: 86-23-68251128
          Email: xzh@swau.cn.

FEATURES
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          /organism="Bombyx mori"
          /mol_type="mRNA"
          /strain="Dazhao (P50)"
          /db_xref="taxon:7091"
          /sex="male"
          /tissue_type="testis"
          /dev_stage="5th-instar day-3 larva"
          /clone_lib="Bwg"
          /note="Vector: pBluescript II SK(+)"

ORIGIN
Query Match      32.0%; Score 16; DB 7; Length 588;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      7 GCTCCATCTACACG 22
      |||||
      222 GCTCCATCTACACG 237

RESULT 34
AZ151143      588 bp      DNA      linear      GSS 28-AUG-2000
LOCUS      SP_0047_A1_F04_T7 Strongylocentrotus purpuratus, purple sea urchin,
DEFINITION sperm genomic BAC library Strongylocentrotus purpuratus genomic
          clone Plate=47 Col=7 Row=K, genomic survey sequence.
          AZ151143
          AZ151143.1 GI:8303044
          GSS.
          Strongylocentrotus purpuratus
          Strongylocentrotus purpuratus
          Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
          Echinoidea; Echinoidea; Echinodermata; Echinozoa;
          Strongylocentrotidae; Strongylocentrotus.
          1 (bases 1 to 588)
REFERENCE Cameron,R.A., Mahairas,G., Rast,J.P., Martinez,P., Biondi,T.R.,
          Swartzell,S., Wallace,J.C., Pousetka,A.J., Livingston,B.T.,
          Wray,G.A., Ettensohn,C.A., Vennrich,H., Bittner,R.J., Davidson,E.H.
          and Hood,L.
          A sea urchin genome project: Sequence scan, virtual map, and
```



JOURNAL additional resources  
Proc. Natl. Acad. Sci. U.S.A. 97 (17), 9514-9518 (2000)  
PUBMED 10920195  
COMMENT Contact: Cameron, RA, Davidson, EH, Hood, L  
Division of Biology 156-29  
California Institute of Technology  
Pasadena California 91125, USA  
Tel: (626) 395-8421  
Fax: (626) 793-1047  
Email: acameron@caltech.edu  
Plate: 47 row: K column: 7  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 588.

## FEATURES

source  
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Location/Qualifiers  
/organism="Strongylocentrotus purpuratus"  
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/clone="Plate=47 Col=7 Row=K"  
/clone\_lib="Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library"  
/note="Organ: sperm; Vector: BACe3.6; BAC Clones in E-Coli DH10B"

## ORIGIN

Query Match 32.0%; Score 16; DB 9; Length 588;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 AACGTTACCAACA 34  
|||||||  
Db 432 AACGTTACCAACA 447

RESULT 35  
BM398361 597 bp mRNA linear EST 28-MAY-2004  
LOCUS BM398361 Yutaka Satou unpublished cDNA library, embryo whole animal  
DEFINITION Ciona intestinalis cDNA clone clem826p22 3', mRNA sequence.  
ACCESSION BM398361  
VERSION BM398361.1 GI:47814189  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 597)  
AUTHORS Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.  
TITLE Expressed genes in Ciona intestinalis (2004)  
JOURNAL Unpublished (2004)  
COMMENT Contact: Yutaka Satou  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4095  
Fax: 81-75-705-1113  
Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

## FEATURES

source  
1..597  
Location/Qualifiers  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="clem826p22"  
/tissue\_type="whole animal"  
/dev\_stage="embryo"  
/clone\_lib="Yutaka Satou unpublished cDNA library, embryo whole animal"

## ORIGIN

Query Match 32.0%; Score 16; DB 5; Length 597;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 TGTACCAAGCACTTC 38  
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Db 199 TGTACCAAGCACTTC 214

RESULT 36  
B1240948/c 613 bp mRNA linear EST 12-JUL-2001  
LOCUS B1240948  
DEFINITION R37915.Sprine RB Drosophila melanogaster normalized Embryo pFlc-1  
Drosophila melanogaster cDNA clone R37915 5 similar to shg:  
FBan0003722 'cell adhesion' located on: 2R 57B16-57B16.1;  
05/12/2001, mRNA sequence.  
B1240948  
ACCESSION B1240948.1 GI:14709591  
VERSION B1240948  
KEYWORDS EST.  
SOURCE Drosophila melanogaster (fruit fly)  
ORGANISM Drosophila melanogaster  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;  
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
Ephydroidea; Drosophilidae; Drosophila.  
REFERENCE 1 (bases 1 to 613)  
AUTHORS Stapleton, M., Brokstein, P., Hong, L., Tyler, D., Berman, B.,  
Carlson, J., Champagne, M., Dorsett, V., Farfan, D., Frise, E.,  
George, R., Mungall, C.J., Nuno, J., Pacled, J., Paragas, V., Park, S.,  
Phouanavong, S., Wan, K., Yu, C., Lewis, S.E., Celinker, S. and  
Rubin, G.M.  
TITLE BDGP/HMI RE Drosophila EST Project  
JOURNAL Unpublished (2001)  
COMMENT Contact: Stapleton, M.  
BDGP Lawrence Berkeley National Lab  
One Cyclotron Rd, Berkeley, CA 94720, USA  
Fax: 510 486 6798  
Email: http://www.fruitfly.org/EST\_estefruitfly.berkeley.edu  
hit genomic AB003452: arm:2R [15705380..16010295]  
estimated-cyto:57B3-57B20: 05/12/2001 hit P element 1(2)10469:  
1(2)10469 G00624 inserted at base unknown 5' end of P element  
Plasmid rescue: 05/12/2001  
Plate: RB.379 row: B column: 3  
High quality sequence stop: 542.

## FEATURES

source  
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Location/Qualifiers  
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/mol\_type="mRNA"  
/db\_xref="taxon:7227"  
/clone="R37915"  
/sex="male and female"  
/dev\_stage="0-24 hours mixed stage embryonic"  
/lab\_host="DH5-alpha TONA"  
/clone\_lib="RE Drosophila melanogaster normalized Embryo pFlc-1"  
/note="Organ: embryo; Vector: pFlc1, Site 1: XhoI, Site 2: BamHI, library was kindly generated by Piero Carninci at the RIKEN. The library was normalized and excised using Cre recombinase. Plasmid cDNA library."

## ORIGIN

Query Match 32.0%; Score 16; DB 2; Length 613;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 GTGTTACCAAGCACTT 37  
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Db 222 GTGTTACCAAGCACTT 207

RESULT 37  
CF645307 628 bp mRNA linear EST 02-OCT-2003  
LOCUS CF645307  
DEFINITION K31 H07 Filamentous Forced Diploid Ustilago maydis cDNA 3', mRNA  
sequence.



ACCESSION CP645307  
 VERSION CF645307.1 GI:37415329  
 KEYWORDS EST  
 SOURCE Ustilago maydis  
 ORGANISM Ustilago maydis  
 Eukaryota; Fungi; Basidiomycota; Ustilaginomycetes; Ustilaginomycetidae; Ustilaginales; Ustilaginaceae; Ustilago.

REFERENCE  
 TITLE 1 (bases 1 to 628)  
 Nugent, K.G., Choffe, K. and Saville, B.J.  
 Gene expression during Ustilago maydis diploid filamentous growth: EST library creation and analyses  
 Fungal Genet. Biol. 41 (3), 349-360 (2004)  
 14761795

JOURNAL PUBMED  
 COMMENT Contact: Barry J. Saville  
 Saville Lab  
 University of Toronto  
 3359 Mississauga Road North, Mississauga, ON, L5L 1C6, Canada  
 Tel: 905 569 4702  
 Fax: 905 828 3792  
 Email: bsaville@utm.utoronto.ca  
 Plate: UTM-UM-D128/9-031-UTM row: 07 column: H  
 Seq primer: T7 Reverse (5' GAGTAATACGACTCAGCTATAGG 3')  
 High quality sequence stop: 628.  
 Location/Qualifiers  
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 /strain="FBD12"  
 /db\_xref="taxon:5270"  
 /cell\_type="mycelia"  
 /dev\_stage="Filamentous forced Diploid"  
 /clone\_lib="Filamentous Forced Diploid"  
 /note="Vector: pSPORT; mRNA was extracted from diploid mycelia. A cDNA library was constructed and unidirectionally cloned into pSPORT plasmid, with the use of the Superscript II cDNA library construction kit."

ORIGIN  
 Query Match 32.0%; Score 16; DB 6; Length 628;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 19 AACGTGTACCAACGA 34  
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 Db 93 AACGTGTACCAACGA 108

RESULT 38  
 CC157381 629 bp DNA linear GSS 29-APR-2003  
 LOCUS ig19c03.g1 WGS-ZmaysF (DH5a methyl filtered) Zea mays genomic clone  
 DEFINITION ig19c03, genomic survey sequence.  
 CC157381  
 VERSION CC157381.1 GI:30182161  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 629)  
 Rabnowicz, P.D., O'Shaughnessy, A.L., Balija, V., Dedhia, N., Katzenburger, F., King, L., Miller, B., Muller, S., Nascimben, L., Zlatavern, I., McCombie, W.R. and Martienssen, R.A.  
 Genomic shotgun sequences from Zea mays (methyl-filtered) Unpublished (2002)  
 Contact: W. Richard McCombie  
 Lita Annenberg Hazen Genome Sequencing Center  
 Cold Spring Harbor Laboratory  
 PO Box 100, Cold Spring Harbor, NY 11724, USA  
 Tel: 516 367 8884  
 Fax: 516 367 8874  
 Email: mcombie@cshl.org

Plate: ig19 row: C column: 03  
 Seq primer: -21M13UnivRev  
 Class: Shotgun  
 High quality sequence stop: 629.  
 Location/Qualifiers  
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 /db\_xref="taxon:4577"  
 /clone="ig19c03"  
 /lab\_host="DH5a"  
 /clone\_lib="WGS-ZmaysF (DH5a methyl filtered)"  
 /note="Organ: immature ears; Site 1: Xba I; Site 2: Xba I; The vector was digested with XbaI and one nucleotide was added by fill in in the recessive 3' end. The genomic DNA was nebulized, end repaired, adaptor ligated and size fractionated using Sephadex. The resulting fragments were between 0.8 and 3 kb and were cloned into the vector (XbaI reads in M13mp19, B/g reads in pUC19). The same ligation was transformed into DH5a."

FEATURES  
 source

ORIGIN  
 Query Match 32.0%; Score 16; DB 9; Length 629;  
 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 22 GTGTACCAAGACTT 37  
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 Db 416 GTGTACCAAGACTT 431

RESULT 39  
 BM012882 645 bp mRNA linear EST 13-OCT-2002  
 LOCUS BM012882 Nori Satoh unpublished cDNA library, blood cells Ciona  
 DEFINITION BM012882 Nori Satoh unpublished cDNA library, blood cells Ciona  
 intestinalis cDNA clone rcibd046101 3', mRNA sequence.  
 BM012882  
 ACCESSION BM012882.1 GI:23928689  
 VERSION BM012882  
 KEYWORDS EST.  
 SOURCE Ciona intestinalis  
 ORGANISM Ciona intestinalis  
 Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cloniidae; Ciona.  
 1 (bases 1 to 645)  
 REFERENCE Satoh, Y., Satake, M., Azumi, K., Nonaka, M., Shin-I, T., Kohara, Y. and Satoh, N.  
 Expressed genes in Ciona intestinalis (2002)  
 TITLE Unpublished (2002)  
 JOURNAL Contact: Nori Satoh  
 COMMENT Department of Zoology  
 Kyoto University  
 Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
 Tel: 81-75-753-4081  
 Fax: 81-75-705-1113  
 Email: satoh@ascidian.zool.kyoto-u.ac.jp.

FEATURES  
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 /organism="Ciona intestinalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:7719"  
 /clone="rcibd046101"  
 /tissue\_type="blood cells"  
 /clone\_lib="Nori Satoh unpublished cDNA library, blood cells"

ORIGIN  
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 Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 TGTACCAAGACTTC 38  
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DB 311 TGTACCAAGACTTC 326

## RESULT 40

LOCUS

DEFINITION BM344262 647 bp mRNA linear EST 27-MAY-2004

ACCESION BM344262 Yutaka Satou unpublished CDNA library, embryo whole animal

VERSION BM344262 Ciona intestinalis cDNA clone ciem826p22 5', mRNA sequence.

KEYWORDS BM344262.1 GI:47756063

SOURCE

ORGANISM

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 647)

Satou,Y., Shin-I,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2004)

Unpublished (2004)

Contact: Yutaka Satou

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Kyoto University

Sakyo-ku, Kyoto, Kyoto 606-8502, Japan

Tel: 81-75-753-4095

Fax: 81-75-705-1113

Email: yutaka@ascidian.zool.kyoto-u.ac.jp.

location/Qualifiers

1. 647

/organism="Ciona intestinalis"

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/clone="ciem826p22"

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whole animal"

## ORIGIN

Query Match

Best Local Similarity 32.0%; Score 16; DB 5; Length 647;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 TGTACCAAGACTTC 38

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DB 399 TGTACCAAGACTTC 384

Search completed: April 11, 2006, 21:43:09  
Job time : 751.433 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 362.437 Seconds  
(without alignments)  
9253.359 Million cell updates/sec

Title: US-10-712-654-24

Perfect score: 59

Sequence: 1 ggtagaagcgcgagatagcgg.....attagaacgactaacgcg 59

Scoring table:

GAPop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

GenEmbl: \*  
1: gb\_ba: \*  
2: gb\_in: \*  
3: gb\_env: \*  
4: gb\_om: \*  
5: gb\_ov: \*  
6: gb\_pat: \*  
7: gb\_ph: \*  
8: gb\_pr: \*  
9: gb\_ro: \*  
10: gb\_rcs: \*  
11: gb\_by: \*  
12: gb\_un: \*  
13: gb\_vi: \*  
14: gb\_htg: \*  
15: gb\_pl: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	59	100.0	867	6	AR366274 Sequence
2	59	100.0	1278	6	AX353779 Sequence
3	59	100.0	1281	6	CS135645 Sequence
4	59	100.0	1694	1	AY921578 Sequence
5	59	100.0	1707	6	CS135643 Sequence
6	59	100.0	1710	6	AR570597 Sequence
7	59	100.0	1785	6	AX353781 Sequence
8	59	100.0	2160	6	169387 Sequence
9	59	100.0	2208	6	CS135652 Sequence
10	59	100.0	2208	6	AX353783 Sequence
11	59	100.0	2211	6	CS061689 Sequence
12	59	100.0	2211	6	AR570595 Sequence
13	59	100.0	2225	1	BAN413937 Sequence
14	59	100.0	2227	1	AT700758 Sequence
15	59	100.0	2231	1	BAN413936 Sequence
16	59	100.0	2292	1	AR570596 Sequence
17	59	100.0	2295	1	AY97299 Sequence
18	59	100.0	2295	6	CS135651 Sequence

19	59	100.0	2295	6	AR570594 Sequence
20	59	100.0	2369	1	AF306778 Bacillus
21	59	100.0	2369	1	AF306779 Bacillus
22	59	100.0	2369	1	AF306780 Bacillus
23	59	100.0	2369	1	AF306781 Bacillus
24	59	100.0	2369	1	AF306782 Bacillus
25	59	100.0	2369	1	AF306783 Bacillus
26	59	100.0	2549	1	AF268967 Bacillus
27	59	100.0	2605	6	AX933603 Sequence
28	59	100.0	2709	6	133400 Sequence
29	59	100.0	2709	6	169378 Sequence
30	59	100.0	4235	1	BACPAG Sequence
31	59	100.0	4235	6	133396 Sequence
32	59	100.0	4235	6	169374 Sequence
33	59	100.0	181654	1	AF065404 Bacillus
34	59	100.0	181677	1	AE011190 Bacillus
35	59	100.0	181677	1	AE011736 Bacillus
36	21	35.6	174720	14	AC111756 Sequence
37	21	35.6	240276	14	AC097773 Rattus
38	21	35.6	249338	14	AC094966 Rattus
39	21	35.6	258249	14	AC094968 Rattus
40	20	33.9	245812	14	AC131444 Rattus
41	20	33.9	247053	14	AC112897 Rattus
42	19	33.9	326183	14	AC137245 Rattus
43	19	32.2	797	10	BV041634 Mus
44	19	32.2	164733	14	AC117341 Rattus
45	19	32.2	166650	9	AC134795 Mus
46	19	32.2	175057	9	AL671893 Mus
47	19	32.2	178929	9	AC121957 Mus
48	19	32.2	188665	9	AC126048 Mus
49	19	32.2	194229	9	AC140214 Mus
50	19	32.2	207168	9	AC157582 Mus
51	19	32.2	220855	9	AC153659 Mus
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53	19	32.2	235417	14	AC136273 Rattus
54	19	32.2	243195	14	AC094523 Rattus
55	19	32.2	259850	14	AC128887 Rattus
56	19	32.2	267417	14	AC096094 Rattus
57	19	32.2	284060	14	AC130058 Rattus
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59	18	30.5	156183	9	BD193698 Enterococ
60	18	30.5	166328	14	AC118877 Rattus
61	18	30.5	190086	14	AC112835 Rattus
62	18	30.5	192016	9	AC102426 Mus
63	18	30.5	200387	9	AC140312 Mus
64	18	30.5	206898	9	AC152949 Mus
65	18	30.5	232877	14	AC094618 Rattus
66	18	30.5	235133	14	AC115375 Rattus
67	18	30.5	236385	14	AC094936 Rattus
68	18	30.5	239747	14	AC079524 Mus
69	18	30.5	243194	14	AC099477 Rattus
70	18	30.5	244675	14	AC094935 Rattus
71	18	30.5	256808	14	AC073766 Mus
72	18	30.5	300225	1	AE016949 Sequence
73	18	30.5	331139	14	AC020958 Mus
74	18	28.8	382	10	BV051279 Mus
75	17	28.8	578	3	AY919663 Sequence
76	17	28.8	696	10	BV649089 Sequence
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79	17	28.8	110000	1	BA000012_14 Continuation
80	17	28.8	119497	14	AC108843 Mus
81	17	28.8	120490	5	AL929339 Mus
82	17	28.8	144370	5	CR383666 Sequence
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84	17	28.8	155062	14	BX005172 Homo
85	17	28.8	155962	8	AC099055 Homo
86	17	28.8	166191	8	AC093745 Homo
87	17	28.8	172546	9	AC124198 Mus
88	17	28.8	191790	9	AC121773 Mus
89	17	28.8	192136	9	AC133508 Mus
90	17	28.8	199065	9	AC116503 Mus
91	17	28.8	199065	9	AC116503 Mus



C 92	17	28.8	199421	8	AL691515	Human DNA	C 165	16	27.1	65625	8	AC145546	AC145546 Homo sapi
C 93	17	28.8	205790	5	AL805965	Mouse DNA	C 166	16	27.1	68378	14	AC113131	AC113131 Homo sapi
C 94	17	28.8	209097	9	CR381673	Zebrafish	C 167	16	27.1	69227	14	AC074060	AC074060 Homo sapi
C 95	17	28.8	212613	9	AC104414	Mus muscu	C 168	16	27.1	70370	14	AC112088	Continuation (4 of
C 96	17	28.8	221603	9	AC133604	AC133604	C 169	16	27.1	71202	14	AC105090	Continuation (4 of
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C 98	17	28.8	227138	14	AC094478	Rattus no	C 171	16	27.1	73320	9	BX897717	BX897717 Mouse DNA
C 99	17	28.8	227837	14	AC125885	Rattus no	C 172	16	27.1	75393	9	BX465839	BX465839 Mouse DNA
C 100	17	28.8	263744	14	AF401201	AC125885	C 173	16	27.1	76437	5	CR252724	CR252724 Zebrafish
C 101	17	28.8	299140	14	AC110368	AF401201 Mus muscu	C 174	16	27.1	80167	14	AC020038	AC020038 Drosophill
C 102	16	27.1	99	6	CS064575	AC110368 Rattus no	C 175	16	27.1	87356	8	AL160160	AL160160 Human DNA
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C 105	16	27.1	403	6	CO113276	CO713462 Sequence	C 178	16	27.1	95577	8	AP005627	AP005627 Homo sapi
C 106	16	27.1	403	6	CO152151	CO113276 Sequence	C 179	16	27.1	95735	8	AC105110	AC105110 Homo sapi
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C 108	16	27.1	403	6	CO235503	CO185622 Sequence	C 181	16	27.1	99392	15	AC000103	AC000103 Genomic B
C 109	16	27.1	403	6	CO273067	CO235503 Sequence	C 182	16	27.1	99595	15	AC151742	AC151742 Medicago
C 110	16	27.1	403	6	CO310585	CO273067 Sequence	C 183	16	27.1	104638	8	AB008921	AB008921 Unculture
C 111	16	27.1	403	6	CO347352	CO310585 Sequence	C 184	16	27.1	10638	3	AL359770	AL359770 Human DNA
C 112	16	27.1	453	6	CS064605	CO347352 Sequence	C 185	16	27.1	110000	1	CP000017	Continuation (8 of
C 113	16	27.1	477	11	AY333963	CS064605 Sequence	C 186	16	27.1	110000	1	CP000017	Continuation (4 of
C 114	16	27.1	531	9	AY041582	AY333963 Cat.A det	C 187	16	27.1	110000	14	AC009575	Continuation (3 of
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C 118	16	27.1	588	6	CO100197	CS106904 Sequence	C 191	16	27.1	110000	15	CR382124	Continuation (11 o
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C 122	16	27.1	588	6	CO260528	CO222575 Sequence	C 195	16	27.1	114032	8	AL137845	AL137845 Homo sapi
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C 124	16	27.1	588	6	CO334660	CO298153 Sequence	C 197	16	27.1	118227	14	AC153114	AC153114 Daerypus n
C 125	16	27.1	588	6	CO072065	CO334660 Sequence	C 198	16	27.1	120571	8	CNS01DT3	AL332633 Human chr
C 126	16	27.1	593	6	CO072065	CO072065 Sequence	C 199	16	27.1	120816	8	AC067890	AC067890 Homo sapi
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C 128	16	27.1	593	6	CO140309	CO101318 Sequence	C 201	16	27.1	123909	15	AC138451	AC138451 Medicago
C 129	16	27.1	593	6	CO176331	CO140309 Sequence	C 202	16	27.1	125452	14	AC139841	AC139841 Medicago
C 130	16	27.1	593	6	CO223639	CO176331 Sequence	C 203	16	27.1	130626	8	HS114G22	AL000056 Human DNA
C 131	16	27.1	593	6	CO261621	CO223639 Sequence	C 204	16	27.1	135055	14	AC010056	AC010056 Drosophill
C 132	16	27.1	593	6	CO262937	CO261621 Sequence	C 205	16	27.1	135055	14	AC011909	AC011909 Drosophill
C 133	16	27.1	593	6	CO289906	CO262937 Sequence	C 206	16	27.1	135351	8	AC068279	AC068279 Homo sapi
C 134	16	27.1	593	6	CO335778	CO289906 Sequence	C 207	16	27.1	137242	8	AC024323	AC024323 Homo sapi
C 135	16	27.1	603	6	AR320160	CO335778 Sequence	C 208	16	27.1	138692	14	CR847500	CR847500 Dario rer
C 136	16	27.1	687	10	BV555221	AR320160 Sequence	C 209	16	27.1	144048	8	AC154782	AC154782 Mus muscu
C 137	16	27.1	713	10	BV542408	BV555221 S21P6014	C 210	16	27.1	144356	8	AC021486	AC021486 Homo sapi
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C 139	16	27.1	829	10	BV321542	BV524475 G591P6047	C 212	16	27.1	145410	15	AC023281	AC023281 Homo sapi
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C 141	16	27.1	935	2	AY078943	AR388681 Sequence	C 214	16	27.1	149205	8	AC010811	AC010811 Homo sapi
C 142	16	27.1	1515	15	AY078943	AY078943 Arabidops	C 215	16	27.1	149831	14	AC026593	AC026593 Homo sapi
C 143	16	27.1	1670	8	BC008030	AY078943 Bombyx mo	C 216	16	27.1	150389	14	BX323581	BX323581 Dario rer
C 144	16	27.1	1946	6	CO588132	BC008030 Homo sapi	C 217	16	27.1	153556	9	AC158687	AC158687 Mus muscu
C 145	16	27.1	1946	6	AX254510	CO588132 Sequence	C 218	16	27.1	154559	8	AC134992	AC134992 Rattus no
C 146	16	27.1	1996	15	BT013782	AX254510 Sequence	C 219	16	27.1	154894	14	AC144898	AC144898 Homo sapi
C 147	16	27.1	2202	6	CS061690	BT013782 Lycopersi	C 220	16	27.1	155112	8	AC102435	AC102435 Mus muscu
C 148	16	27.1	2597	5	BC085378	CS061690 Sequence	C 221	16	27.1	155483	9	AC068413	AC068413 Homo sapi
C 149	16	27.1	2990	2	AY122212	BC085378 Dario rer	C 222	16	27.1	157865	8	HS79C4	HS79C4 Human DNA
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C 151	16	27.1	3557	15	KLA532841	CO740846 Sequence	C 224	16	27.1	159463	14	AC108452	AC108452 Homo sapi
C 152	16	27.1	3791	2	SIMA52	KLA532841 Kluverfom	C 225	16	27.1	160769	8	AC108452	AC108452 Homo sapi
C 153	16	27.1	3946	6	AX254509	X73879 S.lammae DN	C 226	16	27.1	161674	14	AC015567	AC015567 Homo sapi
C 154	16	27.1	4011	1	HD025966	AX254509 Sequence	C 227	16	27.1	162102	14	CR753888	CR753888 Dario rer
C 155	16	27.1	4149	5	BC091271	HD025966 Sequence	C 228	16	27.1	162520	9	AC154440	AC154440 Mus muscu
C 156	16	27.1	4172	5	BC082837	BC091271 Rattus no	C 229	16	27.1	163280	14	AL954240	AL954240 Homo sapi
C 157	16	27.1	9127	5	AB006504	BC082837 Xenopus l	C 230	16	27.1	164591	8	CNS01DVT	AL954240 Pan trogl
C 158	16	27.1	10107	6	CO855052	AB006504 Streptoco	C 231	16	27.1	164628	15	AP004758	AP004758 Oryza sat
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C 161	16	27.1	26258	2	U41018	U41018 Caenorhabdi	C 234	16	27.1	166105	14	AC141029	AC141029 Rattus no
C 162	16	27.1	38146	15	SPAC6B12	Z98531 S.pombe chr	C 235	16	27.1	167621	14	AL162572	AL162572 Homo sapi
C 163	16	27.1	52163	9	AL606917	AL606917 Mouse DNA	C 236	16	27.1	168440	14	AL162572	AL162572 Homo sapi
C 164	16	27.1	56337	14	AC166940	AC166940 Bos tauru	C 237	16	27.1	168524	14	AL356418	AL356418 Homo sapi



238	16	27.1	169124	14	AP001375	311	15	25.4	476	6	AR415121
C 239	16	27.1	169138	2	AC010571	312	15	25.4	476	6	AX971955
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C 242	16	27.1	176247	7	AY940168	C 315	15	25.4	589	10	BV386980
243	16	27.1	179427	14	AC147584	C 316	15	25.4	594	10	BV391654
C 244	16	27.1	181064	9	AL807399	C 317	15	25.4	596	10	BV323724
C 245	16	27.1	181864	8	AL353743	C 318	15	25.4	600	3	AF428709
246	16	27.1	182917	8	AL512603	C 319	15	25.4	613	10	BV279363
247	16	27.1	183498	5	BX072578	C 320	15	25.4	637	10	BV328801
248	16	27.1	183672	8	CNS0507C	C 321	15	25.4	666	10	BV551071
249	16	27.1	188052	8	AC145614	C 322	15	25.4	690	1	AY292954
250	16	27.1	189579	8	AL354733	C 323	15	25.4	713	6	AR354904
251	16	27.1	189590	5	BX470167	C 324	15	25.4	713	6	AR534660
252	16	27.1	191176	9	AC121817	C 325	15	25.4	769	10	BV486676
C 253	16	27.1	191965	8	CNS0505DG	C 326	15	25.4	788	10	BV468041
C 254	16	27.1	192505	8	AL353136	C 327	15	25.4	800	15	AK065957
C 255	16	27.1	193952	14	AC141263	C 328	15	25.4	817	15	IT4581427
256	16	27.1	194184	5	BX510306	C 329	15	25.4	864	10	BV521377
257	16	27.1	197369	8	CNS01RB6	C 330	15	25.4	870	1	AY292960
C 258	16	27.1	198014	14	AC130026	C 331	15	25.4	874	10	CNS06KPS
C 259	16	27.1	198211	14	AC073756	C 332	15	25.4	874	10	CNS06KPS
260	16	27.1	198657	14	AL442648	C 333	15	25.4	877	10	BV465837
261	16	27.1	200190	14	AC115912	C 334	15	25.4	886	10	BV603638
262	16	27.1	200922	14	AC127937	C 335	15	25.4	898	1	AY292959
263	16	27.1	201805	14	CT025155	C 336	15	25.4	902	2	AF007295
C 264	16	27.1	202182	9	AC113304	C 337	15	25.4	916	1	AB073670
265	16	27.1	205291	14	AC147585	C 338	15	25.4	917	10	BV522819
266	16	27.1	205533	9	AC118824	C 339	15	25.4	954	1	AF034847
267	16	27.1	206125	14	CR753872	C 340	15	25.4	1016	15	AF542571
C 268	16	27.1	207647	14	AC150220	C 341	15	25.4	1017	15	AF443619
C 269	16	27.1	208293	14	AC127052	C 342	15	25.4	1020	15	AY437811
C 270	16	27.1	209920	14	AC073682	C 343	15	25.4	1071	8	BT019668
C 271	16	27.1	210580	9	AL606934	C 344	15	25.4	1071	11	AY888401
C 272	16	27.1	211580	9	AC121276	C 345	15	25.4	1071	11	AY891022
C 273	16	27.1	213117	14	AC156141	C 346	15	25.4	1071	11	AY891022
C 274	16	27.1	214911	14	AC098924	C 347	15	25.4	1071	11	AY891023
C 275	16	27.1	215896	14	AC046180	C 348	15	25.4	1071	11	AY891762
C 276	16	27.1	215869	14	AC137412	C 349	15	25.4	1071	11	AY893172
C 277	16	27.1	218963	14	AC154899	C 350	15	25.4	1071	11	AY893643
C 278	16	27.1	219991	14	CT010488	C 351	15	25.4	1071	11	BT019667
C 279	16	27.1	224003	9	AC140326	C 352	15	25.4	1133	15	AB017327
C 280	16	27.1	224054	14	AC097089	C 353	15	25.4	1169	15	AB073699
C 281	16	27.1	227198	14	AC120620	C 354	15	25.4	1203	15	AB060737
C 282	16	27.1	227778	14	AC099371	C 355	15	25.4	1206	15	AF345327
C 283	16	27.1	227940	14	AC151108	C 356	15	25.4	1397	1	AY701757
C 284	16	27.1	228009	14	AC128008	C 357	15	25.4	1402	1	AY701759
C 285	16	27.1	230659	14	AC1550012	C 358	15	25.4	1404	1	AY701758
C 286	16	27.1	230854	9	AC153539	C 359	15	25.4	1477	6	CQ725004
C 287	16	27.1	231896	9	AC115116	C 360	15	25.4	1479	6	CS031561
C 288	16	27.1	231985	14	AC156673	C 361	15	25.4	1479	6	CS040513
C 289	16	27.1	237747	14	CR848674	C 362	15	25.4	1479	6	AX333642
C 290	16	27.1	239102	14	AC137051	C 363	15	25.4	1479	6	AX334314
C 291	16	27.1	245612	14	CT009509	C 364	15	25.4	1479	8	HUMPOLACB
C 292	16	27.1	245693	9	AL844536	C 365	15	25.4	1507	1	TW16SRN
C 293	16	27.1	246958	14	AC159673	C 366	15	25.4	1512	15	AF268124
C 294	16	27.1	248830	14	AC129454	C 367	15	25.4	1518	15	AB038183
C 295	16	27.1	256385	14	AC128721	C 368	15	25.4	1518	15	AY257531
C 296	16	27.1	256862	14	AC111820	C 369	15	25.4	1552	15	AF400590
C 297	16	27.1	265132	14	AC153017	C 370	15	25.4	1552	2	CLORGI68SA
C 298	16	27.1	269576	14	AC073684	C 371	15	25.4	1630	15	AP425238
C 299	16	27.1	270695	9	AC102542	C 372	15	25.4	1630	15	CCCOH1
C 300	16	27.1	294272	2	AE003595	C 373	15	25.4	1703	15	AY084443
C 301	16	27.1	300591	1	AE017155	C 374	15	25.4	1780	15	IT4579965
C 302	16	27.1	301936	1	AE016808	C 375	15	25.4	1877	8	AK222572
C 303	16	27.1	304558	1	AE017501	C 376	15	25.4	1921	2	AK116470
C 304	16	27.1	309771	14	AC117311	C 377	15	25.4	1929	6	AR546872
C 305	16	27.1	320208	14	AC157391	C 378	15	25.4	1947	15	AY336944
C 306	15	25.4	255	1	BS082582	C 379	15	25.4	2040	8	AK090785
C 307	15	25.4	340	2	AF137287	C 380	15	25.4	2167	6	AX713732
C 308	15	25.4	355	2	AF456864	C 381	15	25.4	2167	8	AK054773
C 309	15	25.4	441	6	CO461146	C 382	15	25.4	2331	8	BC000149
C 310	15	25.4	476	6	BD110674	C 383	15	25.4	2352	8	AB169595
					AE001375 Homo sapi						
					AC010571 Drosophila						
					AC024539 Homo sapi						
					BX942829 Dario rer						
					AY940168 Cyanophag						
					AC147584 Otollemitr						
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					AL353743 Human DNA						
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					BX072578 Zebrafish						
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					AL354733 Human DNA						
					BX470167 Zebrafish						
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					AL442648 Homo sapi						
					AC115912 Mus muscu						
					AC127937 Rattus no						
					CT025155 Mus muscu						
					AC113304 Mus muscu						
					AC147585 Otollemitr						
					AC118824 Mus muscu						
					CR753872 Dario rer						
					AC150220 Gallilchri						
					AC127052 Rattus no						
					AC073682 Mus muscu						
					AL606934 Mouse DNA						
					AC156141 Bos tauru						
					AC098924 Rattus no						
					AC046180 Homo sapi						
					AC137412 Rattus no						
					AC154899 Bos tauru						
					CT010488 Mus muscu						
					AC140326 Mus muscu						
					AC097089 Rattus no						
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					AC151108 Mus muscu						
					AC128008 Rattus no						
					AC150012 Gallilchri						
					AC153539 Mus muscu						
					AC115116 Mus muscu						
					AC156673 Bos tauru						
					CR848674 Dario rer						
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					AC128721 Rattus no						
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					AC102542 Mus muscu						
					AE003595 Drosophila						
					AE017155 Haemophil						
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					AE01751 Haemophil						



C 384	15	25.4	2493	15	AY366358	AY366358 Rubus cha	457	15	25.4	95510	14	AP007981	AP007981 Lotus cor
C 385	15	25.4	2522	1	AF155222	AF155222 Escherich	C 458	15	25.4	101046	8	HS925P19	AL022241 Human DNA
C 386	15	25.4	2558	7	P2215P	J04356 Bacterioph	C 459	15	25.4	102151	14	AP007814	AP007814 Lotus cor
C 387	15	25.4	3122	6	AX286962	AX286962 Sequence	C 460	15	25.4	102671	8	BS000241	BS000241 Pan trogl
C 388	15	25.4	3189	6	AX196135	AX196135 Sequence	C 461	15	25.4	103052	8	AT506357	AT506357 Homo sapi
C 389	15	25.4	3861	6	CQ583325	CQ583325 Sequence	C 462	15	25.4	103787	8	AC093659	AC093659 Homo sapi
C 390	15	25.4	3910	2	AJ586562	AJ586562 Acricotop	C 463	15	25.4	103787	14	AC153689	AC153689 Bos tauru
C 391	15	25.4	3984	10	C0611034	C0611034 Sequence	C 464	15	25.4	105907	14	AC026429	AC026429 Homo sapi
C 392	15	25.4	4211	4	AF019298	AF019298 Bos tauru	C 465	15	25.4	106746	15	AC139840	AC139840 Solanum d
C 393	15	25.4	4964	4	AF016589	AF016589 Bos tauru	C 466	15	25.4	110000	1	CR522870	CR522870 27
C 394	15	25.4	5969	6	AX347437	AX347437 Sequence	C 467	15	25.4	110000	1	CR522870	CR522870 28
C 395	15	25.4	5969	6	AX349158	AX349158 Sequence	C 468	15	25.4	110000	1	CR848038	CR848038 10
C 396	15	25.4	5969	6	AX356502	AX356502 Sequence	C 469	15	25.4	110000	1	U00096 16	U00096 16
C 397	15	25.4	5969	6	AX657801	AX657801 Sequence	C 470	15	25.4	110000	1	AE008692	AE008692 17
C 398	15	25.4	5969	6	AX659075	AX659075 Sequence	C 471	15	25.4	110000	1	AB017220	AB017220 00
C 399	15	25.4	6373	6	AX346868	AX346868 Sequence	C 472	15	25.4	110000	1	BA000001	BA000001 02
C 400	15	25.4	7110	6	AR636660	AR636660 Sequence	C 473	15	25.4	110000	1	BA000001	BA000001 03
C 401	15	25.4	7110	6	AX097461	AX097461 Sequence	C 474	15	25.4	110000	1	BA000017	BA000017 19
C 402	15	25.4	8447	6	CTRRNAS	X99212 Chironomus	C 475	15	25.4	110000	1	BA000018	BA000018 18
C 403	15	25.4	9236	6	C0595508	C0595508 Sequence	C 476	15	25.4	110000	1	BA000026	BA000026 08
C 404	15	25.4	9262	6	C0596636	C0596636 Sequence	C 477	15	25.4	110000	1	BA000033	BA000033 19
C 405	15	25.4	9324	13	SMO316084	AJ316084 Scallion	C 478	15	25.4	110000	1	BS571856	BS571856 20
C 406	15	25.4	10049	1	AF291051	AF291051 Carbonell	C 479	15	25.4	110000	1	BS571857	BS571857 19
C 407	15	25.4	10814	7	LBA292531	Lactococc	C 480	15	25.4	110000	1	BS908798	BS908798 15
C 408	15	25.4	11819	1	AE012411	AE012411 Xanthomon	C 481	15	25.4	110000	1	CP000020	CP000020 04
C 409	15	25.4	12775	6	C0611033	C0611033 Sequence	C 482	15	25.4	110000	1	CP000026	CP000026 00
C 410	15	25.4	14759	1	AB004755	AB004755 Pseudomn	C 483	15	25.4	110000	1	CP000026	CP000026 21
C 411	15	25.4	16078	14	AC019969	AC019969 Drosophill	C 484	15	25.4	110000	1	CP000046	CP000046 19
C 412	15	25.4	17300	1	D90800	D90800 E.coli geno	C 485	15	25.4	110000	1	CP000077	CP000077 01
C 413	15	25.4	19465	1	D90798	D90798 E.coli geno	C 486	15	25.4	110000	1	CP000083	CP000083 25
C 414	15	25.4	20521	8	AC073992	AC073992 Homo sapi	C 487	15	25.4	110000	1	AC099306	AC099306 5
C 415	15	25.4	20524	1	D90799	D90799 E.coli geno	C 488	15	25.4	110000	1	AC125548	AC125548 0
C 416	15	25.4	21328	9	AL954700	AL954700 Mouse DNA	C 489	15	25.4	110000	1	AC147965	AC147965 0
C 417	15	25.4	22307	14	AC015297	AC015297 Drosophill	C 490	15	25.4	110000	1	AC147965	AC147965 1
C 418	15	25.4	22359	15	AC145457	AC145457 Cicer ari	C 491	15	25.4	110000	1	AC147965	AC147965 2
C 419	15	25.4	23563	1	AB008695	AB008695 Salmonell	C 492	15	25.4	110000	1	AC151515	AC151515 2
C 420	15	25.4	25478	9	AB083124	AB083124 Mus muscu	C 493	15	25.4	110000	1	CT005263	CT005263 3
C 421	15	25.4	26565	7	AX702505	AX702505 Sequence	C 494	15	25.4	110000	1	CT005269	CT005269 03
C 422	15	25.4	28451	7	AF011378	AF011378 Bacteriop	C 495	15	25.4	110000	1	AC026388	AC026388 2
C 423	15	25.4	31522	15	AP002050	AP002050 Arabidops	C 496	15	25.4	110000	1	AP008214	AP008214 027
C 424	15	25.4	31768	2	CET02D1	Z81135 Caenorhabd	C 497	15	25.4	110000	1	AP008214	AP008214 194
C 425	15	25.4	32965	8	CEN01G7	AC138420 Homo sapi	C 498	15	25.4	110000	1	AP008214	AP008214 237
C 426	15	25.4	36643	5	AC138420	CR749175 Zebrafish	C 499	15	25.4	110000	1	AP008218	AP008218 182
C 427	15	25.4	39229	5	CR749175	CP000055 Rickettsi	C 500	15	25.4	110000	1	CR380958	CR380958 11
C 428	15	25.4	39263	2	CP000055	CEC006A12	C 501	15	25.4	110000	1	CR380958	CR380958 08
C 429	15	25.4	39774	1	CEC006A12	AF217253 Bacteriop	C 502	15	25.4	110000	1	CR382122	CR382122 11
C 430	15	25.4	41724	7	AF217253	AF527608 Bacteriop	C 503	15	25.4	110000	1	AP008210	AP008210 029
C 431	15	25.4	41724	7	AF527608	AC116541	C 504	15	25.4	110000	1	AP008210	AP008210 263
C 432	15	25.4	42511	14	AC116541	AJ872268 Thermotog	C 505	15	25.4	110000	1	AP008210	AP008210 139
C 433	15	25.4	45429	1	AJ872268	AC125605	C 506	15	25.4	110000	1	AP008210	AP008210 114
C 434	15	25.4	45429	8	AC125605	AC125605 Homo sapi	C 507	15	25.4	110000	1	AP008210	AP008210 274
C 435	15	25.4	45834	8	AC125605	AC125605 Homo sapi	C 508	15	25.4	110000	1	AP008210	AP008210 114
C 436	15	25.4	47481	15	NCBI5120	AC107668	C 509	15	25.4	110000	1	AP008210	AP008210 114
C 437	15	25.4	47897	8	AC073360	AC073360 Homo sapi	C 510	15	25.4	110000	1	AP008210	AP008210 221
C 438	15	25.4	48980	14	AC107668	AC130377 Homo sapi	C 511	15	25.4	110000	1	AP008210	AP008210 221
C 439	15	25.4	55337	14	AC130377	AC135255	C 512	15	25.4	112461	15	AP008210	AP008210 221
C 440	15	25.4	55548	8	AC135255	AC135255 Homo sapi	C 513	15	25.4	112945	9	AC023763	AC023763 Homo sapi
C 441	15	25.4	59412	15	NCBI7921	AL389901 Neurospor	C 514	15	25.4	113198	8	AC029963	AC029963 Mouse DNA
C 442	15	25.4	61608	8	AC084360	AC084360 Homo sapi	C 515	15	25.4	113613	8	AC097524	AC097524 Homo sapi
C 443	15	25.4	62829	1	CP000053	CP000053 Rickettsi	C 516	15	25.4	120388	14	CR385049	CR385049 Oryza sat
C 444	15	25.4	63522	14	AC040037	AC040037 Homo sapi	C 517	15	25.4	122214	15	AP004093	AP004093 Strongylo
C 445	15	25.4	68230	14	AC165701	AC165701 Bos tauru	C 518	15	25.4	123022	8	AC090717	AC090717 Homo sapi
C 446	15	25.4	74049	14	AC135331	AC135331 Bos tauru	C 519	15	25.4	124297	14	AC151680	AC151680 Bos tauru
C 447	15	25.4	75413	14	AP007455	AP007455 Lotus cor	C 520	15	25.4	125010	14	AC151626	AC151626 Otolomur
C 448	15	25.4	77313	8	AC110757	AC110757 Homo sapi	C 521	15	25.4	125557	14	AC145820	AC145820 Cicer ari
C 449	15	25.4	77457	1	AF210249	AF210249 Streptomy	C 522	15	25.4	125777	8	AC078927	AC078927 Homo sapi
C 450	15	25.4	78174	2	AC004280	AC004280 Drosophill	C 523	15	25.4	126034	14	AC157958	AC157958 Strongylo
C 451	15	25.4	78568	15	AC007170	AC007170 Arabidops	C 524	15	25.4	126451	5	BS284622	BS284622 Zebrafish
C 452	15	25.4	79355	15	AB012247	AB012247 Arabidops	C 525	15	25.4	127025	8	AC018880	AC018880 Homo sapi
C 453	15	25.4	83659	5	AL353787	AL353787 Human DNA	C 526	15	25.4	129302	14	AC089318	AC089318 Homo sapi
C 454	15	25.4	87539	8	BS571814	BS571814 Zebrafish	C 527	15	25.4	130127	4	AC153760	AC153760 Loxodonta
C 455	15	25.4	88581	8	AC016550	AC016550 Homo sapi	C 528	15	25.4	130370	8	AC133680	AC133680 Homo sapi
C 456	15	25.4	95153	14	CR954248	CR954248 Danio rer	C 529	15	25.4	132336	14	AF215842	AF215842 Homo sapi



530	15	25.4	133019	15	AP006054	AP006054 Oryza sat
531	15	25.4	133967	15	OSJ000257	AL731613 Oryza sat
532	15	25.4	134028	8	AL662906	AL662906 Human DNA
533	15	25.4	136393	14	AC151700	GA115700 Gallus ga
534	15	25.4	136317	8	AP003481	AP003481 Homo sapi
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536	15	25.4	139925	15	AC115071	AC115071 Mus muscu
537	15	25.4	140245	15	AP005658	AP005658 Oryza sat
538	15	25.4	141545	15	OSJ000221	AL663019 Oryza sat
539	15	25.4	141935	15	OSJ000207	AL663004 Oryza sat
540	15	25.4	142080	8	AC079748	AC079748 Homo sapi
541	15	25.4	143391	8	AC005509	AC005509 Homo sapi
542	15	25.4	143499	14	AC141969	AC141969 Rattus no
543	15	25.4	143705	9	AC118351	AC118351 Rattus no
544	15	25.4	144237	9	AC113246	AC113246 Mus muscu
545	15	25.4	144315	14	AY686476	AY686476 Mus muscu
546	15	25.4	146388	9	AC154250	AC154250 Mus muscu
547	15	25.4	147087	2	AC159423	AC159423 Trypanoso
548	15	25.4	147461	15	AP004691	AP004691 Oryza sat
549	15	25.4	147854	5	BX548040	BX548040 Zebratfish
550	15	25.4	148120	14	AC141805	AC141805 Apis mell
551	15	25.4	149697	14	AC109832	AC109832 Oryza sat
552	15	25.4	149837	14	AY686477	AY686477 Mus muscu
553	15	25.4	150339	14	AC141750	AC141750 Apis mell
554	15	25.4	151569	14	AC127473	AC127473 Canis fam
555	15	25.4	152058	15	AP005740	AP005740 Oryza sat
556	15	25.4	152095	15	AC154271	AC154271 Mus muscu
557	15	25.4	152248	14	AC027522	AC027522 Homo sapi
558	15	25.4	152816	14	AC079739	AC079739 Homo sapi
559	15	25.4	152864	14	AC016926	AC016926 Homo sapi
560	15	25.4	153072	15	AC151525	AC151525 Medicago
561	15	25.4	154303	14	AC147860	AC147860 Macropus
562	15	25.4	154715	8	AP005268	AP005268 Pan trogl
563	15	25.4	155210	8	AC007447	AC007447 Homo sapi
564	15	25.4	155887	9	AC134545	AC134545 Mus muscu
565	15	25.4	156282	9	AC125339	AC125339 Mus muscu
566	15	25.4	156614	8	AC109587	AC109587 Homo sapi
567	15	25.4	156826	9	AC124113	AC124113 Mus muscu
568	15	25.4	159480	8	AC021843	AC021843 Homo sapi
569	15	25.4	159973	8	AC020923	AC020923 Homo sapi
570	15	25.4	160561	14	AC017724	AC017724 Drosophill
571	15	25.4	161053	8	AL356608	AL356608 Human DNA
572	15	25.4	161111	18	AC103827	AC103827 Homo sapi
573	15	25.4	161595	14	AC068088	AC068088 Homo sapi
574	15	25.4	163969	9	AC114605	AC114605 Mus muscu
575	15	25.4	164450	2	AC011763	AC011763 Drosophill
576	15	25.4	165274	14	AC163508	AC163508 Bos tauru
577	15	25.4	166036	14	AC041013	AC041013 Homo sapi
578	15	25.4	166128	9	AC131759	AC131759 Mus muscu
579	15	25.4	166346	5	CR361552	CR361552 Zebratfish
580	15	25.4	166427	14	AC069593	AC069593 Homo sapi
581	15	25.4	166462	14	AC027064	AC027064 Homo sapi
582	15	25.4	166548	8	AL807740	AL807740 Human DNA
583	15	25.4	167137	8	AC068631	AC068631 Homo sapi
584	15	25.4	167152	14	AC141796	AC141796 Apis mell
585	15	25.4	167182	5	BX072549	BX072549 Zebratfish
586	15	25.4	167292	14	AC068365	AC068365 Homo sapi
587	15	25.4	167386	14	AC016788	AC016788 Homo sapi
588	15	25.4	167386	14	AC013704	AC013704 Homo sapi
589	15	25.4	167437	8	AC090835	AC090835 Homo sapi
590	15	25.4	167475	14	AC025770	AC025770 Homo sapi
591	15	25.4	167628	8	AC092570	AC092570 Homo sapi
592	15	25.4	167799	8	AC100798	AC100798 Homo sapi
593	15	25.4	167991	8	AC125175	AC125175 Mus muscu
594	15	25.4	168456	9	AC159252	AC159252 Mus muscu
595	15	25.4	168606	8	AC147274	AC147274 Pan trogl
596	15	25.4	169365	9	AC124467	AC124467 Mus muscu
597	15	25.4	169981	14	AC102143	AC102143 Mus muscu
598	15	25.4	170241	8	AC083967	AC083967 Homo sapi
599	15	25.4	170843	8	AC027216	AC027216 Homo sapi
600	15	25.4	171551	5	OSJ000177	AL662916 Oryza sat
601	15	25.4	171783	14	AC146321	AC146321 Papio anu
602	15	25.4	172336	9	AC124083	AC124083 Mus muscu
603	15	25.4	172511	15	AP005688	AP005688 Oryza sat
604	15	25.4	172613	9	AC122475	AC122475 Mus muscu
605	15	25.4	173480	8	CNS00087	AL079343 Human chr
606	15	25.4	173758	8	CNS00144	AC009144 Homo sapi
607	15	25.4	174474	14	AC067968	AC067968 Homo sapi
608	15	25.4	174546	14	AC087688	AC087688 Homo sapi
609	15	25.4	175047	14	AC012521	AC012521 Homo sapi
610	15	25.4	175695	14	AC021717	AC021717 Homo sapi
611	15	25.4	176257	14	AC119444	AC119444 Rattus no
612	15	25.4	176429	8	AP002499	AP002499 Homo sapi
613	15	25.4	176893	5	AL928685	AL928685 Zebratfish
614	15	25.4	177034	15	CNS08CAC	AL813799 Oryza sat
615	15	25.4	177471	2	AC008361	AC008361 Drosophill
616	15	25.4	177688	9	AC127274	AC127274 Mus muscu
617	15	25.4	178420	8	AP003548	AP003548 Homo sapi
618	15	25.4	178630	14	AC109478	AC109478 Homo sapi
619	15	25.4	178929	5	BX470133	BX470133 Zebratfish
620	15	25.4	178994	14	CR384062	CR384062 Danio rer
621	15	25.4	180568	8	AC021325	AC021325 Homo sapi
622	15	25.4	181102	8	AC090058	AC090058 Homo sapi
623	15	25.4	181208	8	AP003063	AP003063 Homo sapi
624	15	25.4	181878	9	AC154690	AC154690 Mus muscu
625	15	25.4	181936	14	AC129128	AC129128 Rattus no
626	15	25.4	182105	9	AC153957	AC153957 Mus muscu
627	15	25.4	182548	15	AP005461	AP005461 Oryza sat
628	15	25.4	182737	14	AP001448	AP001448 Homo sapi
629	15	25.4	183105	2	AC104606	AC104606 Drosophill
630	15	25.4	183861	8	AC117735	AC117735 Mus muscu
631	15	25.4	184036	8	AC147580	AC147580 Oryza sat
632	15	25.4	184079	2	AC008258	AC008258 Drosophill
633	15	25.4	184346	8	AC146236	AC146236 Pan trogl
634	15	25.4	184355	8	CR381572	CR381572 Human DNA
635	15	25.4	184486	8	AC090393	AC090393 Homo sapi
636	15	25.4	184596	8	AC103585	AC103585 Homo sapi
637	15	25.4	184772	9	AC123044	AC123044 Mus muscu
638	15	25.4	184868	14	AC156769	AC156769 Rhinoph
639	15	25.4	185327	8	AC007224	AC007224 Homo sapi
640	15	25.4	185356	14	AC158576	AC158576 Mus muscu
641	15	25.4	185517	8	AC140231	AC140231 Mus muscu
642	15	25.4	185532	8	AL450023	AL450023 Human DNA
643	15	25.4	186286	14	CR854881	CR854881 Danio rer
644	15	25.4	186410	14	AC149244	AC149244 Oryzomur
645	15	25.4	186711	14	AC115885	AC115885 Mus muscu
646	15	25.4	186736	9	AL645912	AL645912 Mouse DNA
647	15	25.4	186779	14	AC154305	AC154305 Mus muscu
648	15	25.4	187386	8	AC099507	AC099507 Homo sapi
649	15	25.4	187716	14	AC162482	AC162482 Bos tauru
650	15	25.4	187845	14	AC118983	AC118983 Rattus no
651	15	25.4	188133	14	AC166242	AC166242 Mus muscu
652	15	25.4	188653	5	CR391991	CR391991 Zebratfish
653	15	25.4	188840	8	AC046144	AC046144 Homo sapi
654	15	25.4	188850	14	AC127475	AC127475 Canis fam
655	15	25.4	188917	14	CR388162	CR388162 Danio rer
656	15	25.4	188917	14	AC160976	AC160976 Mus muscu
657	15	25.4	189036	14	AC019142	AC019142 Homo sapi
658	15	25.4	189190	14	AC129536	AC129536 Mus muscu
659	15	25.4	189219	14	AC009680	AC009680 Homo sapi
660	15	25.4	189263	9	AC134595	AC134595 Mus muscu
661	15	25.4	189612	14	AC051617	AC051617 Mus muscu
662	15	25.4	190009	14	AC163745	AC163745 Mus muscu
663	15	25.4	190015	8	AC087639	AC087639 Homo sapi
664	15	25.4	190116	9	AP003152	AP003152 Mus muscu
665	15	25.4	190996	9	AC163352	AC163352 Mus muscu
666	15	25.4	191680	14	CR753837	CR753837 Danio rer
667	15	25.4	192668	9	AC129020	AC129020 Mus muscu
668	15	25.4	192973	9	AC123645	AC123645 Mus muscu
669	15	25.4	193211	9	AC155275	AC155275 Mus muscu
670	15	25.4	193461	14	CR293529	CR293529 Danio rer
671	15	25.4	194926	9	AC132428	AC132428 Mus muscu
672	15	25.4	195542	14	AC165248	AC165248 Mus muscu
673	15	25.4	195776	14	BX649326	BX649326 Danio rer
674	15	25.4	196532	9	AC152987	AC152987 Mus muscu
675	15	25.4	196536	14	AC023477	AC023477 Homo sapi



676	15	25.4	196946	14	AC067934	AC067934 Homo sapi	c 749	15	25.4	258991	14	AC134223	AC134223 Rattus no
677	15	25.4	197143	5	CR396593	CR396593 Zebrafish	c 750	15	25.4	260417	14	AC106060	AC106060 Rattus no
678	15	25.4	197499	5	BX950214	BX950214 Zebrafish	c 751	15	25.4	260636	14	AC095384	AC095384 Rattus no
679	15	25.4	197637	14	AC158879	AC158879 Bos tauru	c 752	15	25.4	260850	14	CR628328	CR628328 Danio rer
680	15	25.4	198555	14	AC150770	AC150770 Xenopus t	c 753	15	25.4	263323	9	AC097832	AC097832 Rattus no
681	15	25.4	199320	14	CR855325	CR855325 Danio rer	c 754	15	25.4	263388	9	AL670959	AL670959 Mouse DNA
682	15	25.4	199569	8	AC016250	AC016250 Homo sapi	c 755	15	25.4	264227	2	AE003841	AE003841 Drosophill
683	15	25.4	199922	1	BSUB0016	Z99119 Bacillus su	c 756	15	25.4	266427	2	AE003841	AC096262 Rattus no
684	15	25.4	200922	14	BSUB0016	AC148421 Meleagris	c 757	15	25.4	270153	14	AC096348	AC096348 Rattus no
685	15	25.4	201091	5	BX649245	BX649245 Zebrafish	c 758	15	25.4	285946	14	AC114466	AC114466 Rattus no
686	15	25.4	201979	5	AC143329	AC143329 Mus muscu	c 759	15	25.4	285949	2	AE003441	AE003441 Drosophill
687	15	25.4	201982	14	AC027297	AC027297 Mus muscu	c 760	15	25.4	287029	1	AE017266	AE017266 Rattus no
688	15	25.4	202507	8	AC021856	AC021856 Homo sapi	c 761	15	25.4	292767	14	AC048333	AC048333 Rattus no
689	15	25.4	202635	8	AC160133	AC160133 Mus muscu	c 762	15	25.4	295957	14	BX294151	AC122619 Rattus no
690	15	25.4	203462	8	AC099346	AC099346 Homo sapi	c 763	15	25.4	295957	14	AC122619	AC122619 Rattus no
691	15	25.4	203612	14	AP001498	AP001498 Homo sapi	c 764	15	25.4	296500	1	SC099128	SC099128 Rattus no
692	15	25.4	204603	14	AC066591	AC066591 Homo sapi	c 765	15	25.4	301475	14	AC157842	AC157842 Rattus no
693	15	25.4	205162	9	AC127296	AC127296 Mus muscu	c 766	15	25.4	302605	1	AE016938	AE016938 Bacteroid
694	15	25.4	206098	14	AC156915	AC156915 Bos tauru	c 767	15	25.4	304985	14	CR385070	CR385070 Danio rer
695	15	25.4	207333	9	AC130532	AC130532 Mus muscu	c 768	15	25.4	305325	1	AE016765	AE016765 Escherich
696	15	25.4	208391	14	AC130009	AC130009 Rattus no	c 769	15	25.4	310193	14	AC131872	AC131872 Rattus no
697	15	25.4	208710	5	AC126262	AC126262 Mus muscu	c 770	15	25.4	315743	14	AC162474	AC162474 Bos tauru
698	15	25.4	209295	5	BX545856	BX545856 Zebrafish	c 771	15	25.4	315743	14	AC162474	AC162474 Bos tauru
699	15	25.4	211034	9	AL731709	AL731709 Mouse DNA	c 772	15	25.4	317050	1	AL935254	AL935254 Mycoplasm
700	15	25.4	211076	9	AC012214	AC012214 Homo sapi	c 773	15	25.4	321250	1	MPULM02	CR378668 Photobact
701	15	25.4	211076	9	AC154592	AC154592 Mus muscu	c 774	15	25.4	348128	1	CR378668	CR378668 Photobact
702	15	25.4	213269	5	AL844452	AL844452 Zebrafish	c 775	14	23.7	163	13	AY713381	AY713381 Apicom P
703	15	25.4	213272	14	AC135668	AC135668 Mus muscu	c 776	14	23.7	166	10	GD4716	GD4716 human SRS W
704	15	25.4	213984	14	AC099349	AC099349 Rattus no	c 777	15	23.7	175	15	AY170872	AY170872 Metroside
705	15	25.4	214061	14	AC164027	AC164027 Bos tauru	c 778	14	23.7	175	15	AY170873	AY170873 Metroside
706	15	25.4	214625	9	AC116582	AC116582 Mus muscu	c 779	14	23.7	207	15	AB079155	AB079155 Human rhl
707	15	25.4	215137	9	AC128672	AC128672 Mus muscu	c 780	14	23.7	233	15	AB032763	AB032763 Paraflior
708	15	25.4	215499	14	AC152530	AC152530 Bos tauru	c 781	14	23.7	243	6	C0055391	C0055391 Sequence
709	15	25.4	216728	14	AC147966	AC147966 Gallus ga	c 782	14	23.7	243	6	C0074655	C0074655 Sequence
710	15	25.4	217558	14	AC111489	AC111489 Rattus no	c 783	14	23.7	243	6	C0105558	C0105558 Sequence
711	15	25.4	217725	2	AE003717	AE003717 Drosophill	c 784	14	23.7	243	6	C0144250	C0144250 Sequence
712	15	25.4	219395	14	AC112094	AC112094 Rattus no	c 785	14	23.7	243	6	C0179724	C0179724 Sequence
713	15	25.4	220060	1	AP008820	AP008820 Bacillus	c 786	14	23.7	243	6	C0204088	C0204088 Sequence
714	15	25.4	220562	8	AC007500	AC007500 Homo sapi	c 787	14	23.7	243	6	C0227455	C0227455 Sequence
715	15	25.4	221612	9	AC164250	AC164250 Mus muscu	c 788	14	23.7	243	6	C0265609	C0265609 Sequence
716	15	25.4	224038	14	AC109747	AC109747 Rattus no	c 789	14	23.7	243	6	C0302696	C0302696 Sequence
717	15	25.4	224098	8	BS000242	BS000242 Pan trogl	c 790	14	23.7	243	6	C0339866	C0339866 Sequence
718	15	25.4	224331	14	AC132674	AC132674 Rattus no	c 791	14	23.7	302	10	G29483	G29483 human SRS S
719	15	25.4	225413	9	AC124474	AC124474 Mus muscu	c 792	14	23.7	305	10	BV102328	BV102328 RPAMMSBO
720	15	25.4	226567	9	AC093316	AC093316 Mus muscu	c 793	14	23.7	310	2	AY143639	AY143639 Echinoscar
721	15	25.4	227872	2	AE003720	AE003720 Drosophill	c 794	14	23.7	310	14	BV312080	BV312080 S226P6311
722	15	25.4	228842	14	AC125805	AC125805 Rattus no	c 795	14	23.7	314	10	BX296514	BX296514 Arabidops
723	15	25.4	228889	14	AC096485	AC096485 Bos tauru	c 796	14	23.7	316	5	AY089896	AY089896 Xiphodrym
724	15	25.4	229531	14	AC164363	AC164363 Rattus no	c 797	14	23.7	354	5	BV214491	BV214491 S233P679F
725	15	25.4	230465	14	AC095139	AC095139 Rattus no	c 798	14	23.7	361	10	RP282463	RP282463 R. prowazeki
726	15	25.4	233569	14	AC098273	AC098273 Rattus no	c 799	14	23.7	378	10	BV252612	BV252612 S234P6305
727	15	25.4	233977	14	AC099296	AC099296 Rattus no	c 800	14	23.7	393	13	AF418344	AF418344 HIV-1 180
728	15	25.4	234156	14	AC163295	AC163295 Mus muscu	c 801	14	23.7	393	13	AF418448	AF418448 HIV-1 180
729	15	25.4	235816	14	AC109667	AC109667 Rattus no	c 802	14	23.7	394	10	BV265446	BV265446 S235P6315
730	15	25.4	236932	14	AC097171	AC097171 Rattus no	c 803	14	23.7	394	10	AF418313	AF418313 HIV-1 180
731	15	25.4	237066	14	AC134080	AC134080 Rattus no	c 804	14	23.7	395	13	AF418315	AF418315 HIV-1 180
732	15	25.4	238090	14	AC118768	AC118768 Rattus no	c 805	14	23.7	395	13	AF418335	AF418335 HIV-1 180
733	15	25.4	238330	14	AC106176	AC106176 Rattus no	c 806	14	23.7	396	13	AF418337	AF418337 HIV-1 180
734	15	25.4	239139	14	AC103026	AC103026 Rattus no	c 807	14	23.7	396	13	AF418338	AF418338 HIV-1 180
735	15	25.4	240928	5	BX322606	BX322606 Zebrafish	c 808	14	23.7	396	13	AF418338	AF418338 HIV-1 180
736	15	25.4	245476	14	AC098496	AC098496 Rattus no	c 809	14	23.7	396	13	AF418339	AF418339 HIV-1 180
737	15	25.4	245486	14	AC125575	AC125575 Rattus no	c 810	14	23.7	396	13	AF418340	AF418340 HIV-1 180
738	15	25.4	246382	14	AC117563	AC117563 Rattus no	c 811	14	23.7	396	13	AF418341	AF418341 HIV-1 180
739	15	25.4	247633	14	AC094650	AC094650 Rattus no	c 812	14	23.7	396	13	AF418342	AF418342 HIV-1 180
740	15	25.4	248499	14	AC107190	AC107190 Bos tauru	c 813	14	23.7	396	13	AF418343	AF418343 HIV-1 180
741	15	25.4	248676	14	AC157007	AC157007 Bos tauru	c 814	14	23.7	396	13	AF418345	AF418345 HIV-1 180
742	15	25.4	249010	14	AC153581	AC153581 Mus muscu	c 815	14	23.7	396	13	AF418347	AF418347 HIV-1 180
743	15	25.4	249021	14	AC094500	AC094500 Rattus no	c 816	14	23.7	396	13	AF418348	AF418348 HIV-1 180
744	15	25.4	249732	14	AC154444	AC154444 Mus muscu	c 817	14	23.7	396	13	AF418349	AF418349 HIV-1 180
745	15	25.4	252509	14	AC098338	AC098338 Rattus no	c 818	14	23.7	396	13	AF418350	AF418350 HIV-1 180
746	15	25.4	253360	14	AC096943	AC096943 Rattus no	c 819	14	23.7	396	13	AF418351	AF418351 HIV-1 180
747	15	25.4	255502	14	AC102144	AC102144 Mus muscu	c 820	14	23.7	396	13	AF418352	AF418352 HIV-1 180
748	15	25.4	257403	14	AC153564	AC153564 Mus muscu	c 821	14	23.7	396	13	AF418352	AF418352 HIV-1 180



822	14	23.7	396	13	AP418353	HIV-1	180	895	14	23.7	547	10	BV395024	BV395024	S243P6117
823	14	23.7	396	13	AP418354	HIV-1	180	896	14	23.7	549	10	BV298220	BV298220	S239P640F
824	14	23.7	396	13	AP418355	HIV-1	180	897	14	23.7	550	10	BV412984	BV412984	S229P6387
825	14	23.7	396	13	AP418356	HIV-1	180	898	14	23.7	551	10	BV414848	BV414848	S229P6553
826	14	23.7	396	13	AP418357	HIV-1	180	899	14	23.7	552	10	BV364367	BV364367	S231P675R
827	14	23.7	396	13	AP418358	HIV-1	180	900	14	23.7	553	10	BV254871	BV254871	S235P6163
828	14	23.7	396	13	AP418359	HIV-1	180	901	14	23.7	553	10	BV282923	BV282923	S232P6147
829	14	23.7	396	13	AP418360	HIV-1	180	902	14	23.7	554	10	BV346803	BV346803	S230P6285
830	14	23.7	396	13	AP418361	HIV-1	180	903	14	23.7	555	10	BV246781	BV246781	S234P6248
831	14	23.7	396	13	AP418362	HIV-1	180	904	14	23.7	555	10	BV387197	BV387197	S244P6243
832	14	23.7	396	13	AP418363	HIV-1	180	905	14	23.7	555	15	BT014696	BT014696	ArabIdops
833	14	23.7	396	13	AP418364	HIV-1	180	906	14	23.7	555	15	BT015492	BT015492	ArabIdops
834	14	23.7	396	13	AP418365	HIV-1	180	907	14	23.7	556	10	BV255082	BV255082	S235P6428
835	14	23.7	396	13	AP418366	HIV-1	180	908	14	23.7	556	10	BV296033	BV296033	S239P6244
836	14	23.7	396	13	AP418446	HIV-1	180	909	14	23.7	556	10	BV421105	BV421105	S229P6503
837	14	23.7	396	13	AP418447	HIV-1	180	910	14	23.7	556	10	BV301226	BV301226	S239P610F
838	14	23.7	396	13	AP418450	HIV-1	180	911	14	23.7	557	10	BV277774	BV277774	S232P6553
839	14	23.7	396	13	AP418451	HIV-1	180	912	14	23.7	558	10	BV416883	BV416883	S229P6331
840	14	23.7	396	13	AP418452	HIV-1	180	913	14	23.7	558	15	AF145261	AF145261	NiCotI:ana
841	14	23.7	396	13	AP418453	HIV-1	180	914	14	23.7	559	10	BV377454	BV377454	S245P6201
842	14	23.7	397	13	AP418314	HIV-1	180	915	14	23.7	560	10	BV253616	BV253616	S234P63FE
843	14	23.7	397	13	AP418323	HIV-1	180	916	14	23.7	560	10	BV287742	BV287742	S232P6146
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852	14	23.7	468	10	BV422651	S232P6414R		925	14	23.7	566	10	BV441473	BV441473	S237P6145
853	14	23.7	473	10	BV291988	S232P6404		926	14	23.7	568	10	BV372987	BV372987	S231P64405
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864	14	23.7	484	6	CO253013	Sequence		937	14	23.7	575	10	BV293354	BV293354	S232P676F
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866	14	23.7	484	6	CO327115	Sequence		939	14	23.7	577	10	BV247140	BV247140	S234P6109
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884	14	23.7	525	15	AB181184	Populus n		957	14	23.7	587	10	BV274012	BV274012	S235P65FD
885	14	23.7	526	10	BV308568	S236P6105		958	14	23.7	587	10	BV397845	BV397845	S236P60FC
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969 14 23.7 590 10 BV374025 BV374025 S231P6153  
970 14 23.7 591 10 BV381242 BV381242 S245P62FD  
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973 14 23.7 594 10 BV275880 BV275880 S232P6155  
974 14 23.7 594 10 BV280707 BV280707 S232P6109  
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977 14 23.7 596 10 BV374367 BV374367 S231P6612  
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981 14 23.7 598 10 BV387305 BV387305 S244P6340  
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987 14 23.7 599 10 BV406565 BV406565 S229P684R  
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998 14 23.7 601 10 BV305723 BV305723 S236P6191  
999 14 23.7 601 10 BV393059 BV393059 S243P617F  
1000 14 23.7 601 10 BV429585 BV429585 S237P6103

## ALIGNMENTS

RESULT 1  
LOCUS AR366274 867 bp DNA linear PAT 12-SRP-2003  
DEFINITION Sequence 7 from patent US 6329156.  
ACCESSION AR366274  
VERSION AR366274.1 GI:34598679  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 867)  
AUTHORS Ciriaco N.M., Jackson, P.J. and Lehnert, B.B.  
TITLE Method for screening inhibitors of the toxicity of Bacillus anthracis  
JOURNAL Patent: US 6329156-A 7 11-DEC-2001;  
The Regents of the University of California; Los Alamos, NM;  
FOX;  
FEATURES  
source location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 3e-25;  
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DB 129 GGTAAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTTAGAAAGCACTAAACCGG 187  
RESULT 2  
LOCUS AX353779 1278 bp DNA linear PAT 06-FEB-2002  
AX353779

DEFINITION Sequence 10 from Patent WO0204646.  
ACCESSION AX353779  
VERSION AX353779.1 GI:18618829  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Williamson, E.D., Miller, J., Walker, N.J., Ballile, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifent, H.L., Tibbail, R.W. and Topping, A.W.  
TITLE Expression system  
JOURNAL Patent: WO 0204646-A 10 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
source location/Qualifiers  
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RESULT 3  
LOCUS CS135645 1281 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 10 from Patent WO2005068493.  
ACCESSION CS135645  
VERSION CS135645.1 GI:72056311  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 10 28-JUN-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
source location/Qualifiers  
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RESULT 4  
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DEFINITION Bacillus anthracis isolate 34F2 plasmid pX01 protective antigen  
ACCESSION AY921578  
VERSION AY921578.1 GI:62467684  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus



REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 1694)  
Vahedi, F., Moazeni Julia, G. and Mahmoudi, M.  
Humoral immunity in mice induced by vaccination with a plasmid encoding anthrax protective antigen  
Unpublished  
2 (bases 1 to 1694)  
Vahedi, F., Moazeni Julia, G. and Mahmoudi, M.  
Direct Submission  
Submitted (06-FEB-2005) Immunology Research Center, BuAli Research Institute, Mashhad University of Medical Sciences, BuAli Sq., Mashhad, Iran

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Db 979 GGTAGAAAGCGGATAGCGGGGTTAATCTTAGATCCATTAGAAACGACTAAACCGG 1037  
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RESULT 5  
CS135643 1707 bp DNA linear PAT 09-AUG-2005  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Sequence 8 from Patent WO2005068493.  
CS135643.1 GI:72056309  
Bacillus anthracis  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Cutting, S.M.  
Anthrax vaccine in the form of a spore  
Patent: WO 2005068493-A 8 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)

FEATURES  
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Query Match 100.0%; Score 59; DB 6; Length 1707;

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RESULT 6  
AR570597 1710 bp DNA linear PAT 14-DEC-2004  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Sequence 4 from patent US 6770479.  
AR570597  
AR570597.1 GI:56571410  
Unknown.  
Unknown.  
Unclassified.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

1 (bases 1 to 1710)  
Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
Anthrax vaccine  
Patent: US 6770479-A 4 03-AUG-2004;  
The United States of America as represented by the Secretary of the Army; Washington, DC;  
MOX;

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RESULT 7  
AX353781 1785 bp DNA linear PAT 06-FEB-2002  
LOCUS  
DEFINITION  
ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM

Sequence 12 from Patent WO0204646.  
AX353781  
AX353781.1 GI:18618830  
synthetic construct  
synthetic construct  
Other sequences; artificial sequences.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Williamson, B.D., Miller, D., Walker, N.J., Baillie, L.W., Holden, P.T.,  
Flick-Smith, H.C., Bullifant, H.L., Tibball, R.W. and Topping, A.W.  
Expression system  
Patent: WO 0204646-A 12 17-JAN-2002;  
The Secretary of State for Defense (GB)

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RESULT 8  
LOCUS 169387 2160 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 30 from patent US 5677274.  
ACCESSION 169387  
VERSION 169387.1 GI:2831509  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2160)  
AUTHORS Leppia,S.H., Klumpel,K.R., Arora,N., Singh,Y. and Nichols,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 30 14-OCT-1997;  
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Query Match 100.0%; Score 59; DB 6; Length 2160;  
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RESULT 9  
LOCUS CS135652 2208 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 17 from Patent WO2005068493.  
ACCESSION CS135652  
VERSION CS135652.1 GI:72056316  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
AUTHORS Cutting,S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNAL Patent: WO 2005068493-A 17 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)  
FEATURES  
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RESULT 10  
LOCUS AX353783 2208 bp DNA linear PAT 06-FEB-2002  
DEFINITION Sequence 14 from Patent WO0204646.  
ACCESSION AX353783  
VERSION AX353783.1 GI:18618831  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
other sequences; artificial sequences.

REFERENCE 1  
AUTHORS Williamson,B.D., Miller,J., Walker,N.J., Baillie,L.W., Holden,P.T.,

FLICK-Smith,H.C., Bullifent,H.L., Tibball,R.W. and Topping,A.W.  
Expression system  
Patent: WO 0204646-A 14 17-JAN-2002;  
The Secretary of State for Defense (GB)  
FEATURES  
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Qy 1 GGTAAGAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
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RESULT 11  
LOCUS CS061689 2211 bp DNA linear PAT 13-APR-2005  
DEFINITION Sequence 9 from Patent WO2005026203.  
ACCESSION CS061689  
VERSION CS061689.1 GI:62553664  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
AUTHORS Kopecko,D.J., Osorio,M., Bhattacharyya,S., Girt,C.P. and Blake,M.  
TITLE DNA promoters and anthrax vaccines  
JOURNAL Patent: WO 2005026203-A 9 24-MAR-2005;  
Department of Health and Human Services (US)  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAAGAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 1503 GGTAAGAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1561

RESULT 12  
LOCUS AR570595 2211 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 2 from patent US 6770479.  
ACCESSION AR570595  
VERSION AR570595.1 GI:56571408  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 2211)  
AUTHORS Lee,J.S., Pushko,P., Parker,M.D., Smith,J.F. and Welkos,S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 2 03-AUG-2004;  
The United States of America as represented by the Secretary of the Army; Washington, DC;  
WOX;  
FEATURES  
source 1..2211  
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ORIGIN /mol\_type="genomic DNA"

Query Match 100.0%; Score 59; DB 6; Length 2211;  
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGCGATAGCGCGGTTAATCTCTAGTATCATTTAGAAACGACTAAACCGG 59  
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Db 1503 GGTAGAAAGCGCGATAGCGCGGTTAATCTCTAGTATCATTTAGAAACGACTAAACCGG 1561

RESULT 13  
BAN413937  
LOCUS 2225 bp DNA linear BCT 22-MAY-2002  
DEFINITION Bacillus anthracis partial pag gene, isolate IT-Carbl-6241.  
ACCESSION AJ413937.1 GI:16031494  
KEYWORDS pag gene.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
AUTHORS Adone, R., Pasquali, P., La Rosa, G., Marianelli, C., Muscillo, M., Fasanella, A., Francia, M. and Ciuchini, F.  
TITLE Sequence analysis of the gene encoding for the major virulence factors of Bacillus anthracis vaccine strain 'Carbosap J. Appl. Microbiol. 92, 1-5 (2002)

JOURNAL  
REFERENCE 2 (bases 1 to 2225)  
AUTHORS Muscillo, M.  
TITLE Direct Submision  
JOURNAL Submitted (11-SEP-2001) Muscillo M., Environmental Hygiene, Istituto Superiore di Sanita, Viale Regina Elena 299, Rome 00199, Italy

FEATURES  
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Query Match 100.0%; Score 59; DB 1; Length 2225;

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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1557 GGTAGAAAGCGCGATAGCGCGGTTAATCTCTAGTATCATTTAGAAACGACTAAACCGG 1615

RESULT 14  
AY700758  
LOCUS 2227 bp DNA linear BCT 18-AUG-2004  
DEFINITION Bacillus anthracis strain Sterne plasmid pXOI protective antigen  
gene, complete cds.  
ACCESSION AY700758  
KEYWORDS AY700758.1 GI:51235129  
SOURCE  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 2227)  
AUTHORS Aziz, M.A. and Bhatnagar, R.  
TITLE Mature protective antigen gene with prokaryotic ribosomal binding site

JOURNAL  
REFERENCE 2 (bases 1 to 2227)  
AUTHORS Aziz, M.A. and Bhatnagar, R.  
TITLE Direct Submission  
JOURNAL Submitted (29-JUL-2004) Centre for Biotechnology, Jawaharlal Nehru University, New Mehrauli Road, New Delhi, Delhi 110067, India

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source location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 59; DB 1; Length 2227;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
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Db 1519 GGTAGAAAGCGCGATAGCGCGGTTAATCTCTAGTATCATTTAGAAACGACTAAACCGG 1577

RESULT 15  
BAN413936  
LOCUS 2231 bp DNA linear BCT 22-MAY-2002  
DEFINITION Bacillus anthracis partial pag gene, isolate IT-Carbl-6254.  
ACCESSION AJ413936  
VERSION AJ413936.1 GI:16031492



KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
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ORIGIN  
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Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGCTTAATCCTAGTATCCATTGAAACGACTAAACCGG 59  
DB 1564 GGTAGAAAGCGGATAGCGCGGCTTAATCCTAGTATCCATTGAAACGACTAAACCGG 1622

RESULT 16  
ARS70596 2292 bp DNA linear PAT 14-DEC-2004  
LOCUS ARS70596  
DEFINITION Sequence 3 from patent US 6770479.  
ACCESSION ARS70596  
VERSION ARS70596.1 GI:56571409  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.

Unclassified.  
1 (bases 1 to 2292)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNAL Patent: US 6770479-A 3 03-AUG-2004;  
The United States of America as represented by the Secretary of the  
Army; Washington, DC;  
WOK;

FEATURES  
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ORIGIN  
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 17  
AY997299 2295 bp DNA linear BCT 26-APR-2005  
LOCUS AY997299  
DEFINITION Bacillus anthracis strain A16r protective antigen (pag) gene,  
complete cds.  
ACCESSION AY997299  
VERSION AY997299.1 GI:62823103  
KEYWORDS  
SOURCE  
ORGANISM  
Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 2295)  
XU, J., Dong, D., and Chen, W.  
Protective antigen gene of Bacillus anthracis strain A16r  
Unpublished  
2 (bases 1 to 2295)  
XU, J., Dong, D., and Chen, W.  
Direct Submission  
Submitted (03-APR-2005) Department of Molecular Biology, Beijing  
Institute of Microbiology and Epidemiology, 20 Dongdajie, Fengtai,  
Beijing 100071, China

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ORIGIN ENGDSTNGIKILIFSKGYEIG"

Query Match 100.0%; Score 59; DB 1; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 59  
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Db 1587 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1645

RESULT 18  
LOCUS CS135651 2295 bp DNA linear PAT 09-AUG-2005  
DEFINITION Sequence 16 from Patent WO2005068493.  
ACCESSION CS135651  
VERSION CS135651.1 GI:72056315  
KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1  
AUTHORS Cutting, S.M.  
TITLE Anthrax vaccine in the form of a spore  
JOURNML Patent: WO 2005068493-A 16 28-JUL-2005;  
Royal Holloway and Bedford New College (GB)

FEATURES  
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Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1587 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1645

RESULT 19  
LOCUS AR570594 2295 bp DNA linear PAT 14-DEC-2004  
DEFINITION Sequence 1 from patent US 6770479.  
ACCESSION AR570594  
VERSION AR570594.1 GI:56571407  
KEYWORDS  
SOURCE  
ORGANISM Unknown.  
Unclassified.

REFERENCE 1 (bases 1 to 2295)  
AUTHORS Lee, J.S., Pushko, P., Parker, M.D., Smith, J.F. and Welkos, S.L.  
TITLE Anthrax vaccine  
JOURNML Patent: US 6770479-A 1 03-AUG-2004;  
The United States of America as represented by the Secretary of the Army; Washington, DC;  
WOX;

FEATURES  
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Location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 59; DB 6; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 59  
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Db 1587 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1645

RESULT 20  
LOCUS AF306778 2369 bp DNA linear BCT 01-OCT-2003  
DEFINITION Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306778  
VERSION AF306778.1 GI:10880942

KEYWORDS  
SOURCE  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus anthracis

JOURNML J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNML Submitted (20-SEP-2000) Biological Sciences, Northern Arizona University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA

FEATURES  
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Location/Qualifiers  
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CDS

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ORIGIN

Query Match 100.0%; Score 59; DB 1; Length 2369;  
Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1635 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1693

RESULT 21  
LOCUS AF306779 2369 bp DNA linear BCT 01-OCT-2003  
DEFINITION Bacillus anthracis isolate 28 protective antigen (pag) gene,  
complete cds.  
ACCESSION AF306779  
VERSION AF306779.1 GI:10880944







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NAQDFSTPTITMNVNQLPELTKQRLADTDQYGNATYFNGRVRVDTGSNWS
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GNLYOGKDIETEDPFPDQTSQNIKNQALNATNITYVLADIKLAKAKNMLIRDRK
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## ORIGIN

Query Match 100.0%; Score 59; DB 1; Length 2369;

Best Local Similarity 100.0%; Pred. No. 2.9e-25; Mismatches 0; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59  
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Db 1635 GGTAGAAAGCGGATAGCGGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1693

RESULT 24  
AF306782 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis plasmid pX01 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306782  
VERSION AF306782.1 GI:10880950  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
FEATURES  
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Best Local Similarity 100.0%; Pred. No. 2.9e-25; Mismatches 0; Indels 0; Gaps 0;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59  
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Db 1635 GGTAGAAAGCGGATAGCGGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1693

RESULT 25  
AF306783 2369 bp DNA linear BCT 01-OCT-2003  
LOCUS Bacillus anthracis isolate BAI024 protective antigen (pag) gene,  
DEFINITION complete cds.  
ACCESSION AF306783  
VERSION AF306783.1 GI:10880952  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Genetic diversity in the protective antigen gene of Bacillus  
anthracis  
JOURNAL J. Bacteriol. 181 (8), 2358-2362 (1999)  
PUBMED 10197996  
REFERENCE 2 (bases 1 to 2369)  
AUTHORS Price, L.B., Hugh-Jones, M., Jackson, P.J. and Keim, P.  
TITLE Direct Submission  
JOURNAL Submitted (20-SEP-2000) Biological Sciences, Northern Arizona  
University, P.O. Box 5640, Flagstaff, AZ 86011-5640, USA  
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FKLYMTDSQNKKEVISSDNLQPELKOKSSNRKRSSTAGPTVPDRDNGI PPSLEY  
EGYTVDKNKRTPLSFWISNIHEKKGITLKYSPEKSTASDPYDPEKVTGRIDKRV  
SPEARHPVLAAYPIVHVDMENIILSKNEDSTONTDSQTRTISKNTSRTHTSEVHG  
NAEVHASFDDIGSVSAGFSNSSTVAIDHSLSAERTMAETGMLNTADTALAN  
IRYVNTGTAPIYVNLPTTSLVLGKNOQTATIKAKENQLSQILAFNNYTPSKNLAIAL  
NAQDFSTPTITMNVNQLPELTKQRLADTDQYGNATYFNGRVRVDTGSNWS  
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GNLYOGKDIETEDPFPDQTSQNIKNQALNATNITYVLADIKLAKAKNMLIRDRK  
PHYDRNNIYAGABSVKAEHREYINSGTGLNLINDKDIRKILISGTVIETDEGLK  
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FKLYMTDSQNKKEVISSDNLQPELKOKSSNRKRSSTAGPTVPDRDNGI PPSLEY  
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ORIGIN

Query Match 100.0%; Score 59; DB 1; Length 2369;  
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 1635 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 1693

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 NAODPFSTPIITMNNVNOFLBETKQQLDLDVYGNLATYFNGRVRVDTGSNMS  
 VLPJOETTARIIIFNGKDNLVERRIAANVPSDPLETTKPDMLKEALKIAFGNEPN  
 GNLQYQKDITFEFNPDOQTSONIKQALBANVTNYITVLDKIKLANAKNIIILDRK  
 FHYDRNNIAGVADSVVKEAREVINSSTEGLLNIDDKIKLISGYVELEDGK  
 EVINDRYMNLNSSLRODGKTFIDPKYKNDKPLIYISPNKVVAVATKENTIIINPS  
 ENGDTSTNGIKILIFSKGYEIG"

RESULT 26  
 AF268967 2549 bp DNA linear BCT 31-JUL-2000  
 LOCUS Bacillus anthracis plasmid pX01 protective antigen (paga) gene,  
 DEFINITION complete cds.  
 ACCESSION AF268967  
 VERSION AF268967.1 GI:9280532  
 KEYWORDS  
 SOURCE  
 ORGANISM Bacillus anthracis  
 Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
 cereus group.  
 1 (bases 1 to 2549)  
 Cohen, S., Mendelson, I., Alboun, Z., Kobiler, D., Elhanany, E.,  
 Bino, T., Leitner, M., Imbar, I., Rosenberg, H., Gozes, Y., Barak, R.,  
 Fisher, M., Kromann, C., Velan, B. and Shaffer, A.  
 Attenuated nontoxicogenic and nonencapsulated recombinant Bacillus  
 anthracis spore vaccines protect against anthrax  
 Infect. Immun. 68 (8), 4549-4558 (2000)  
 10899854  
 2 (bases 1 to 2549)  
 Cohen, S., Mendelson, I. and Shaffer, A.  
 Direct Submision  
 Submitted (18-MAY-2000) Department of Biochemistry, Israel  
 Institute for Biological Research, P.O. Box 19, Ness Ziona 74100,  
 Israel

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 SPEARHPVAAVPIVHVDMENIILSKNDSQNTDSTRTISKNTSRTTSHSVHG  
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ORIGIN

Query Match 100.0%; Score 59; DB 1; Length 2549;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
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 ENGDTSTNGIKILIFSKGYEIG"

RESULT 27  
 AX933603 2605 bp DNA linear PAT 22-DEC-2003  
 LOCUS Sequence 3 from Patent WO03087378.  
 DEFINITION AX933603  
 ACCESSION AX933603  
 VERSION AX933603.1 GI:40312826  
 KEYWORDS  
 SOURCE  
 ORGANISM Bacillus anthracis  
 Bacillus anthracis  
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
 cereus group.  
 1 Schmaljohn, C. U. and Fuller, J.  
 Nucleic acid immunization  
 Patent: WO 03087378-A.3 23-OCT-2003;  
 Powderject Research Limited (GB)  
 location/Qualifiers  
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ORIGIN

Query Match 100.0%; Score 59; DB 6; Length 2605;  
 Best Local Similarity 100.0%; Pred. No. 2.9e-25;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 59  
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 1760 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 1818



RESULT 28  
LOCUS I33400 2709 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 11 from patent US 5591631.  
ACCESSION I33400  
VERSION I33400.1 GI:1824191  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 2709)  
AUTHORS Leppla,S.H., Klimpel,K.R., Arora,N., Singh,Y. and Nicholas,P.J.  
TITLE Anthrax toxin fusion proteins, nucleic acid encoding same  
JOURNAL Patent: US 5591631-A 11 07-JAN-1997;  
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Db 1500 GGTAGAAAGCGGATAGCGGGTTAATCCTAGTATCGATCACTTAAGAAAGAAACCGG 1558  
RESULT 29  
LOCUS I69378 2709 bp DNA linear PAT 04-FEB-1998  
DEFINITION Sequence 11 from patent US 5677274.  
ACCESSION I69378  
VERSION I69378.1 GI:2831500  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
1 (bases 1 to 2709)  
AUTHORS Leppla,S.H., Klimpel,K.R., Arora,N., Singh,Y. and Nicholas,P.J.  
TITLE Anthrax toxin fusion proteins and related methods  
JOURNAL Patent: US 5677274-A 11 14-OCT-1997;  
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Query Match 100.0%; Score 59; DB 6; Length 2709;  
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OY 1 GGTAGAAAGCGGATAGCGGGTTAATCCTAGTATCGATCACTTAAGAAAGAAACCGG 59  
Db 1500 GGTAGAAAGCGGATAGCGGGTTAATCCTAGTATCGATCACTTAAGAAAGAAACCGG 1558

and Schmidt,J.J.  
Sequence and analysis of the DNA encoding protective antigen of  
Bacillus anthracis  
JOURNAL Gene 69 (2), 287-300 (1988)  
PUBMED 3148491  
REFERENCE 2 (bases 1 to 4235)  
AUTHORS Welkos,S.  
TITLE Direct Submission  
JOURNAL Submitted (15-JUN-1989) Bacteriology, USAMRIID, Ft. Detrick,  
Frederick, MD 21702, USA  
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RESULT 31  
LOCUS I13396 4235 bp DNA linear PAT 06-FEB-1997  
DEFINITION Sequence 3 from patent US 5591631.  
ACCESSION I13396  
VERSION I13396.1 GI:1824187







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 complement (6544. 8352)  
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Best Local Similarity	100.0%; Pred. No. 2.6e-25;
Matches	59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Db	133869 GGTGAAAGGCGGTACGCGCGGTAACTCTAGTATCCATTGAAACGACTAAACCGG 59
LOCUS	AB011190 181677 bp DNA circular BCT 14-JUN-2002
DEFINITION	Bacillus anthracis str. A2012 plasmid pxoi, complete sequence.
ACCESSION	AB011190
VERSION	AB011190.1 GI:20520075
KEYWORDS	
SOURCE	Bacillus anthracis str. A2012
ORGANISM	Bacillus anthracis str. A2012
REFERENCE	1 (bases 1 to 181677) Read,T.D., Salberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L., Holtzapfe,E., Busch,J.D., Smith,K.L., Schupp,J.M., Solomon,D., Keim,P. and Fraser,C.M. Comparative genome sequencing for discovery of novel polymorphisms in Bacillus anthracis Science 296 (5575), 2028-2033 (2002)
TITLE	
JOURNAL	12004073
PUBMED	2 (bases 1 to 181677) Read,T.D., Salberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L., Holtzapfe,E., Busch,J.D., Smith,K.L., Schupp,J.M., Solomon,D., Keim,P. and Fraser,C.M. Direct Submission Submitted (09-MAY-2002) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
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Query Match 100.0%; Score 59; DB 1; Length 181677;  
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RESULT 35  
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LOCUS Bacillus anthracis str. 'Ames Ancestor' plasmid pXOI, complete  
DEFINITION  
ACCESSION AB017336  
VERSION AB017336.2 GI:47552137  
KEYWORDS  
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ORGANISM  
Bacillus anthracis str. 'Ames Ancestor'  
Bacillus anthracis str. 'Ames Ancestor'  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
1 (bases 1 to 181677)  
Ravel,J., Raeko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,  
Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,  
Salzberg,S. and Fraser,C.M.  
Direct Submission  
Bacillus anthracis comparative genomics  
Unpublished  
2 (bases 1 to 181677)  
Ravel,J., Raeko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,  
Federova,N.B., Salzberg,S. and Fraser,C.M.  
Submitted (17-MAY-2004) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
On May 21, 2004 this sequence version replaced gi:47499967.  
This sequence is to be utilized as the reference strain for  
Bacillus anthracis research - all other sequences should be  
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Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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RESULT 36  
AC111756/C  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-248C14, \*\*\* SEQUENCING IN PROGRESS  
AC111756  
AC111756.4 GI:25073664  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
1 (bases 1 to 174720)  
Muzny, D., Marie, Metcker, M. Lee, Abramson, S., Adams, C., Alder, J.,  
Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D.,  
Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, B., Baden, H.,  
Baldwin, B., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,  
Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,  
Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,  
Cardenas, V., Carter, K., Cavazos, I., Cesaar, H., Center, A.,  
Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,  
Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,  
Devila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
Diegado, O., Denson, S., Deramo, C., Ding, Y., Din, H., Divya, K.,  
Drepper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K.,  
Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G.,  
Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
Frazer, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
Gebregeorgis, B., Geer, K., Gill, R., Grady, M., Guert, W., Guevara, W.,  
Gunnarane, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K.,  
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Herrandez, R., Hines, S., Hledum, S. L., Hodgson, A., Hogues, M.,  
Hollins, B., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A.,  
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Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, D.,  
Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J.,  
Lorenshewa, L., Louissege, H., Lozada, R. U., Lu, X., Ma, T.,  
Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A.,  
Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, B.,  
Mawhinney, S., McLeod, M. P., McNeill, T. Z., Meenen, B.,



TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S.,  
Morgan,M., Morris,K., Morris,S., Mundaasa,M., Murphy,M., Nair,L.,  
Nakkeris,C., Neal,D., Newton,N., Nguyen,N., Norris,S.,  
Nwokilemech,O., Okunolu,G., Olampunagoon,A., Pal,S., Parke,K.,  
Paternak,S., Paul,H., Perez,A., Perez,L., Plankkoch,C.,  
Plopper,F., Polindexter,A., Popovic,D., Primus,B., Pu,L.,D.,  
Puzo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R.,  
Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F.,  
Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.,J.,  
Sanders,W., Savery,G., Scherer,S., Scott,G., Shatman,S., Shen,H.,  
Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajic,D.,  
Sned,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J.,  
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Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Umami,K.,  
Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J.,  
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Wright,D., Wright,R., Wu,J., Yakub,S., Yen,J., Yoon,L., Yoon,V.,  
Yu,F., Zhang,J., Zhou,J., Zhou,X., Zhao,S., Dunn,D., von  
Niederhausern,A., Weiss,R., Smith,D.R., Holt,R.A., Smith,H.O.,  
Weinstock,G. and Gibbs,R.A.

Unpublished  
2 (bases 1 to 174720)  
Worley,K.C.

Direct Submission  
Submitted (19-FEB-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 174720)  
Rat Genome Sequencing Consortium.

Direct Submission  
Submitted (19-NOV-2002) Human Genome Sequencing Center, Department  
of Molecular and Human Genetics, Baylor College of Medicine, One  
Baylor Plaza, Houston, TX 77030, USA

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

The sequence in this assembly is a combination of BAC based reads  
and whole genome shotgun sequencing reads assembled using Atlas  
(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described  
in the feature table below represents a scaffold in the Atlas  
assembly (a 'contig-scaffold'). Within each contig-scaffold,  
individual sequence contigs are ordered and oriented, and separated  
by sized gaps filled with Ns to the estimated size. The sequence  
may extend beyond the ends of the clone and there may be sequence  
contigs within a contig-scaffold that consist entirely of whole  
genome shotgun sequence reads. Both end sequences and whole genome  
shotgun sequence only contigs will be indicated in the feature  
table.

----- Genome Center  
Center: Baylor College of Medicine

Center code: BCM  
Web site: http://www.hgsc.bcm.tmc.edu/  
Contact: hgsc-help@bcm.tmc.edu

----- Project Information  
Center project name: GOAO

----- Summary Statistics  
Center clone name: CH230-248C14

Assembly program: Phrap; version 0.990329  
Consensus quality: 150282 bases at least Q40  
Consensus quality: 154752 bases at least Q30  
Consensus quality: 157508 bases at least Q20  
Estimated insert size: 151567; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

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\* NOTE: Estimated insert size may differ from sequence length  
\* (see http://www.hgsc.bcm.tmc.edu/docs/genbankdraftdata.html).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will

FEATURES  
source

\* be preserved.  
1 44325: contig of 44325 bp in length  
\* 44326 44425: gap of unknown length  
\* 44426 170547: contig of 126122 bp in length  
\* 170548 170647: gap of unknown length  
\* 170648 171732: contig of 1085 bp in length  
\* 171733 171832: gap of unknown length  
\* 171833 173391: contig of 1559 bp in length  
\* 173392 173491: gap of unknown length  
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ORIGIN

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Best Local Similarity 100.0%; Pred. NO. 0.098;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 TTAATCTAGTATCATTTAG 44  
Db 72120 TTAATCTAGTATCATTTAG 72100

RESULT 37  
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LOCUS Rattus norvegicus clone CH230-41C1, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
DEFINITION 5 unordered pieces.  
ACCESSION AC097773  
VERSION AC097773.6 GI:30521558  
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
1 (bases 1 to 240276)  
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 Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstein, G. and Gibbs, R.A.

# TITLE JOURNAL REFERENCE AUTHORS JOURNAL

2 (bases 1 to 240276)  
 Direct Submission

Morley, K.C.  
 Direct Submission  
 Submitted (23-OCT-2001) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 240276)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (10-MAY-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA

On May 10, 2003 this sequence version replaced gi:24942826.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: hgsc-help@bcm.tmc.edu  
 ----- Project Information  
 Center project name: GRPK  
 Center clone name: CH230-41C1  
 ----- Summary Statistics  
 Assembly program: Atlas 3.0;  
 Consensus quality: 198296 bases at least Q40

Consensus quality: 201912 bases at least Q30  
 Consensus quality: 204554 bases at least Q20  
 Estimated insert size: 201878; sum-of-contigs estimation  
 Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

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 \* NOTE: Estimated insert size may differ from sequence length  
 \* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 5 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

1 222276: contig of 222276 bp in length  
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 \* 222377 236055: contig of 13679 bp in length  
 \* 236056 237418: gap of unknown length  
 \* 237419 237518: contig of 1263 bp in length  
 \* 237519 238717: gap of unknown length  
 \* 238718 238817: contig of 1199 bp in length  
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## gap

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## ORIGIN

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 Best Local Similarity 100.0%; Pred. No. 0.057;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

24 TTAATCCTAGTGCATCATTTAG 44  
 Db 236604 TTAATCCTAGTGCATCATTTAG 236584

## RESULT 38

AC094966 249338 bp DNA linear HTG 09-MAY-2003  
 LOCUS Rattus norvegicus clone CH230-6L24, \*\*\* SEQUENCING IN PROGRESS \*\*\*  
 DEFINITION 6 unordered pieces.  
 AC094966  
 AC094966.5 GI:30467141  
 VERSION HTG: HTGS PHASE1; HTGS DRAFT; HTGS ENRICHED.  
 KEYWORDS Rattus norvegicus (Norway rat)  
 SOURCE Rattus norvegicus  
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;



REFERENCE  
AUTHORS

Sciurognathi; Muroidea; Muridae; Murinae; Rattus.

1 (bases 1 to 249338)

Murphy D. Marie, Metzger M. Lee, Abramson S., Adams C., Alder J., Allen C., Allen H., Albrooks S., Amin A., Angiano D., Anylebech V., Aoyagi A., Ayodeji M., Baca E., Baden H., Baldwin D., Bandanaike D., Barber M., Barnstead M., Bernhied F., Biewald K., Blair J., Blankenburg K., Blyth P., Brown M., Bryant N., Buhay C., Burch P., Burrell K., Calderon E., Cardenas V., Carter K., Cavazos I., Caesar H., Center A., Chacko J., Chavez D., Chen G., Chen R., Chen Y., Chen Z., Chu J., Cleveland C., Cockrell R., Cox C., Coyle M., Cree A., D'Souza L., Davila M. L., Davis C., Davy-Carroll L., De Anda C., Dederich D., Delgado O., Denson S., Deramo C., Ding Y., Dinh H., Divya K., Draper H., Dugan-Rocha S., Dunn A., Durbin K., Duval B., Evans K., Egan A., Escotto M., Eugene C., Evans C. A., Fails T., Fan G., Fernandez S., Finley M., Flagg N., Forbes L., Foster M., Foster P., Fraser C. M., Gabisi A., Ganta R., Garcia A., Garner T., Garza M., Gebregeorgis E., Geer K., Gill R., Grady M., Guerra M., Guevara W., Gunaratne P., Haaland W., Hamill C., Hamilton C., Hamilton K., Harvey Y., Havlak P., Hawes A., Henderson N., Hernandez J., Hernandez R., Hines S., Hladun S. L., Hodgson A., Hognes M., Hollins B., Howells S., Huiyk S., Hume J., Idlebird D., Jackson A., Jackson L., Jacob L., Jiang H., Johnson B., Johnson R., Jolivet A., Karpathy S., Kelly S., Kelly S., Khan Z., King L., Kovar C., Kowis C., Kraft C. L., Lebow H., Levan J., Lewis L., Li Z., Liu J., Liu J., Liu W., Liu Y., London P., Longacre S., Lopez J., Losheneva L., Louisedge H., Lozano R. J., Lu X., Ma J., Maheshwari M., Mahindartne M., Mahmoud M., Malloy K., Mangum A., Mangum B., Mapua P., Martin K., Martin R., Martinez E., Mahoney S., McLeod M. P., McNeill T. Z., Meenen E., Miosavljovic A., Miner G., Minja E., Montemayor J., Moore S., Morgan M., Morris K., Morris S., Munidasa M., Murphy M., Nair L., Nankervis C., Neal D., Newton N., Nguyen N., Norris S., Nwokediemo O., Okwoum G., Olarnpungsaon A., Pal S., Parks K., Patelrak S., Paul H., Perez A., Perez L., Pfannkuch C., Plopper F., Poindexter A., Popovic D., Primus E., Pu L., Pu L., Puazo M., Quiroz J., Rachlin R., Reeves K., Regier M. A., Reigh R., Reilly B., Reilly M., Ren Y., Reuter M., Richards S., Riggs F., Rivers C., Rodkey T., Rojce A., Rose R., Rose R., Ruiz S. J., Sanders W., Savery G., Scherer S., Scott G., Shatman S., Shen H., Shetty J., Shvartsbeyn A., Sison I., Sitter C. D., Smajic D., Sneed A., Sodergren E., Song X.-Z., Sorrelle R., Sosa J., Steimle M., Strong R., Sutton A., Svatek A., Taber P., Taylor C., Taylor T., Thomas N., Thomas S., Tingey A., Trejos Z., Usmani K., Valas R., Vera V., Villaseana D., Waldron L., Walker B., Wang J., Wang Q., Wang S., Warren J., Warren R., Wei X., White F., Williams G., Willson R., Wleczek R., Wooden H., Worley K., Wright D., Wright R., Wu J., Yakub S., Yen J., Yoon L., Yoon V., Yu F., Zhang J., Zhou J., Zhou X., Zhao S., Dunn D., von Niederhausen A., Weise R., Smith D. R., Holt R. A., Smith H. O., Weinstock G. and Gibbs R. A.

## TITLE

Direct Submission

## JOURNAL

Unpublished

## REFERENCE

2 (bases 1 to 249338)

## AUTHORS

Worley K. C.

## JOURNAL

Direct Submission

Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## REFERENCE

3 (bases 1 to 249338)

## AUTHORS

Rat Genome Sequencing Consortium.

## JOURNAL

Direct Submission

Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

## COMMENT

The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)

Project Information

Center project name: GBVC

Center clone name: CH230-6L24

Summary Statistics

Assembly program: Atlas;

Consensus quality: 204902 bases at least Q40

Consensus quality: 209721 bases at least Q30

Consensus quality: 213215 bases at least Q20

Estimated insert size: 222181; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

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Quality coverage: 5x in Q20 bases; sum-of-contigs estimation

Quality coverage: 5x in Q20 bases; sum-of-contigs estimation



RESULT 39  
AC094968/c  
LOCUS AC094968 258249 bp DNA linear HTG 09-MAY-2003  
DEFINITION Rattus norvegicus clone CH230-6M2. \*\*\* SEQUENCING IN PROGRESS \*\*\*  
15 unordered pieces.  
AC094968  
AC094968.9 GI:30467153  
KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Rattus.  
REFERENCE  
AUTHORS Muzny, D. Marie, Metzker, M. Lee, Abramson, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angiulo, D., Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biwalto, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Evans, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Frazer, C. M., Gabisi, A., Gant, R., Garcia, A., Garner, T., Garza, M., Gebregiorgis, B., Geer, K., Gill, R., Grady, M., Guerra, M., Guetara, W., Guenard, P., Haaland, W., Hamil, C., Hamilton, C., Hamilton, K., Harey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulys, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshew, L., Louised, H., Lozano, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapua, P., Martin, K., Martin, R., Martinez, E., Mathiney, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nandertis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Ntali, L., Nwackeme, O., Okunolu, G., Olafunmoye, A., Pal, S., Parks, K., Paeternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Polinder, A., Popovic, D., Primus, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. U., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartbeyn, A., Sisson, I., Sitter, C. D., Smajls, D., Sneed, A., Sodergren, B., Song, X.-Z., Sorelle, R., Soza, D., Steimle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tinney, A., Trejos, Z., Uman, J., Vais, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Wilson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, S., Zhou, S., Dunn, D., von Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstein, G. and Gibbs, R. A.  
TITLE Direct Submission  
JOURNAL Unpublished  
2 (bases 1 to 258249)  
AUTHORS Worley, K. C.  
JOURNAL Direct Submission  
Submitted (15-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
REFERENCE 3 (bases 1 to 258249)  
AUTHORS Rat Genome Sequencing Consortium.

TITLE  
JOURNAL  
COMMENT  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On May 9, 2003 this sequence version replaced gi:2518885.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/project/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.  
----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GSVB  
Center clone name: CH230-6M2  
----- Summary Statistics  
Assembly program: Atlas  
Consensus quality: 189965 bases at least Q40  
Consensus quality: 197194 bases at least Q20  
Consensus quality: 203248 bases at least Q20  
Estimated insert size: 199666; sum-of-contigs estimation  
Quality coverage: 5x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 15 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 17695: contig of 17695 bp in length  
\* 17696 17795: gap of unknown length  
\* 17796 20724: contig of 2929 bp in length  
\* 20725 20824: gap of unknown length  
\* 20825 238279: contig of 217455 bp in length  
\* 238280 238379: gap of unknown length  
\* 238380 239535: contig of 1156 bp in length  
\* 239536 239635: gap of unknown length  
\* 239636 241396: contig of 1761 bp in length  
\* 241397 241496: gap of unknown length  
\* 241497 242724: contig of 1228 bp in length  
\* 242725 242824: gap of unknown length  
\* 242825 244618: contig of 1793 bp in length  
\* 244618 244717: gap of unknown length  
\* 244718 246834: contig of 2117 bp in length  
\* 246835 246934: gap of unknown length  
\* 246935 248127: contig of 1193 bp in length  
\* 248128 248227: gap of unknown length  
\* 248228 249390: contig of 1163 bp in length  
\* 249391 249490: gap of unknown length  
\* 249491 250641: contig of 1151 bp in length  
\* 250642 250741: gap of unknown length  
\* 250742 252772: contig of 1531 bp in length  
\* 252773 252872: gap of unknown length  
\* 252873 253719: contig of 1347 bp in length  
\* 253720 253819: gap of unknown length  
\* 253820 255194: contig of 1375 bp in length  
\* 255195 255294: gap of unknown length  
\* 255295 258249: contig of 2955 bp in length.  
Location/Qualifiers



	source	1.. 258249	/organism="Rattus norvegicus"	
			/mol_type="genomic DNA"	
			/db_xref="taxon:10116"	
			/clone="CH230-GM2"	
	gap	1796.. 17795	/estimated_length=unknown	
	misc_feature	17796.. 19700	/note="wgs_contig"	
	gap	20725.. 20824	/estimated_length=unknown	
	misc_feature	106696.. 108927	/note="wgs_contig"	
	misc_feature	170450.. 1172616	/note="wgs_contig"	
	gap	238280.. 238379	/estimated_length=unknown	
	gap	239536.. 239635	/estimated_length=unknown	
	gap	241397.. 241496	/estimated_length=unknown	
	gap	242725.. 242824	/estimated_length=unknown	
	gap	244618.. 244717	/estimated_length=unknown	
	gap	246835.. 246934	/estimated_length=unknown	
	gap	248128.. 248227	/estimated_length=unknown	
	gap	249391.. 249490	/estimated_length=unknown	
	gap	250642.. 250741	/estimated_length=unknown	
	gap	252273.. 252372	/estimated_length=unknown	
	gap	253720.. 253819	/estimated_length=unknown	
	gap	255195.. 255294	/estimated_length=unknown	
	ORIGIN			
	Query Match	35.6% Score 21; DB 14; Length 258249;		
	Best Local Similarity	100.0%; Pred.No. 0.097;		
	Matches	21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
Oy	24 TTAATCCTAGTGCATTG 44			
Db	65437 TTAACTCTAGTGATCCATTG 65417			
RESULT 40	AC131444	245812 bp	DNA	linear HTG 09-MAY-2003
LOCUS	AC131444/C			
DEFINITION	Rattus norvegicus clone CH230-5A7, *** SEQUENCING IN PROGRESS ***,			
	8 unordered pieces.			
ACCESSION	AC131444			
VERSION	AC131444.4 GI:30466292			
KEYWORDS	HTG; HTGS PHASEI; HTGS DRAFT; HTGS_ENRICHED.			
SOURCE	Rattus norvegicus (Norway rat)			
ORGANISM	Rattus norvegicus			
	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;			
	Sciurognathi; Muridea; Muridae; Murinae; Rattus.			
	1 (bases 1 to 245812)			
	Muzny, D.Marie, Metzker, M.Lee., Abramson, S., Adams, C., Alder, J.,			
	Allen, C., Allen, H., Alpbroske, S., Amin, A., Angiano, D.,			
	Anylalech, V., Ayogei, A., Ayodeji, M., Baca, E., Baden, H.,			
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	Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,			

Devila, M.L., Davis, C., Davy-Carroll, L., De Anda, C., Dederich, D.,  
 Delgado, O., Denison, S., Deramo, C., Ding, Y., Dinth, H., Diya, K.,  
 Draper, H., Dugan-Rocha, S., Dunn, A., Dublin, K., Duval, B., Eaves, K.,  
 Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falle, T., Fan, G.,  
 Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P.,  
 Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,  
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 Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K.,  
 Hernandez, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J.,  
 Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hoques, M.,  
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 Niederhausen, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O.,  
 Weinstock, G. and Gibbs, R.A.

Direct Submission  
 Unpublished  
 2 (bases 1 to 245812)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (22-APR-2002) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 245812)  
 Rat Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (09-MAY-2003) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 On May 9, 2003 this sequence version replaced gi:24818488.  
 The sequence in this assembly is a combination of BAC based reads  
 and whole genome shotgun sequencing reads assembled using Atlas  
 (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described  
 in the feature table below represents a scaffold in the Atlas  
 assembly (a 'contig-scaffold'). Within each contig-scaffold,  
 individual sequence contigs are ordered and oriented, and separated  
 by sized gaps filled with Ns to the estimated size. The sequence  
 may extend beyond the ends of the clone and there may be sequence  
 contigs within a contig-scaffold that consist entirely of whole  
 genome shotgun sequence reads. Both end sequences and whole genome  
 shotgun sequence only contigs will be indicated in the feature  
 table.

----- Genome Center  
 Center: Baylor College of Medicine  
 Center code: BCM  
 Web site: <http://www.hgsc.bcm.tmc.edu/>  
 Contact: [hgsc-help@bcm.tmc.edu](mailto:hgsc-help@bcm.tmc.edu)  
 ----- Project Information -----



Center project name: GRAD  
Center clone name: CH230-5A7  
----- Summary Statistics -----

Assembly program: Atlas;  
Consensus quality: 232192 bases at least Q40  
Consensus quality: 235216 bases at least Q30  
Consensus quality: 237217 bases at least Q20  
Estimated insert size: 243602; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/Genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 8 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

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1      5768: contig of 5768 bp in length
*      1      5769      5868: gap of unknown length
*      5869      229450: contig of 223582 bp in length
*      229451      229550: gap of unknown length
*      229551      235483: contig of 5933 bp in length
*      235484      235583: gap of unknown length
*      235584      238991: contig of 3408 bp in length
*      238992      239091: gap of unknown length
*      239092      241301: contig of 2110 bp in length
*      241302      242547: contig of 1246 bp in length
*      242548      243774: contig of 1127 bp in length
*      243775      243874: gap of unknown length
*      243875      245812: contig of 1938 bp in length.
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## FEATURES

Location/Qualifiers

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             /note="clone_boundary
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             site:ECORI
             end sequence: BH334419"
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             /estimated_length=unknown
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## ORIGIN

Query Match 33.9%; Score 20; DB 14; Length 245812;  
Best Local Similarity 100.0%; Pred. No. 0.41;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 24 TTAATCCAGATGCATTA 43  
|||||  
Db 22838 TTAATCCAGATGCATTA 22819

Search completed: April 11, 2006, 18:09:57  
Job time : 426.437 secs







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C 94	16	27.1	749	6	ABQ23415	AbQ23415 Oligonuc1	167	15	25.4	26565	10	ADH80491	Adh80491 Becherich
C 95	16	27.1	749	6	ABQ23414	AbQ23414 Oligonuc1	168	15	25.4	58326	13	ACN37226	Acn37226 Human per
C 96	16	27.1	781	6	ABQ27463	AbQ27463 Oligonuc1	C 169	15	25.4	58857	3	AA58471	Aa58471 Nucleotid
C 97	16	27.1	781	6	ABQ27462	AbQ27462 Oligonuc1	170	15	25.4	72383	14	ABE96530	Abe96530 Human EGF
C 98	16	27.1	879	6	ABQ15031	AbQ15031 Oligonuc1	171	15	25.4	14391	10	ADL13648	Adl13648 Osteocarth
C 99	16	27.1	879	6	ABQ15030	AbQ15030 Oligonuc1	C 172	15	25.4	168407	13	ABD33266	Abd33266 Murine ca
C 100	16	27.1	891	8	ACA35744	AcA35744 Prokaryot	173	15	23.7	243	4	AAI20522	Aai20522 Probe #10
C 101	16	27.1	891	8	ACA19368	AcA19368 Prokaryot	174	14	23.7	243	4	ABA65565	Aba65565 Human foe
C 102	16	27.1	912	11	ACH96615	AcH96615 Klebsiell	175	14	23.7	243	4	AAI45731	Aai45731 Probe #14
C 103	16	27.1	978	6	ABQ31366	AbQ31366 Oligonuc1	176	14	23.7	243	4	ABA47670	Aba47670 Human bre
C 104	16	27.1	978	6	ABQ31367	AbQ31367 Oligonuc1	177	14	23.7	243	4	ABA32654	AbA32654 Probe #11
C 105	16	27.1	1206	10	ADFS8441	Adf58441 Human pol	178	14	23.7	243	4	AAK39715	Aak39715 Human bon
C 106	16	27.1	1221	5	AA569154	Aa569154 DNA encod	179	14	23.7	243	4	AAK13969	Aak13969 Human bra
C 107	16	27.1	1221	5	AA567826	Aa567826 DNA encod	180	14	23.7	243	4	AB539304	Ab539304 Human liv
C 108	16	27.1	1221	5	AA567898	Aa567898 DNA encod	181	14	23.7	243	6	AAI06220	Aai06220 Probe #62
C 109	16	27.1	1266	13	ADS95145	AdS95145 Human the	182	14	23.7	262	12	ADQ05799	AdQ05799 Soybean z
C 110	16	27.1	1266	13	ADS94983	AdS94983 Human the	C 183	14	23.7	262	12	ADQ05799	AdQ05799 Soybean z
C 111	16	27.1	1266	13	ADV68002	Adv68002 Biologica	C 184	14	23.7	302	6	ABK64714	AbK64714 Human den
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C 113	16	27.1	1884	5	AA581725	Aa581725 DNA encod	C 186	14	23.7	361	13	ACF88030	Acf88030 Human SIR
C 114	16	27.1	1884	5	AA567592	Aa567592 DNA encod	C 187	14	23.7	374	12	ADQ06865	AdQ06865 Soybean t
C 115	16	27.1	1886	5	AA580612	Aa580612 DNA encod	C 188	14	23.7	386	12	ADQ06863	AdQ06863 Soybean t
C 116	16	27.1	1946	4	AB112433	Ab112433 Drosophill	C 189	14	23.7	402	4	AAK70026	Aak70026 Human lmm
C 117	16	27.1	1946	4	AA557123	Aa557123 CDNA enco	C 190	14	23.7	409	12	ADQ06859	AdQ06859 Soybean t
C 118	16	27.1	1946	10	ADC35825	AdC35825 Drosophill	C 191	14	23.7	423	12	ADQ06856	AdQ06856 Soybean t
C 119	16	27.1	2202	14	ADY84836	AdY84836 Bacillus	C 192	14	23.7	429	12	ADQ05814	AdQ05814 Soybean z
C 120	16	27.1	3946	4	AB112432	Ab112432 Drosophill	C 193	14	23.7	429	12	ADQ05815	AdQ05815 Soybean z
C 121	16	27.1	3946	4	AA557122	Aa557122 DNA encod	C 194	14	23.7	437	12	ADQ06861	AdQ06861 Soybean t
C 122	16	27.1	3946	10	ADC35824	AdC35824 Drosophill	C 195	14	23.7	437	12	ADQ06861	AdQ06861 Soybean t
C 123	16	27.1	3946	10	ADY84836	AdY84836 Bacillus	C 196	14	23.7	441	10	ADQ06855	AdQ06855 Soybean t
C 124	15	25.4	441	6	AB180946	Ab180946 Human ova	197	14	23.7	447	10	ADQ06855	AdQ06855 Soybean t
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C 129	15	25.4	714	6	ABQ32676	AbQ32676 Oligonuc1	202	14	23.7	484	4	ABA22745	Aba22745 Probe #12
C 130	15	25.4	715	6	ABQ25515	AbQ25515 Oligonuc1	203	14	23.7	484	4	AAK26678	Aak26678 Human bon
C 131	15	25.4	715	6	ABQ25514	AbQ25514 Oligonuc1	204	14	23.7	484	4	AAK01218	Aak01218 Human bra
C 132	15	25.4	734	6	ABQ49600	AbQ49600 Oligonuc1	205	14	23.7	484	4	ABS26269	AbS26269 Human liv
C 133	15	25.4	734	6	ABQ49601	AbQ49601 Oligonuc1	206	14	23.7	484	5	AAI01220	Aai01220 Probe #12
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C 135	15	25.4	800	6	ABQ18148	AbQ18148 Oligonuc1	C 208	14	23.7	520	6	ABQ24710	AbQ24710 Oligonuc1
C 136	15	25.4	1080	13	ADT45444	AdT45444 Bacteriat	209	14	23.7	520	6	ABQ24711	AbQ24711 Oligonuc1
C 137	15	25.4	1479	6	AB165814	Ab165814 Lung canc	210	14	23.7	546	12	ACH70181	Ach70181 Human gen
C 138	15	25.4	1479	6	AB165814	Ab165814 Lung canc	C 211	14	23.7	546	12	ACH70181	Ach70181 Human gen
C 139	15	25.4	1479	12	ADO19431	AdO19431 Human PRO	212	14	23.7	569	6	ABQ16771	AbQ16771 Oligonuc1
C 140	15	25.4	1479	12	ADO59198	AdO59198 MSI-H car	C 213	14	23.7	569	6	ABQ16770	AbQ16770 Oligonuc1
C 141	15	25.4	1479	13	ACN39625	AcN39625 Tumour-as	C 214	14	23.7	570	13	ACN57532	AcN57532 Cocton gy
C 142	15	25.4	1479	14	ADY15261	AdY15261 DNA encod	C 215	14	23.7	571	6	ABQ25518	AbQ25518 Oligonuc1
C 143	15	25.4	1703	3	AA429014	Aa429014 Arabidops	216	14	23.7	571	6	ABQ25519	AbQ25519 Oligonuc1
C 144	15	25.4	1703	3	AA429014	Aa429014 Arabidops	C 217	14	23.7	576	6	ABQ44461	AbQ44461 Oligonuc1
C 145	15	25.4	2000	11	ACL37624	AcL37624 Rice stre	218	14	23.7	576	6	ABQ44460	AbQ44460 Oligonuc1
C 146	15	25.4	2067	13	ADS58456	AdS58456 Bacteriat	C 219	14	23.7	600	4	ABK61087	AbK61087 Human foe
C 147	15	25.4	2167	10	ADA52848	AdA52848 Human cod	C 220	14	23.7	600	4	AA140985	Aa140985 Probe #96
C 148	15	25.4	2331	12	ADO19429	AdO19429 Human PRO	C 221	14	23.7	600	4	ABA28985	Aba28985 Probe #74
C 149	15	25.4	2380	14	ADX07434	AdX07434 Cyclin-de	C 222	14	23.7	600	4	AAK35269	Aak35269 Human bon
C 150	15	25.4	2483	12	ADO23245	AdO23245 Human sof	C 223	14	23.7	600	4	AAK09380	Aak09380 Human bra
C 151	15	25.4	3122	6	AA595278	Aa595278 long term	C 224	14	23.7	600	4	ABS35014	AbS35014 Human liv
C 152	15	25.4	3861	4	AB109228	Ab109228 Drosophill	C 225	14	23.7	603	6	ABS09680	AbS09680 Human gen
C 153	15	25.4	3861	4	AB109228	Ab109228 Drosophill	C 226	14	23.7	603	6	ABQ09092	AbQ09092 M. capuli
C 154	15	25.4	4300	10	AAH42107	AaH42107 Nucleotid	C 227	14	23.7	606	11	ABD01706	AbD01706 Pseudomon
C 155	15	25.4	4576	10	AD567446	Ad567446 Rat gene	228	14	23.7	612	6	ABQ36798	AbQ36798 Oligonuc1
C 156	15	25.4	5969	6	ABK33998	AbK33998 Human DNA	C 229	14	23.7	612	6	ABQ14898	AbQ14898 Oligonuc1
C 157	15	25.4	5969	6	AB192337	Ab192337 Chemicall	C 230	14	23.7	612	6	ABQ14899	AbQ14899 Oligonuc1
C 158	15	25.4	5969	8	ADA20381	Ada20381 Prostate	C 231	14	23.7	612	6	ABQ36799	AbQ36799 Oligonuc1
C 159	15	25.4	5969	8	ADA84188	Ada84188 Human ren	C 232	14	23.7	645	8	ACA48035	Aca48035 Prokaryot
C 160	15	25.4	6373	6	AB133966	Ab133966 Human imm	C 233	14	23.7	656	6	ABQ26142	AbQ26142 Oligonuc1
C 161	15	25.4	7059	13	AD514647	Ad514647 Pseudomon	C 234	14	23.7	656	8	ABQ26143	AbQ26143 Oligonuc1
C 162	15	25.4	7110	4	AAE81351	Aae81351 Quorum se	C 235	14	23.7	675	8	ACA44343	AcA44343 Prokaryot
C 163	15	25.4	9236	4	AB117350	Ab117350 Drosophill	C 236	14	23.7	683	6	ABQ49973	AbQ49973 Oligonuc1
C 164	15	25.4	9236	4	AB120102	Ab120102 Drosophill	C 237	14	23.7	683	6	ABQ49972	AbQ49972 Oligonuc1
C 165	15	25.4	12775	4	AB127700	Ab127700 Drosophill	238	14	23.7	696	6	ABK81019	AbK81019 Bacillus



239	14	23.7	703	6	ABQ51131	Abg51131 Oligonuc	c 312	14	23.7	1519	6	AA562428	AA562428 cDNA sequ
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242	14	23.7	709	6	ABQ25069	Abq25069 Oligonuc	315	14	23.7	1698	2	AAT68198	AAT68198 H. pylori
243	14	23.7	725	6	ABQ37532	Abq37532 Oligonuc	316	14	23.7	1708	12	ADQ25517	ADQ25517 Human sof
244	14	23.7	725	6	ABQ37533	Abq37533 Oligonuc	317	14	23.7	1731	13	ADX13183	ADX13183 Plant ful
245	14	23.7	733	6	ABQ17418	Abq17418 Oligonuc	c 318	14	23.7	1743	13	ADT48711	ADT48711 Bacterial
246	14	23.7	733	6	ABQ17419	Abq17419 Oligonuc	c 319	14	23.7	1872	10	ADK11452	ADK11452 Drosophi
247	14	23.7	738	10	ADF02629	Adf02629 Bacterial	c 320	14	23.7	1884	14	ABL17221	ABL17221 Drosophi
248	14	23.7	738	13	ADR64765	Adr64765 Cotton cd	321	14	23.7	2000	8	ADA72822	ADA72822 Rice gene
249	14	23.7	741	6	ABQ32307	Abq32307 Oligonuc	322	14	23.7	2000	11	ACL37579	ACL37579 Rice stre
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251	14	23.7	764	6	ABQ24113	Abq24113 Oligonuc	324	14	23.7	2000	11	ACL37064	ACL37064 Rice stre
252	14	23.7	764	6	ABQ24112	Abq24112 Oligonuc	325	14	23.7	2000	12	ADT41129	ADT41129 Plant cdn
253	14	23.7	764	6	ABQ24758	Abq24758 Oligonuc	326	14	23.7	2038	12	ADQ64816	ADQ64816 Novel hum
254	14	23.7	764	6	ABQ24759	Abq24759 Oligonuc	327	14	23.7	2073	2	AAV58675	AAV58675 Artichoke
255	14	23.7	772	6	ABQ52628	Abq52628 Oligonuc	328	14	23.7	2298	9	ABV24470	ABV24470 Fruit fly
256	14	23.7	772	6	ABQ52629	Abq52629 Oligonuc	329	14	23.7	2492	5	ABV24285	ABV24285 Human pro
257	14	23.7	795	11	ABD01740	Abd01740 Pseudomon	330	14	23.7	2499	4	ABL28943	ABL28943 Drosophi
258	14	23.7	814	4	AAH33473	Aah33473 Human col	c 331	14	23.7	2549	4	ABL23632	ABL23632 Drosophi
259	14	23.7	842	6	ABO53508	Abg53508 Oligonuc	332	14	23.7	2760	6	ABZ1783	ABZ1783 Arabidops
260	14	23.7	842	6	ABO53509	Abg53509 Oligonuc	333	14	23.7	2760	8	ADA68392	ADA68392 Arabidops
261	14	23.7	860	6	ABQ28534	Abq28534 Oligonuc	334	14	23.7	2760	12	ADN72258	ADN72258 Thale cre
262	14	23.7	860	6	ABQ28535	Abq28535 Oligonuc	335	14	23.7	2761	5	AA584709	AA584709 DNA encod
263	14	23.7	864	8	ACA47540	Acg47540 Prokaryot	336	14	23.7	2887	4	ABL29042	ABL29042 Drosophi
264	14	23.7	900	2	AAO34590	Aag34590 A4 fragme	337	14	23.7	3060	2	AAK07383	AAK07383 Arabidops
265	14	23.7	927	2	ACA22164	Acg22164 Prokaryot	338	14	23.7	3060	2	AAK07377	AAK07377 Arabidops
266	14	23.7	929	2	AAT60139	Aat60139 Antirrhin	339	14	23.7	3060	2	AAK07378	AAK07378 Arabidops
267	14	23.7	930	8	ACA51097	Acas1097 Prokaryot	340	14	23.7	3060	2	AAK07374	AAK07374 Arabidops
268	14	23.7	930	8	ACA51834	Acas1834 Prokaryot	341	14	23.7	3060	2	AAK07376	AAK07376 Arabidops
269	14	23.7	933	8	ACE72803	Act72803 Staphyloc	342	14	23.7	3060	2	AAK07379	AAK07379 Arabidops
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271	14	23.7	949	6	ABQ43869	Abq43869 Oligonuc	344	14	23.7	3177	4	ABL16832	ABL16832 Drosophi
272	14	23.7	949	6	ABQ43868	Abq43868 Oligonuc	345	14	23.7	3187	4	ABL08798	ABL08798 Drosophi
273	14	23.7	958	4	AA188905	Aa188905 Human pol	346	14	23.7	3187	4	AA557088	AA557088 DNA encod
274	14	23.7	986	13	ADX32246	Adx32246 Plant ful	347	14	23.7	3187	10	ADC35773	ADC35773 Drosophi
275	14	23.7	987	13	ADT45337	Adt45337 Bacterial	c 348	14	23.7	3481	13	ACN42608	ACN42608 Human dia
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283	14	23.7	1080	12	ADP98705	Adp98705 C. albica	c 356	14	23.7	3798	14	ADV14820	ADV14820 Protein r
284	14	23.7	1101	12	ADQ02792	Ado02792 Soybean c	c 357	14	23.7	3798	14	ADV14797	ADV14797 Protein r
285	14	23.7	1101	13	AD142430	Adi142430 Plant tra	c 358	14	23.7	3825	14	ADV14829	ADV14829 Protein r
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287	14	23.7	1137	10	ACPF67410	Acf67410 Photorhab	c 360	14	23.7	4393	10	ADH54362	ADH54362 Human gen
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289	14	23.7	1141	6	ABQ31403	Abq31403 Oligonuc	362	14	23.7	4731	4	ABL19382	ABL19382 Drosophi
290	14	23.7	1200	4	ABA82970	Abg82970 Enterococ	c 363	14	23.7	5076	6	ABL28942	ABL28942 Drosophi
291	14	23.7	1229	6	ABQ24598	Abq24598 Oligonuc	364	14	23.7	5244	8	ABZ10026	ABZ10026 Haemato
292	14	23.7	1229	6	ABQ24599	Abq24599 Oligonuc	c 365	14	23.7	5304	6	ABK28356	ABK28356 DNA trans
293	14	23.7	1252	8	ABS58051	Abs58051 Gene enco	c 366	14	23.7	5368	6	ABN80099	ABN80099 Human che
294	14	23.7	1252	14	ADW72704	Adw72704 Rhinodact	c 367	14	23.7	5455	4	ABL17220	ABL17220 Drosophi
295	14	23.7	1260	8	ACF74455	Act74455 Staphyloc	c 368	14	23.7	5572	6	ABL132815	ABL132815 Human imm
296	14	23.7	1317	13	ADX28715	Adx28715 Plant ful	c 369	14	23.7	5777	12	ADM92541	ADM92541 Thalecres
297	14	23.7	1320	8	ABN66156	Abn66156 Streptoco	370	14	23.7	5912	12	ADQ26103	ADQ26103 Arabidops
298	14	23.7	1320	8	ACA50596	Acg50596 Prokaryot	371	14	23.7	5912	12	ADQ26103	ADQ26103 Arabidops
299	14	23.7	1350	11	ABD01732	Abd01732 Pseudomon	372	14	23.7	5912	12	ADQ26103	ADQ26103 Arabidops
300	14	23.7	1389	2	AAV74636	Aav74636 Staphyloc	373	14	23.7	6185	9	ACD19127	ACD19127 E. coli 0
301	14	23.7	1413	4	AA552437	Aa552437 E. coli D	374	14	23.7	6185	10	ADC01397	ADC01397 Enteroha
302	14	23.7	1413	4	ACA32509	Acg32509 Prokaryot	c 375	14	23.7	6283	6	ABK39992	ABK39992 Human che
303	14	23.7	1413	13	AD541130	Ades4101 Bacterial	c 376	14	23.7	6526	6	ABL32835	ABL32835 Human imm
304	14	23.7	1425	13	ADSS1130	Adss1130 Bacterial	377	14	23.7	6526	6	ABL34237	ABL34237 Human imm
305	14	23.7	1442	4	ABL05895	Ab105895 Drosophi	378	14	23.7	6526	6	ABN80307	ABN80307 Human che
306	14	23.7	1478	6	ABQ44619	Abq44619 Oligonuc	379	14	23.7	6527	2	AAT60141	AAT60141 Antirrhin
307	14	23.7	1478	6	ABQ44618	Abq44618 Oligonuc	c 380	14	23.7	6948	6	ABL33409	ABL33409 Human imm
308	14	23.7	1495	8	AAA89197	Aa89197 Caenorhab	c 381	14	23.7	6948	6	AA561230	AA561230 Human gen
309	14	23.7	1495	8	ABX93665	Abx93665 DNA encod	c 382	14	23.7	7131	6	ABK31451	ABK31451 Signal tr
310	14	23.7	1500	10	ACC61841	Acc61841 Gene sequ	c 383	14	23.7	7131	6	ABL70428	ABL70428 Chemical
311	14	23.7	1500	10	ADK63767	Adk63767 Disease t	c 384	14	23.7	7131	6	AA561361	AA561361 Human gen



385	14	23.7	7143	2	AAV58287	Aav58287 S. pyogen	C 458	13	22.0	19	14	ADZ25975	Adz25975 PCR prime
386	14	23.7	8244	6	AA546396	AA546396 Tumour su	459	13	22.0	21	13	ADU41692	Adu41692 knock-dow
C 387	14	23.7	8244	6	ABL32993	Abi32993 Human imm	460	13	22.0	42	2	AAQ88081	Aaq88081 Primer us
C 388	14	23.7	8244	6	ABO67032	Abb67032 Human ang	C 461	13	22.0	50	6	ABZ28951	Abz28951 Candida g
C 389	14	23.7	8244	10	ADBS4134	ADB54134 Pretreat	C 462	13	22.0	60	8	ABV93692	Abv93692 Bacillus
C 390	14	23.7	8955	14	ADW94117	Adw94117 Staphyloc	C 463	13	22.0	64	8	ACAI1967	Acai1967 prokaryot
391	14	23.7	9496	5	ABAI6328	Abai6328 Human ner	C 464	13	22.0	67	8	ACAI5949	Acai5949 prokaryot
C 392	14	23.7	10517	13	ADSR89438	Adsr89438 Oligonuc	465	13	22.0	66	4	AAD10961	Aad10961 E. coli E
C 393	14	23.7	10925	4	ABL27602	Abi27602 Drosophi	466	13	22.0	78	12	ACH84532	Ach84532 Human gen
C 394	14	23.7	13815	4	ABL05454	Abi05454 Drosophi	C 467	13	22.0	100	8	ACD80650	Adc80650 E. coli K
C 395	14	23.7	17841	4	ABL04868	Abi04868 Drosophi	C 468	13	22.0	100	8	ADH87542	Adh87542 Bovine la
C 396	14	23.7	21890	4	ABL15986	Abi15986 Drosophi	469	13	22.0	100	10	ADH87542	Adh87542 Lactate d
C 397	14	23.7	22055	9	ADA02879	Ada02879 Mouse Pap	C 470	13	22.0	100	10	ADH87542	Adh87542 Primer us
C 398	14	23.7	22055	10	ADB72617	Adb72617 Mouse Pap	C 471	13	22.0	111	12	ADL80499	Adl80499 Human rec
C 399	14	23.7	22055	10	ADC85358	Adc85358 Human Dpt	C 472	13	22.0	146	4	AA511170	Aa511170 Salmonell
C 400	14	23.7	22055	12	ADM74474	Adm74474 Murine ca	C 473	13	22.0	146	8	ACAI6009	Acai6009 prokaryot
C 401	14	23.7	22582	14	ADZ12706	Adz12706 Murine ca	C 474	13	22.0	152	4	AAI98740	Aai98740 Human exc
C 402	14	23.7	23732	4	ABL30302	Abi30302 Drosophi	C 475	13	22.0	152	4	AA51212	AA51212 Salmonell
C 403	14	23.7	26047	11	ACN44246	Acn44246 Human gen	C 476	13	22.0	152	5	AAI63136	AAI63136 Human kid
404	14	23.7	28690	2	AAI13075	AAi13075 Enterococ	C 477	13	22.0	152	8	ACA16017	ACA16017 prokaryot
405	14	23.7	28690	2	ABS98870	Ab988870 Enterococ	C 478	13	22.0	152	8	ABZ38327	Abz38327 N. gonorr
406	14	23.7	28690	2	ABD42098	Abd42098 Poly aden	C 479	13	22.0	156	10	ADCT6300	Adct6300 DNA homol
407	14	23.7	29793	6	ABK14948	Abk14948 Worm poly	C 480	13	22.0	156	10	ADD16960	Add16960 DNA (segi
408	14	23.7	29793	6	ABK14930	Abk14930 Worm poly	C 481	13	22.0	156	10	ABD16960	Abd16960 DNA (segi
409	14	23.7	29793	8	ABX14494	Abx14494 Cosmid p2	C 482	13	22.0	198	14	AB56863	AB56863 Human gen
410	14	23.7	29793	14	ABR63618	Abbr63618 Caenorhab	483	13	22.0	208	3	AAA31871	AAA31871 Plant mtc
411	14	23.7	30069	6	ABD45553	Abd45553 Human tra	484	13	22.0	210	8	ABX49901	Abx49901 Bovine ES
412	14	23.7	32987	13	ABD33318	Abd33318 Human can	C 485	13	22.0	222	10	ADH85022	Adh85022 Enterococ
C 413	14	23.7	55008	6	AAK80495	Aak80495 Human imm	C 486	13	22.0	238	14	AB56864	AB56864 Human ech
C 414	14	23.7	71428	10	ACF65373	Acf65373 Phototrab	C 487	13	22.0	252	11	ABD03980	Abd03980 Pseudomon
C 415	14	23.7	73103	14	ABR35708	Ab35708 L. pneumo	C 488	13	22.0	268	4	AA511167	AA511167 Salmonell
C 416	14	23.7	73195	10	ACF65375	Acf65375 Phototrab	C 489	13	22.0	268	8	ACA16006	ACA16006 prokaryot
C 417	14	23.7	74234	11	ACN44594	Acn44594 Human gen	C 490	13	22.0	270	2	AA511148	AA511148 Salmonell
C 418	14	23.7	90583	8	ACD13447	Act13447 Human DNA	C 491	13	22.0	270	8	ACA15990	ACA15990 prokaryot
C 419	14	23.7	110000	2	AAT58840_2	Continuati	C 492	13	22.0	273	8	ACA21985	ACA21985 prokaryot
420	14	23.7	110000	2	AAT58840_3	Continuati	C 493	13	22.0	297	4	AAH84614	AAH84614 DNA encod
C 421	14	23.7	110000	6	ABO69245_15	Continuati	C 494	13	22.0	300	5	AA568161	AA568161 Kiebslell
422	14	23.7	110000	10	ADP77343_00	Continuati	C 495	13	22.0	303	11	ABD00983	Abd00983 Kiebslell
C 423	14	23.7	110000	10	ADP77343_05	Continuati	C 496	13	22.0	303	13	AD084189	Ad084189 Human pro
C 424	14	23.7	110000	10	ACF67367_05	Continuati	C 497	13	22.0	319	4	AA511129	AA511129 Salmonell
C 425	14	23.7	110000	10	ACF67367_05	Continuati	C 498	13	22.0	319	9	AA511131	AA511131 Salmonell
426	14	23.7	110000	14	ADZ45062_03	Continuati	C 499	13	22.0	319	8	ACA15979	ACA15979 prokaryot
427	14	23.7	110000	14	ADZ45062_04	Continuati	C 500	13	22.0	319	8	ACA15981	ACA15981 prokaryot
428	14	23.7	110000	14	ADZ45062_04	Continuati	C 501	13	22.0	324	10	ADP81227	Adp81227 Leukaemia
C 429	14	23.7	110000	14	ABR39174_02	Continuati	C 502	13	22.0	324	8	ACD05725	ACD05725 CDNA enco
C 430	14	23.7	110000	14	ABR39174_05	Continuati	C 503	13	22.0	337	5	ABV17905	Abv17905 Human pro
C 431	14	23.7	110000	14	ABR39174_06	Continuati	C 504	13	22.0	337	11	ABD14801	Abd14801 Pseudomon
C 432	14	23.7	110000	14	ABR39175_13	Continuati	C 505	13	22.0	345	4	AAK61339	AAK61339 Human imm
C 433	14	23.7	110000	14	ABR39175_16	Continuati	C 506	13	22.0	351	10	ACF67506	Acf67506 Phototrab
C 434	14	23.7	110000	14	ABR42401_13	Continuati	C 507	13	22.0	356	4	AA511187	AA511187 Salmonell
C 435	14	23.7	110000	14	ABR42401_16	Continuati	C 508	13	22.0	356	8	ACA16025	ACA16025 prokaryot
C 436	14	23.7	110000	14	ABR42401_16	Continuati	C 509	13	22.0	375	8	ACA40239	ACA40239 prokaryot
437	14	23.7	110000	14	ABR42401_16	Continuati	C 510	13	22.0	377	8	AA511187	AA511187 Salmonell
C 438	14	23.7	121062	12	ADO97213	ADO97213 Human can	C 511	13	22.0	378	12	AD047914	Ad047914 Human che
C 439	14	23.7	163350	6	AD46127	AD46127 Human tum	C 512	13	22.0	388	3	AACT74474	Aact74474 Human ORF
440	14	23.7	164702	8	ACF62730	ACF62730 Cancer ba	C 513	13	22.0	388	6	AA511166	AA511166 Salmonell
441	14	23.7	164702	8	ADB20845	ADB20845 MKP1 base	C 514	13	22.0	388	6	ABM20697	Abm20697 Human ORF
442	14	23.7	164702	10	ADB87934	ADB87934 Human UGT	C 515	13	22.0	388	8	ACA15948	ACA15948 prokaryot
443	14	23.7	164702	10	ADB96917	ADB96917 Human MDR	C 516	13	22.0	388	8	ACA15948	ACA15948 prokaryot
444	14	23.7	164702	10	ADB96917	ADB96917 Human MDR	C 517	13	22.0	389	4	AA511132	AA511132 Salmonell
445	14	23.7	164702	6	ABT11173	Abt11173 Human 5-1	C 518	13	22.0	389	4	AA511127	AA511127 Salmonell
C 446	14	23.7	168273	6	ABT11114	Abt11114 Human 5-1	C 519	13	22.0	389	8	ACA15978	ACA15978 prokaryot
447	14	23.7	175590	10	ADD50650	ADD50650 BAC seque	C 520	13	22.0	389	8	ACA15982	ACA15982 prokaryot
448	14	23.7	175590	10	ADV77908	Adv77908 Human BAC	C 521	13	22.0	389	8	ACA15980	ACA15980 prokaryot
C 449	14	23.7	184368	14	ABE35722	ABe35722 L. pneumo	C 522	13	22.0	391	4	ABV47695	ABv47695 Human exc
C 450	14	23.7	184368	14	ADZ13837	Adz13837 Human can	C 523	13	22.0	391	5	AAV47695	AAV47695 Human kid
451	14	23.7	188794	12	AD059476	Ad059476 Human gen	C 524	13	22.0	391	5	AAI63578	AAI63578 Salmonell
C 452	14	23.7	204621	12	ACN44486	Acn44486 Human gen	C 525	13	22.0	396	11	ACH95470	ACH95470 prokaryot
C 453	14	23.7	210920	11	ADQ97123	Adq97123 Mouse can	526	13	22.0	397	5	AA564427	AA564427 Novel hum
454	14	23.7	238484	11	ACN44210	Acn44210 Human gen	527	13	22.0	411	8	ABX53820	ABX53820 Bovine ES
C 455	14	23.7	317425	14	ABR35720	Ab35720 L. pneumo	528	13	22.0	411	8	ACA28192	ACA28192 prokaryot
C 456	14	23.7	349980	5	AAH41224	Aah41224 Pyrococcu	529	13	22.0	414	12	ADL03165	Adl03165 DNA encod
C 457	13	22.0	19	14	ADY79613	Ady79613 Bacillus	530	13	22.0	420	14	ADV74402	Adv74402 Human col



531	13	22.0	421	13	ADx48766	Adx48766 Plant full	c 604	13	22.0	538	6	ABQ37054	Abq37054 Oligonuc1
532	13	22.0	422	4	AA183820	Aa183820 Human pol	c 605	13	22.0	538	13	ADx10588	Adx10588 Plant full
533	13	22.0	422	4	AA185434	Aa185434 Human pol	c 606	13	22.0	541	10	ADD33244	Add33244 Mouse mit
534	13	22.0	422	8	ABX62215	Abx62215 Arabidops	c 607	13	22.0	542	12	ADP20377	Adp20377 Pinus rad
535	13	22.0	423	6	AD07787	Aad07787 Human sec	c 608	13	22.0	543	4	AA507082	Aa507082 DNA encod
536	13	22.0	423	6	AAD29122	Aad29122 Bacillus	c 609	13	22.0	543	6	ABQ19739	Abq19739 Oligonuc1
537	13	22.0	425	8	ABX54177	Abx54177 Bovine ES	c 610	13	22.0	545	6	ABQ19738	Abq19738 Oligonuc1
538	13	22.0	426	14	ABE63721	Abb63721 DNA encod	c 611	13	22.0	546	6	ABQ16650	Abq16650 Oligonuc1
539	13	22.0	456	6	ABL66120	Ab166120 Lung canc	c 612	13	22.0	546	6	ABQ16651	Abq16651 Oligonuc1
540	13	22.0	460	3	AA559162	AAa559162 CDNA enco	c 613	13	22.0	546	12	ACH74382	Ach74382 Human gen
541	13	22.0	460	3	AA558995	AAa58995 CDNA enco	c 614	13	22.0	547	2	AAV86332	Aav86332 EST clone
542	13	22.0	460	10	ADB32015	Adb32015 Human par	c 615	13	22.0	548	6	ABQ14934	Abq14934 Oligonuc1
543	13	22.0	460	12	ADR13819	Adr13819 Human int	c 616	13	22.0	548	6	ABQ14935	Abq14935 Oligonuc1
544	13	22.0	464	2	AAO37717	Aag37717 K1ADH4 pr	c 617	13	22.0	549	6	ABQ18056	Abq18056 Oligonuc1
545	13	22.0	465	4	AAK84321	Aa84321 Human imm	c 618	13	22.0	549	6	ABQ18057	Abq18057 Oligonuc1
546	13	22.0	470	13	ADV40068	Adv40068 Rat cardl	c 619	13	22.0	549	6	ABQ43554	Abq43554 Oligonuc1
547	13	22.0	472	14	ADM05977	Adm05977 Human gen	c 620	13	22.0	554	6	ABQ44354	Abq44354 Oligonuc1
548	13	22.0	473	5	ABV52481	Abv52481 Human pro	c 621	13	22.0	554	11	ADT94719	Adt94719 Colon can
549	13	22.0	482	4	AA139092	Aa139092 Probe #77	c 622	13	22.0	554	11	ADX41201	Adx41201 Human cdn
550	13	22.0	482	4	AAK33303	Aak33303 Human bon	c 623	13	22.0	558	6	ABQ51572	Abq51572 Oligonuc1
551	13	22.0	482	4	AAK07511	Aak07511 Human bra	c 624	13	22.0	558	6	ABQ51573	Abq51573 Oligonuc1
552	13	22.0	482	4	AB533035	Ab533035 Human liv	c 625	13	22.0	558	12	ADN13447	Adn13447 Human pro
553	13	22.0	482	6	AB508137	Ab508137 Human gen	c 626	13	22.0	561	11	ABD06739	Abd06739 Pseudomon
554	13	22.0	485	4	AA111556	Aa111556 Probe #14	c 627	13	22.0	569	6	ABQ29686	Abq29686 Oligonuc1
555	13	22.0	485	4	ABA53240	Ab53240 Human foe	c 628	13	22.0	569	6	ABQ29687	Abq29687 Oligonuc1
556	13	22.0	485	4	ABA42817	Ab42817 Human bre	c 629	13	22.0	570	10	ADD35011	Add35011 Mouse mit
557	13	22.0	485	4	AAK26940	Aak26940 Human bon	c 630	13	22.0	573	8	ACA33457	Aca33457 Prokaryot
558	13	22.0	485	4	AAK01493	Aak01493 Human bra	c 631	13	22.0	576	13	ADX29772	Adx29772 Plant full
559	13	22.0	485	5	AA101477	AA101477 Probe #14	c 632	13	22.0	578	6	ABQ36481	Abq36481 Oligonuc1
560	13	22.0	487	10	ADP82597	Adp82597 Leukemia	c 633	13	22.0	578	6	ABQ36480	Abq36480 Oligonuc1
561	13	22.0	489	8	ACA45758	Ac445758 Prokaryot	c 634	13	22.0	579	6	ABN70892	Abn70892 Streptoco
562	13	22.0	490	2	AAT47069	Aat47069 Pinto bea	c 635	13	22.0	581	6	ABN65793	Abn65793 Human can
563	13	22.0	490	14	ADK57939	Adk57939 Caprine a	c 636	13	22.0	582	6	ABQ51352	Abq51352 Oligonuc1
564	13	22.0	495	4	AA551205	AAa551205 Salmonell	c 637	13	22.0	582	6	ABQ51353	Abq51353 Oligonuc1
565	13	22.0	495	8	ACA16005	Ac16005 Prokaryot	c 638	13	22.0	584	6	ABQ45770	Abq45770 Oligonuc1
566	13	22.0	497	9	ACH47873	Ach47873 Human lun	c 639	13	22.0	584	6	ABQ18334	Abq18334 Oligonuc1
567	13	22.0	497	11	ADT96219	Adt96219 Colon can	c 640	13	22.0	584	6	ABQ18335	Abq18335 Oligonuc1
568	13	22.0	497	11	ADX42701	Adx42701 Human cdn	c 641	13	22.0	584	6	ABQ45771	Abq45771 Oligonuc1
569	13	22.0	499	9	ACH14374	Ach14374 Human adu	c 642	13	22.0	588	12	ACH70829	Ach70829 Human gen
570	13	22.0	501	8	AB252716	Ab252716 Aspergill1	c 643	13	22.0	590	2	AAV88437	Aav88437 EST clone
571	13	22.0	505	6	ABQ15474	Abq15474 Oligonuc1	c 644	13	22.0	594	11	ACL28217	ACL28217 Rice abio
572	13	22.0	505	6	ABQ15475	Abq15475 Oligonuc1	c 645	13	22.0	599	5	ADM19583	Adm19583 Novel hum
573	13	22.0	507	2	AAT47070	Aat47070 Pinto bea	c 646	13	22.0	599	6	ABQ32352	Abq32352 Oligonuc1
574	13	22.0	508	6	ABQ47766	Abq47766 Oligonuc1	c 647	13	22.0	599	6	ABQ32353	Abq32353 Oligonuc1
575	13	22.0	508	6	ABQ47767	Abq47767 Oligonuc1	c 648	13	22.0	600	4	ABL07321	Ab107321 Drosoph11
576	13	22.0	510	6	ABQ49760	Abq49760 Oligonuc1	c 649	13	22.0	600	9	ADA29700	Ada29700 DNA encod
577	13	22.0	510	6	ABQ49761	Abq49761 Oligonuc1	c 650	13	22.0	601	6	ABQ17521	Abq17521 Oligonuc1
578	13	22.0	510	13	ADT06245	Adt06245 Bacillus	c 651	13	22.0	601	6	ABQ17520	Abq17520 Oligonuc1
579	13	22.0	513	13	ACF86684	Acf86684 Human STR	c 652	13	22.0	604	6	ABQ47114	Abq47114 Oligonuc1
580	13	22.0	519	6	ABQ50277	Abq50277 Oligonuc1	c 653	13	22.0	604	6	ABQ47115	Abq47115 Oligonuc1
581	13	22.0	519	6	ABQ50276	Abq50276 Oligonuc1	c 654	13	22.0	608	6	ABQ31774	Abq31774 Oligonuc1
582	13	22.0	519	10	ADK53713	Adk53713 Plant DNA	c 655	13	22.0	608	6	ABQ31775	Abq31775 Oligonuc1
583	13	22.0	521	11	ADT96876	Adt96876 Colon can	c 656	13	22.0	610	6	ABQ17772	Abq17772 Oligonuc1
584	13	22.0	521	11	ADK43358	Adk43358 Human cdn	c 657	13	22.0	610	6	ABQ17773	Abq17773 Oligonuc1
585	13	22.0	525	10	ADC03379	Adc03379 Rice flow	c 658	13	22.0	618	2	AAK30612	Aak30612 H. pylori
586	13	22.0	525	12	ACH67438	Ach67438 Human gen	c 659	13	22.0	618	6	ABN66682	Abn66682 Streptoco
587	13	22.0	525	12	ACH73117	Ach73117 Human gen	c 660	13	22.0	618	6	ABN70327	Abn70327 Streptoco
588	13	22.0	527	6	ABQ19486	Abq19486 Oligonuc1	c 661	13	22.0	618	10	ADC92594	Adc92594 E. faeciu
589	13	22.0	527	6	ABQ19487	Abq19487 Oligonuc1	c 662	13	22.0	619	6	ABQ18198	Abq18198 Oligonuc1
590	13	22.0	530	6	ABQ46543	Abq46543 Oligonuc1	c 663	13	22.0	619	6	ABQ18199	Abq18199 Oligonuc1
591	13	22.0	530	6	ABQ46542	Abq46542 Oligonuc1	c 664	13	22.0	619	6	ABQ15485	Abq15485 Oligonuc1
592	13	22.0	530	12	AD062817	Ad062817 Transcriptp	c 665	13	22.0	619	6	ABQ15484	Abq15484 Oligonuc1
593	13	22.0	530	13	ACN55272	Acn55272 Cotton an	c 666	13	22.0	622	6	ABQ20756	Abq20756 Oligonuc1
594	13	22.0	533	6	ABQ49731	Abq49731 Oligonuc1	c 667	13	22.0	622	6	ABQ29054	Abq29054 Oligonuc1
595	13	22.0	533	6	ABQ49730	Abq49730 Oligonuc1	c 668	13	22.0	623	6	ABQ29055	Abq29055 Oligonuc1
596	13	22.0	534	6	ABQ53164	Abq53164 Oligonuc1	c 669	13	22.0	623	6	ABQ34265	Abq34265 Oligonuc1
597	13	22.0	534	6	ABQ53165	Abq53165 Oligonuc1	c 670	13	22.0	625	6	ABQ34264	Abq34264 Oligonuc1
598	13	22.0	535	6	ABQ15754	Abq15754 Oligonuc1	c 671	13	22.0	625	6	ABQ46678	Abq46678 Oligonuc1
599	13	22.0	535	6	ABQ15755	Abq15755 Oligonuc1	c 672	13	22.0	625	6	ABQ46679	Abq46679 Oligonuc1
600	13	22.0	537	6	ABQ16735	Abq16735 Oligonuc1	c 673	13	22.0	629	14	ACU55132	Acu55132 Human col
601	13	22.0	537	6	ABQ16734	Abq16734 Oligonuc1	c 674	13	22.0	633	6	ABQ39592	Abq39592 Oligonuc1
602	13	22.0	537	6	ABQ37055	Abq37055 Oligonuc1	c 675	13	22.0	633	6	ABQ39593	Abq39593 Oligonuc1
603	13	22.0	538	6	ABQ37055	Abq37055 Oligonuc1	c 676	13	22.0	633	6	ABQ39593	Abq39593 Oligonuc1



677	13	635	13	ADs49739	Ads49739 Bacterial	750	13	798	6	ABO16633	Abq16633 Oligonuc1
678	13	636	13	ADSS5254	Adss5254 Bacterial	751	13	798	6	ABQ67692	Abq67692 Listeria
679	13	637	6	ABQ35205	Abq35205 Oligonuc1	752	13	800	10	ADK56066	Adk56066 Plant DNA
680	13	637	6	ABQ35204	Abq35204 Oligonuc1	753	13	800	13	ADK54597	Adk54597 plant ful
681	13	638	6	ABQ22408	Abq22408 Oligonuc1	754	13	807	8	ACF75141	Acf75141 Staphyloc
682	13	638	6	ABQ22409	Abq22409 Oligonuc1	755	13	809	6	ABN99012	Abn99012 Arabidops
683	13	645	10	ADP90826	Adp90826 Human hep	756	13	810	12	ADQ39600	Adq39600 Yeast ub1
684	13	647	6	ABQ49369	Abq49369 Oligonuc1	757	13	819	6	ABQ33538	Abq33538 Oligonuc1
685	13	647	6	ABQ49368	Abq49368 Oligonuc1	758	13	819	6	ABQ33539	Abq33539 Oligonuc1
686	13	648	10	ABD33419	Abd33419 Mouse mit	759	13	822	10	ADH82337	Adh82337 Enterococ
687	13	648	11	ABD06626	Abd06626 Pseudomon	760	13	822	13	ADK53940	Adk53940 Plant ful
688	13	650	5	AAS05540	Aas05540 Mammalian	761	13	825	3	AAC47711	Aac47711 Arabidops
689	13	650	10	ADK59764	Adk59764 Plant DNA	762	13	828	4	ABL18041	AbL18041 Drosophil
690	13	653	3	AAA78491	Aaa78491 Plant SDP	763	13	828	6	ABQ51698	Abq51698 Oligonuc1
691	13	654	6	ABQ16860	Abq16860 Oligonuc1	764	13	828	6	ABQ51699	Abq51699 Oligonuc1
692	13	654	6	ABQ16861	Abq16861 Oligonuc1	765	13	835	2	AAV27370	Aav27370 Streptoco
693	13	663	11	ABD01216	Abd01216 Klebsiell	766	13	835	6	ABQ4838	Abq4838 S. pneumo
694	13	666	2	AAQ37718	Aaq37718 K1ADH4 pr	767	13	835	10	ADC45174	Adc45174 S. pneumo
695	13	673	6	ABQ20069	Abq20069 Oligonuc1	768	13	836	6	ADR60703	Adr60703 Cotton CD
696	13	673	6	ABQ20068	Abq20068 Oligonuc1	769	13	836	13	ADR04272	Adr04272 Soybean F
697	13	676	14	ADY65169	Ady65169 S. mansoni	770	13	837	6	ABQ69526	Abq69526 Listeria
698	13	677	6	ABQ14424	Abq14424 Oligonuc1	771	13	842	6	ABQ25796	Abq25796 Oligonuc1
699	13	677	6	ABQ14425	Abq14425 Oligonuc1	772	13	842	6	ABQ25797	Abq25797 Oligonuc1
700	13	678	10	ACA54562	Aca54562 Human NF-	773	13	850	4	AAH04116	Aah04116 Human CDN
701	13	678	14	ADU83039	Adu83039 Human NFk	774	13	850	4	AAH98527	Aah98527 Human EST
702	13	680	10	ADK53724	Adk53724 Plant DNA	775	13	853	4	AAH98527	Abh51914 Oligonuc1
703	13	681	10	ADK53724	Adk53724 Plant DNA	776	13	855	6	ABQ51915	Abq51915 Oligonuc1
704	13	681	10	ADK53724	Adk53724 Plant DNA	777	13	855	6	ABQ51915	Abq24872 Oligonuc1
705	13	684	6	ABQ14546	Abq14546 Oligonuc1	778	13	856	6	ABQ24872	Abq24872 Oligonuc1
706	13	684	6	ABR80227	Abk80227 Bacillus	779	13	856	6	ABQ24872	Abq24872 Oligonuc1
707	13	684	6	ABQ34722	Abq34722 Oligonuc1	780	13	856	13	AACT5932	Abq24873 Oligonuc1
708	13	692	6	ABQ34723	Abq34723 Oligonuc1	781	13	858	10	ACF68784	Abq24872 Oligonuc1
709	13	695	13	ADX31571	Adx31571 Plant ful	782	13	858	6	ABQ25574	Abq25574 Oligonuc1
710	13	700	6	ABQ45981	Abq45981 Oligonuc1	783	13	861	6	ABQ22575	Abq22575 Oligonuc1
711	13	700	6	ABQ45980	Abq45980 Oligonuc1	784	13	861	6	ABQ22575	Abq22575 Oligonuc1
712	13	703	10	ACF66684	Acf66684 Photorhab	785	13	864	2	AAV72072	Abq22574 Oligonuc1
713	13	713	10	AAZ52328	Aaz52328 Klebsiell	786	13	864	6	ABQ50201	Abq50201 Oligonuc1
714	13	715	6	ABQ17778	Abq17778 Oligonuc1	787	13	864	6	ABQ50201	Abq50201 Oligonuc1
715	13	715	6	ABQ17779	Abq17779 Oligonuc1	788	13	866	6	ABQ41555	Abq41555 Oligonuc1
716	13	720	6	ABQ39058	Abq39058 Oligonuc1	789	13	866	6	ABQ41555	Abq41555 Oligonuc1
717	13	720	6	ABQ39059	Abq39059 Oligonuc1	790	13	866	2	AAK15332	Abq41554 Oligonuc1
718	13	721	10	ACF67230	Acf67230 Photorhab	791	13	867	6	ABQ15332	Abq41554 Oligonuc1
719	13	723	6	ABN66671	Abn66671 Streptoco	792	13	873	8	ACA25530	Abq41554 Oligonuc1
720	13	726	8	ACA50527	Acas0527 Prokaryot	793	13	876	6	ABQ15665	Abq15664 Oligonuc1
721	13	729	14	ADY65181	Ady65181 S. mansoni	794	13	876	8	ACD05704	AcD05704 CDNA enco
722	13	741	11	ABD08021	Abd08021 Pseudomon	795	13	876	11	ABD02570	Abd02570 Pseudomon
723	13	741	13	ADK561847	Adk561847 Bacterial	796	13	879	11	ACH99914	Ach99914 Klebsiell
724	13	742	6	ABQ46920	Abq46920 Oligonuc1	797	13	882	6	ABQ14648	Abq14648 Oligonuc1
725	13	742	6	ABQ46921	Abq46921 Oligonuc1	798	13	882	6	ABQ14649	Abq14649 Oligonuc1
726	13	747	6	ABZ14676	Abz14676 Arabidops	799	13	884	4	AAH05565	AAH05565 Human CDN
727	13	747	8	ACA35166	Acas35166 Prokaryot	800	13	884	11	ABD00349	Abd00349 Klebsiell
728	13	750	11	ABD03653	Abd03653 Pseudomon	801	13	885	11	ACH91006	Ach91006 Human gen
729	13	754	5	AAH94145	Aah94145 Human foe	802	13	886	12	ABQ46695	Abq46695 Oligonuc1
730	13	757	6	ABQ48775	Abq48775 Oligonuc1	803	13	887	6	ABQ46694	Abq46694 Oligonuc1
731	13	757	6	ABQ48774	Abq48774 Oligonuc1	804	13	887	6	ABQ46694	Abq46694 Oligonuc1
732	13	760	6	ABQ17652	Abq17652 Oligonuc1	805	13	890	6	ABQ20793	Abq20792 Oligonuc1
733	13	760	6	ABQ17653	Abq17653 Oligonuc1	806	13	890	6	ABQ20792	Abq20792 Oligonuc1
734	13	762	10	ACF65851	Acf65851 Photorhab	807	13	891	10	ADP00345	Adp00345 Wheat flo
735	13	768	10	ADK55445	Adk55445 Human gen	808	13	891	10	ADP00345	Adp00345 Wheat flo
736	13	768	10	ADK55449	Adk55449 Human gen	809	13	891	10	ADP00345	Adp00345 Wheat flo
737	13	769	6	ABQ44674	Abq44674 Oligonuc1	810	13	891	12	ADJ43131	Adj43131 Plant CDN
738	13	769	6	ABQ44675	Abq44675 Oligonuc1	811	13	892	6	ABK34314	Abk34314 Human CDN
739	13	771	6	ABQ44166	Abq44166 Oligonuc1	812	13	906	8	ACA32809	AcA32809 Prokaryot
740	13	771	6	ABQ44167	Abq44167 Oligonuc1	813	13	909	10	ADH83399	Adh83399 Enterococ
741	13	779	4	AAI93470	Aai93470 Human pol	814	13	920	6	ABQ54052	Abq54052 Oligonuc1
742	13	779	4	AAI93470	Aai93470 Human pol	815	13	920	6	ABQ54052	Abq54052 Oligonuc1
743	13	782	10	ACR65502	AcR65502 Photorhab	816	13	930	10	ACA48768	AcA48768 Prokaryot
744	13	786	10	ACR66134	AcR66134 Photorhab	817	13	939	10	ADC93088	AdC93088 Bacterial
745	13	787	6	ABQ50996	Abq50996 Oligonuc1	818	13	942	4	AA553084	AA553084 Enterococ
746	13	787	6	ABQ50997	Abq50997 Oligonuc1	819	13	945	13	ADT47395	Adt47395 Bacterial
747	13	789	8	ACA48140	Aca48140 Prokaryot	820	13	957	8	ACA35552	AcA35552 Prokaryot
748	13	797	10	ACF67039	AcF67039 Photorhab	821	13	957	8	ACA22979	AcA22979 Prokaryot
749	13	798	6	ABQ16632	Abq16632 Oligonuc1	822	13	961	6	ABQ42297	Abq42297 Oligonuc1



C 823	13	22.0	961	6	ABQ42296	Abq42296 Oligonuc	C 896	13	22.0	1136	2	AAT35254	Aat35254 Recombina
C 824	13	22.0	964	6	ABQ46458	Abq46458 Oligonuc	C 897	13	22.0	1139	6	ABQ51149	Abq51149 Oligonuc
C 825	13	22.0	964	6	ABQ46459	Abq46459 Oligonuc	C 898	13	22.0	1139	6	ABQ51148	Abq51148 Oligonuc
C 826	13	22.0	966	8	ACA44769	Ac44769 Prokaryot	C 899	13	22.0	1140	12	ADN74883	Adn74883 Rice RCN2
C 827	13	22.0	967	6	ABQ14297	Abq14297 Oligonuc	C 900	13	22.0	1164	6	ABZ31747	Abz31747 Candida a
C 828	13	22.0	967	6	ABQ14296	Abq14296 Oligonuc	C 901	13	22.0	1164	11	ACH99274	Ach99274 Klebsiell
C 829	13	22.0	969	5	AAS92780	Aas92780 DNA encod	C 902	13	22.0	1165	14	AEB26888	Aeb26888 Pimus rad
C 830	13	22.0	970	6	ABN98521	Abn98521 Arabidops	C 903	13	22.0	1175	6	ABO23061	Abg23061 Oligonuc
C 831	13	22.0	971	6	ABQ42017	Abq42017 Oligonuc	C 904	13	22.0	1175	6	ABO23060	Abg23060 Oligonuc
C 832	13	22.0	971	6	ABQ42016	Abq42016 Oligonuc	C 905	13	22.0	1182	10	ADC91116	Adc91116 E. faeciu
C 833	13	22.0	972	10	ADH84245	Adh84245 Enterococ	C 906	13	22.0	1183	6	ABZ11881	Abz11881 Human pol
C 834	13	22.0	972	10	ADH84245	Adh84245 Enterococ	C 907	13	22.0	1183	12	ADM44399	Adm44399 Novel hum
C 835	13	22.0	975	8	ACL72710	Ac172710 M. xanthu	C 908	13	22.0	1185	5	ABAI4252	Abi44252 Human ner
C 836	13	22.0	980	6	AD42245	Ad42245 Corn Ft h	C 909	13	22.0	1185	13	AD545745	Ad545745 Bacterial
C 837	13	22.0	980	13	AD42245	Ad42245 Corn Ft h	C 910	13	22.0	1189	5	ABV28964	Abv28964 Human pro
C 838	13	22.0	1000	6	ABQ45122	Abq45122 Oligonuc	C 911	13	22.0	1189	5	ABV23123	Abv23123 Human pro
C 839	13	22.0	1000	6	ABQ45123	Abq45123 Oligonuc	C 912	13	22.0	1193	6	ABQ30906	Abq30906 Oligonuc
C 840	13	22.0	1001	3	AAC57888	Aac57888 Atrachidn	C 913	13	22.0	1193	6	ABQ30907	Abq30907 Oligonuc
C 841	13	22.0	1007	6	ABQ22166	Abq22166 Oligonuc	C 914	13	22.0	1195	6	ABQ31773	Abq31773 Oligonuc
C 842	13	22.0	1007	6	ABQ22167	Abq22167 Oligonuc	C 915	13	22.0	1195	6	ABQ31772	Abq31772 Oligonuc
C 843	13	22.0	1014	3	AAC51053	Aac51053 Arabidops	C 916	13	22.0	1199	8	ACA44307	Ac444307 Prokaryot
C 844	13	22.0	1014	11	ABD15086	Abd15086 Pseudomon	C 917	13	22.0	1205	4	AAH34731	Aah34731 Human col
C 845	13	22.0	1017	6	ABQ13922	Abq13922 Oligonuc	C 918	13	22.0	1211	2	AAQ37716	Aaq37716 KlADH4 pr
C 846	13	22.0	1017	6	ABQ13923	Abq13923 Oligonuc	C 919	13	22.0	1239	10	ADC91504	Adc91504 E. faeciu
C 847	13	22.0	1017	10	ACF71967	Acf71967 Photorhab	C 920	13	22.0	1263	2	AAK61371	Aak61371 DNA encod
C 848	13	22.0	1020	6	ABN68326	Abn68326 Streptoco	C 921	13	22.0	1263	6	ABO50084	Abg50084 Oligonuc
C 849	13	22.0	1020	6	ABK65340	Abk65340 Arabidops	C 922	13	22.0	1263	6	ABO50085	Abg50085 Oligonuc
C 850	13	22.0	1020	10	ADC46732	Adc46732 Thalectes	C 923	13	22.0	1265	6	ABQ28515	Abq28515 Oligonuc
C 851	13	22.0	1020	10	ADD30247	Add30247 Plant yie	C 924	13	22.0	1265	6	ABQ28514	Abq28514 Oligonuc
C 852	13	22.0	1020	10	ADP00612	Adp00612 Bacterial	C 925	13	22.0	1284	6	ABN68250	Abn68250 Streptoco
C 853	13	22.0	1020	10	AD144112	Ad144112 Plant tra	C 926	13	22.0	1287	13	ADV85433	Adv85433 Streptoco
C 854	13	22.0	1023	9	ADA31897	Ada31897 DNA encod	C 927	13	22.0	1290	2	AAV36619	Aav36619 Nucleotid
C 855	13	22.0	1023	10	ADH85236	Adh85236 Enterococ	C 928	13	22.0	1290	9	ACC83894	Acc83894 Bacillus
C 856	13	22.0	1023	13	ADV83746	Adv83746 Streptoco	C 929	13	22.0	1290	14	ADVA3792	Adv43792 Human psy
C 857	13	22.0	1024	6	ABK66450	Abk66450 Helicobac	C 930	13	22.0	1293	4	ABL04971	Ab104971 Drosophil
C 858	13	22.0	1026	6	ABN91350	Abn91350 Staphyloc	C 931	13	22.0	1295	6	AAD42250	Aad42250 Rice FT h
C 859	13	22.0	1026	10	ADH85021	Adh85021 Enterococ	C 932	13	22.0	1295	13	ADRO4264	Adr04264 Rice FT h
C 860	13	22.0	1038	11	ACH99267	Ach99267 Klebsiell	C 933	13	22.0	1308	2	AAK29773	Aak29773 L.lactis
C 861	13	22.0	1040	3	AAC76126	Aac76126 Human ORF	C 934	13	22.0	1326	5	ABV24705	Abv24705 Human pro
C 862	13	22.0	1041	8	ACA24310	Ac24310 Prokaryot	C 935	13	22.0	1326	5	ADL45865	Adl45865 Human ova
C 863	13	22.0	1047	12	ADH88986	Adh88986 Escherich	C 936	13	22.0	1337	8	ACA24703	Ac24703 Prokaryot
C 864	13	22.0	1050	2	AAK61454	Aak61454 DNA encod	C 937	13	22.0	1342	2	AAV31252	Aav31252 E. coli J
C 865	13	22.0	1050	8	ADA39871	Ada39871 Human sec	C 938	13	22.0	1360	2	AAK14180	Aax14180 H. pylori
C 866	13	22.0	1050	10	ADC73535	Adc73535 Human sec	C 939	13	22.0	1364	13	ADK63772	Adk63772 Plant ful
C 867	13	22.0	1050	10	ADD37601	Add37601 Human sec	C 940	13	22.0	1365	13	ADT45879	Adt45879 Bacterial
C 868	13	22.0	1050	10	ADA56059	Ada56059 Gene enco	C 941	13	22.0	1368	14	ADVA3793	Adv43793 Human psy
C 869	13	22.0	1055	13	ADO84563	Ado84563 Plant ful	C 942	13	22.0	1377	6	ABQ42699	Abq42699 Oligonuc
C 870	13	22.0	1057	3	AAC39647	Aac39647 Arabidops	C 943	13	22.0	1377	6	ABQ42698	Abq42698 Oligonuc
C 871	13	22.0	1059	13	ADU69345	Adu69345 S agalact	C 944	13	22.0	1377	12	ADL03707	Adl03707 DNA encod
C 872	13	22.0	1059	13	ADV85219	Adv85219 Streptoco	C 945	13	22.0	1378	6	ABQ26065	Abq26065 Oligonuc
C 873	13	22.0	1062	13	ADT46073	Adt46073 Bacterial	C 946	13	22.0	1378	6	ABQ26064	Abq26064 Oligonuc
C 874	13	22.0	1065	3	AAC37478	Aac37478 Arabidops	C 947	13	22.0	1380	13	ADXL1686	Adxl1686 Plant ful
C 875	13	22.0	1078	6	ABQ22896	Abq22896 Oligonuc	C 948	13	22.0	1383	10	ACC61524	Acc61524 Gene sequ
C 876	13	22.0	1078	6	ABQ22897	Abq22897 Oligonuc	C 949	13	22.0	1383	10	ADK64565	Adk64565 Disease t
C 877	13	22.0	1080	4	AAS52712	Aas52712 E. coli D	C 950	13	22.0	1392	13	ADT18831	Adt18831 Plant CDN
C 878	13	22.0	1080	8	ACA32732	Ac32732 Prokaryot	C 951	13	22.0	1392	9	ADB07093	Adb07093 Altiococ
C 879	13	22.0	1089	8	ACA21094	Ac21094 Prokaryot	C 952	13	22.0	1392	9	ADB07089	Adb07089 Altiococ
C 880	13	22.0	1092	11	ABD09877	Abd09877 Pseudomon	C 953	13	22.0	1392	9	ADB07095	Adb07095 Altiococ
C 881	13	22.0	1096	6	ABQ16837	Abq16837 Oligonuc	C 954	13	22.0	1392	9	ADB07097	Adb07097 Altiococ
C 882	13	22.0	1096	6	ABQ16836	Abq16836 Oligonuc	C 955	13	22.0	1392	9	ADB07099	Adb07099 Altiococ
C 883	13	22.0	1098	6	ABQ46497	Abq46497 Oligonuc	C 956	13	22.0	1392	9	ADB07091	Adb07091 Altiococ
C 884	13	22.0	1098	6	ABQ46496	Abq46496 Oligonuc	C 957	13	22.0	1401	12	ADO29801	Ado29801 Human GPC
C 885	13	22.0	1098	8	ACA29971	Ac29971 Prokaryot	C 958	13	22.0	1401	13	ADS59963	Ads59963 Bacterial
C 886	13	22.0	1104	9	ADA32249	Ada32249 DNA encod	C 959	13	22.0	1401	14	ADVA3790	Adv43790 Human psy
C 887	13	22.0	1104	13	ADS59783	Ads59783 Bacterial	C 960	13	22.0	1406	6	ABQ43494	Abq43494 Oligonuc
C 888	13	22.0	1104	13	ADS63216	Ads63216 Bacterial	C 961	13	22.0	1406	6	ABQ43495	Abq43495 Oligonuc
C 889	13	22.0	1109	5	AAS82291	Aas82291 DNA encod	C 962	13	22.0	1407	8	ACA37275	Ac37275 Prokaryot
C 890	13	22.0	1109	6	ABO53587	Abg53587 Oligonuc	C 963	13	22.0	1414	6	ABQ36704	Abq36704 Oligonuc
C 891	13	22.0	1109	6	ABO53586	Abg53586 Oligonuc	C 964	13	22.0	1414	6	ABQ36705	Abq36705 Oligonuc
C 892	13	22.0	1109	6	ADC32333	Adc32333 Human nov	C 965	13	22.0	1419	13	ADK63296	Adk63296 Bacterial
C 893	13	22.0	1112	10	ADK45530	Adk45530 Plant ful	C 966	13	22.0	1419	13	ADK63296	Adk45530 Plant ful
C 894	13	22.0	1131	9	ADB11001	Adb11001 Altiococ	C 967	13	22.0	1419	13	ADK15102	Adk15102 Plant ful
C 895	13	22.0	1131	9	ADB11003	Adb11003 Altiococ	C 968	13	22.0	1424	6	ABQ54034	Abq54034 Oligonuc



```

c 969 13 22.0 1424 6 ABG54035
970 13 22.0 1425 8 ACA21787
971 13 22.0 1425 8 ABT18979
972 13 22.0 1426 8 AA296372
973 13 22.0 1434 8 ACA48521
974 13 22.0 1442 5 AAS93560
975 13 22.0 1449 13 ADT43999
976 13 22.0 1455 11 ACH96566
977 13 22.0 1464 12 ADQ63366
978 13 22.0 1473 8 ABT20201
979 13 22.0 1473 8 ABT20799
c 980 13 22.0 1478 14 AEA23803
981 13 22.0 1486 10 ADE56979
982 13 22.0 1488 6 ABM69252
983 13 22.0 1491 13 ADV84236
c 984 13 22.0 1497 2 AAT47066
985 13 22.0 1500 12 ADV43791
c 986 13 22.0 1501 14 ADM47947
c 987 13 22.0 1506 13 ADT48832
c 988 13 22.0 1507 10 ADC30526
989 13 22.0 1518 8 ABT18385
c 990 13 22.0 1522 10 ADE62973
991 13 22.0 1526 12 ADQ63748
992 13 22.0 1551 13 ADT48559
c 993 13 22.0 1554 12 ADH56217
994 13 22.0 1563 8 ACA43108
995 13 22.0 1564 13 ADX63830
996 13 22.0 1575 8 ACA31033
997 13 22.0 1581 2 AAX55982
998 13 22.0 1582 2 AAG94037
999 13 22.0 1584 10 ADC92297
1000 13 22.0 1586 13 ADR85606

```

## ALIGNMENTS

## RESULT 1

ID ADR48526 standard; DNA; 59 BP.

XX ADR48526;

DT 04-NOV-2004 (first entry)

XX paga target sequence #4.

XX Bacillus anthracis; cutaneous; respiratory anthrax infection; paga; capB;

KW pXO1; pXO2; target sequence; ds.

XX Bacillus anthracis.

OS WO2004070001-A2.

XX 19-AUG-2004.

PD 12-NOV-2003; 2003WO-US036240.

XX 15-NOV-2002; 2002US-0426552P.

PR 16-MAY-2003; 2003US-0471082P.

XX (GENP-) GEN-PROBE INC.

PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;

XX WPI; 2004-604428/58.

PT New oligonucleotides that hybridize specifically to a *Bacillus anthracis* sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis* infections.

XX Claim 1; SEQ ID NO 24; 61pp; English.

CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC *anthracis* target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from paga and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pXO1 and pXO2, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a paga  
CC target sequence.

XX Sequence 59 BP; 19 A; 11 C; 18 G; 11 T; 0 U; 0 Other;

SO Query Match 100.0%; Score 59; DB 13; Length 59;  
Best Local Similarity 100.0%; Pred. No. 2.8e-24; Mismatches 0; Gaps 0;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 GGTAGAAAGCGGATGACGGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
Db 1 GGTAGAAAGCGGATGACGGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59

```

## RESULT 2

ID ADL16360 standard; DNA; 723 BP.

XX ADL16360;

DT 06-MAY-2004 (first entry)

XX pBP15 vector DNA for expression of 27 kDa PA deletion mutant (PA27).

KW Immunogenic; vaccine; lethal infection; protective antigen; PA;  
lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.

XX *Bacillus anthracis*.

OS Synthetic.

XX Key Location/Qualifiers

FT CDS 1..723

XX US2004028695-A1.

XX 12-FEB-2004.

XX 28-MAR-2003; 2003US-00402466.

XX 12-APR-2002; 2002US-0372152P.

XX (PARK/) PARK S.

XX (GIRI/) GIRI L.

XX Park S, Giri L;

XX WPI; 2004-168865/16.

PT Immunogenic composition for preparing a vaccine against a lethal  
PT infection of *Bacillus anthracis* in an animal, comprises an immunizing  
PT amount of a recombinant *B. anthracis* protective antigen protein and/or  
PT lethal factor protein.

XX Disclosure; SEQ ID NO 25; 143pp; English.

XX The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant *B. anthracis* protective antigen (rPA) protein and a  
CC recombinant *B. anthracis* lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by *B. anthracis*. The present sequence is pBP15 vector DNA for the  
CC expression of *Bacillus anthracis* 27 kDa N-terminal PA deletion mutant



CC (PA27). This sequence is used in the invention.  
XX Sequence 723 BP; 302 A; 81 C; 131 G; 209 T; 0 U; 0 Other;  
SQ

Query Match 100.0%; Score 59; DB 12; Length 723;  
Best Local Similarity 100.0%; Pred. No. 2,7e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 59  
DB 15 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 73

RESULT 3  
ADT06243  
ID ADT06243 standard; DNA; 852 BP.  
XX  
XX ADT06243;  
XX  
XX  
XX 30-DEC-2004 (first entry)  
XX  
XX  
XX Bacillus anthracis detection aptamer oligonucleotide #151.  
XX  
XX ss; antibacterial; aptamer; binding affinity; pathogen; virulence; spore;  
XX high throughput screening assay; diagnosis.  
XX  
XX Bacillus anthracis.  
XX  
XX MO2004085665-A2.  
XX  
XX 07-OCT-2004.  
XX  
XX 19-JUN-2003; 2003WO-US020844.  
XX  
XX 19-JUN-2002; 2002US-0390214P.  
XX PR 07-FEB-2003; 2003US-0445977P.  
XX PR 10-MAR-2003; 2003US-0453259P.  
XX PR 15-APR-2003; 2003US-0492930P.  
XX  
XX PA (ARCH-) ARCHEMIX CORP.  
XX  
XX Wilson C, Epstein D, Cload ST, Marsh N, Hamaguchi N;  
XX WPI; 2004-737328/72.  
XX  
XX Novel nucleic acid aptamer having binding affinity to target of Bacillus  
XX PT anthracis, useful for treating Bacillus anthracis disease.  
XX  
XX PS Claim 4; SEQ ID NO 157; 144pp; English.  
XX  
XX The invention relates to a nucleic acid (I) aptamer having binding  
XX CC affinity to one or more pathogen (e.g., Bacillus anthracis ) targets,  
XX CC where binding of (I) to the target reduces virulence of the target. (I)  
XX CC is useful for detecting a Bacillus anthracis protective antigen in a  
XX CC sample. (I) is useful for treating B.anthraxis disease in subjects  
XX CC exposed to B.anthraxis spores. (I) has high affinity and specificity for  
XX CC the protective antigen of B.anthraxis , and is cost effective. (I)  
XX CC enables high throughput screening assays. This sequence corresponds to a  
XX CC nucleic acid used in the invention.  
XX  
XX SQ Sequence 852 BP; 339 A; 106 C; 167 G; 240 T; 0 U; 0 Other;  
XX

Query Match 100.0%; Score 59; DB 13; Length 852;  
Best Local Similarity 100.0%; Pred. No. 2,7e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 59  
DB 144 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 202

RESULT 4  
ADT06241  
ADT06241

ID ADT06241 standard; DNA; 852 BP.  
XX  
XX AC ADT06241;  
XX  
XX 30-DEC-2004 (first entry)  
XX  
XX  
XX Bacillus anthracis detection aptamer oligonucleotide #150.  
XX  
XX ss; antibacterial; aptamer; binding affinity; pathogen; virulence; spore;  
XX high throughput screening assay; diagnosis.  
XX  
XX Bacillus anthracis.  
XX  
XX OS  
XX  
XX MO2004085665-A2.  
XX  
XX 07-OCT-2004.  
XX  
XX 19-JUN-2003; 2003WO-US020844.  
XX  
XX  
XX 19-JUN-2002; 2002US-0390214P.  
XX PR 07-FEB-2003; 2003US-0445977P.  
XX PR 10-MAR-2003; 2003US-0453259P.  
XX PR 15-APR-2003; 2003US-0492930P.  
XX  
XX PA (ARCH-) ARCHEMIX CORP.  
XX  
XX Wilson C, Epstein D, Cload ST, Marsh N, Hamaguchi N;  
XX WPI; 2004-737328/72.  
XX  
XX Novel nucleic acid aptamer having binding affinity to target of Bacillus  
XX PT anthracis, useful for treating Bacillus anthracis disease.  
XX  
XX PS Claim 4; SEQ ID NO 155; 144pp; English.  
XX  
XX The invention relates to a nucleic acid (I) aptamer having binding  
XX CC affinity to one or more pathogen (e.g., Bacillus anthracis ) targets,  
XX CC where binding of (I) to the target reduces virulence of the target. (I)  
XX CC is useful for detecting a Bacillus anthracis protective antigen in a  
XX CC sample. (I) is useful for treating B.anthraxis disease in subjects  
XX CC exposed to B.anthraxis spores. (I) has high affinity and specificity for  
XX CC the protective antigen of B.anthraxis , and is cost effective. (I)  
XX CC enables high throughput screening assays. This sequence corresponds to a  
XX CC nucleic acid used in the invention.  
XX  
XX SQ Sequence 852 BP; 340 A; 105 C; 166 G; 241 T; 0 U; 0 Other;  
XX

Query Match 100.0%; Score 59; DB 13; Length 852;  
Best Local Similarity 100.0%; Pred. No. 2,7e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 59  
DB 144 GGTAGAAAGCGGATGACGGCGGTTAATCCTAGTATCATTAGAAAGACTAAACCGG 202

RESULT 5  
ABA91381  
ID ABA91381 standard; DNA; 867 BP.  
XX  
XX AC ABA91381;  
XX  
XX 15-APR-2002 (first entry)  
XX  
XX  
XX Bacillus anthracis protective antigen PA32 DNA.  
XX  
XX PA32; protective antigen 32; anthrax; inhibitor; screening;  
XX KW antibacterial; therapy; vaccine; DNA immunisation; gene; de-  
XX OS Bacillus anthracis.  
XX  
XX PN US6329156-B1.  
XX



```
PD 11-DEC-2001.
XX
XX 22-MAR-1999; 99US-00273839.
XX
XX 22-MAR-1999; 99US-00273839.
XX
XX (REGC ) UNIV CALIFORNIA.
XX
XX Citino NM, Jackson PJ, Lehnert BE;
XX
XX WPI; 2002-121130/16.
XX
XX P-PSDB; AAM50707.
XX
XX Screening Bacillus anthracis toxicity inhibitor (?) by generating
XX recombinant protective antigen 32, comparing fluorescence of cells
XX contacted with PA32-fluorescent marker fusion protein before, after
XX contact with T.
XX
XX Claim 1, Col 13-14; 14pp; English.
XX
XX The present sequence is that of DNA encoding Bacillus anthracis 32 kDa
XX protective antigen PA32 (see AAM50707), comprising domain 4 of protective
XX antigen PA83. The PA32 DNA was obtained by PCR amplification using B.
XX anthracis Sterne strain pXOI as template and the PA83 gene-derived
XX primers given in ABA91382-83. A claimed method for screening inhibitors
XX of the toxicity of B. anthracis involves: generating recombinant PA32 DNA
XX and ligating it to enhanced green fluorescent protein (EGFP); expressing
XX the gene fusion to produce EGFP-PA32 protein; contacting this with a
XX first sample of mammalian cells; measuring the fluorescence from
XX individual cells in the sample; mixing EGFP-PA32 with a potent toxicity
XX inhibitor of B. anthracis; contacting this mixture with individual cells
XX in a second sample of mammalian cells; measuring the fluorescence from
XX individual cells in the second sample; and comparing the effectiveness
XX of the toxicity inhibitor being determined from a decrease of
XX fluorescence from cells in the second sample. The mammalian cells are
XX preferably A549 human bronchial epithelial cells, and fluorescence is
XX detected using flow cytometry. The assay can be used as a rapid screen
XX for compounds which disrupt binding of PA to cells. 4 Human scFvs (see
XX ABA91388-91) have been identified as potential prophylactics or
XX therapeutics against anthrax poisoning. High intracellular expression
XX levels and ease of purification make recombinant PA32 an attractive
XX vaccine candidate or therapeutic for anthrax poisoning. DNA vaccines are
XX also envisaged
XX
XX Sequence 867 BP; 335 A; 122 C; 175 G; 235 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 6; Length 867;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTAGAAAGCGCGATAGCGCGGTTAATCTAGTATCCATTGAAACGACTTAACCGG 59
XX |||||
XX 129 GGTAGAAAGCGCGATAGCGCGGTTAATCTAGTATCCATTGAAACGACTTAACCGG 187
XX
XX RESULT 6
XX ADI39009
XX ID ADI39009 standard; DNA; 867 BP.
XX
XX ADI39009;
XX
XX 22-APR-2004 (first entry)
XX
XX B. anthracis protective antigen PA32 DNA.
XX
XX Anthrax; protective antigen; PA32; ds; antibacterial; vaccine;
XX single-chain F v fragment; scFv; PA83; EGFP;
XX enhanced green fluorescent protein.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
```

```
FT CDS 1..867
FT /*tag= a
FT /product= "PA32"
XX
XX US2004014707-A1.
XX
XX 22-JAN-2004.
XX
XX 27-FEB-2003; 2003US-00375356.
XX
XX 22-MAR-1999; 99US-00273839.
XX
XX 16-NOV-2001; 2001US-00992742.
XX
XX (CIRI/) CIRINO N M.
XX (JACK/) JACKSON P J.
XX (LEHN/) LEHNERT B E.
XX
XX Citino NM, Jackson PJ, Lehnert BE;
XX
XX WPI; 2004-121598/12.
XX
XX P-PSDB; ADI39010.
XX
XX Inhibiting toxicity of Bacillus anthracis, useful for treating anthrax
XX poisoning comprising introducing a DNA-encoding single-chain Fv fragment
XX protein against protective antigen PA83.
XX
XX Disclosure; SEQ ID NO 7; 20pp; English.
XX
XX The invention relates to inhibiting the toxicity of Bacillus anthracis
XX comprising introducing at least one type of DNA-encoding single-chain F v
XX fragment (scFv) protein into host mammalian cells, where the host
XX mammalian cells produce an immunoglobulin that functions in an immune
XX response against protective antigen PA83 (and also PA32) of B. anthracis.
XX Also disclosed is a method for screening for inhibitors of the toxicity
XX for B. anthracis. The scFv protein is selected from scFv 1 protein, scFv
XX 4 protein or its mixtures. The host mammalian cells comprise human
XX epithelial cells. The method is useful for inhibiting the toxicity of
XX Bacillus anthracis. The protein can be used as a vaccine or for treating
XX anthrax poisoning. It can also be used as a rapid assay for other small
XX molecule inhibitors of PA binding to cell receptors. EGFP (enhanced green
XX fluorescent protein)-PA32 fusion proteins were used in assays designed to
XX identify scFv proteins which may protect against B. anthracis infection.
XX The present sequence encodes B. anthracis PA32.
XX
XX Sequence 867 BP; 335 A; 122 C; 175 G; 235 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 12; Length 867;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTAGAAAGCGCGATAGCGCGGTTAATCTAGTATCCATTGAAACGACTTAACCGG 59
XX |||||
XX 129 GGTAGAAAGCGCGATAGCGCGGTTAATCTAGTATCCATTGAAACGACTTAACCGG 187
XX
XX RESULT 7
XX ADR48535
XX ID ADR48535 standard; DNA; 1108 BP.
XX
XX ADR48535;
XX
XX 04-NOV-2004 (first entry)
XX
XX paga target sequence #5.
XX
XX Bacillus anthracis; cutaneous; respiratory anthrax infection; paga; capB;
XX pXOI; pXO2; target sequence; de.
XX
XX Bacillus anthracis.
XX
XX WO2004070001-A2.
XX
XX 19-AUG-2004.
```



XX		12-NOV-2003; 2003WO-US036240.	
Pf			
XX		15-NOV-2002; 2002US-0426552P.	
PR		16-MAY-2003; 2003US--0471082P.	
XX			
PA	(GENP-) GEN-PROBE INC.		
XX			
XI	Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;		
DR	WPI; 2004-604428/58.		
Pt	New oligonucleotides that hybridize specifically to a Bacillus anthracis sequence, useful for detecting cutaneous and respiratory Bacillus anthrax infections.		
Pt			
PS	Claim 21; SEQ ID NO 33; 61pp; English.		
XX			
CC	The present invention relates to an oligonucleotide of 20-40 nucleotides that specifically hybridizes to a sequence contained in a Bacillus anthracis target sequence. The methods and compositions of the present invention are useful for detecting the presence of Bacillus anthracis nucleic acid in a sample, in particular for detecting cutaneous and respiratory anthrax infections. Two synthetic genetic target sequences, derived from pagA and capB gene sequences, were synthesized to provide known standards for testing oligonucleotides for detection of the genes carried by the plasmids pXO1 and pXO2, without requiring handling of virulent Bacillus anthracis. The present sequence represents a pagA target sequence.		
SQ	Sequence 1108 BP; 409 A; 188 C; 224 G; 287 T; 0 U; 0 Other;		
Oy	Query Match Best Local Similarity 100.0%; Score 59; DB 13; Length 1108; Matches 59; Conservative 100.0%; Pred. No. 2.6e-24; Mismatches 0; Indels 0; Gaps 0;		
Dn	1 GGTAGAAAGCGGGATACGCGCGCTTAATTCTTAGTATCATTAGAAGCACTAAACC GG 59       998 GGTAGAAAGCGGGATACGCGCGCTTAATTCTTAGTATCATTAGAAGCACTAAACC GG 1056		
RESULT 8			
ID	ADL16358		
XX	ADL16358 standard; DNA; 1272 BP.		
AC	ADL16358;		
DT	06-MAY-2004 (first entry)		
DE	pPB113 vector DNA for expression of 47kDa PA deletion mutant (PA47).		
KM	Immunogenic; vaccine; lethal infection; protective antigen; PA;		
XX	lethal factor; LF; anthrax; antibacterial; gene; mutant; ds.		
OS	Bacillus anthracis.		
FH	Key	Location/Qualifiers	
FT	CDS	1..1272	
FT		/tag= a	
FT		/product= "PA deletion mutant protein (PA47)"	
FT		/partial	
FT		/note= "No start codon"	
PN	US2004028695-A1.		
PD	12-FEB-2004.		
PF	28-MAR-2003; 2003US--00402466.		
PR	12-APR-2002; 2002US--0372152P.		
XX			
XX	(PARK/) PARK S.		

PA	(GIRI//) GIRI L.
XX	
PI	Park S, Giri L;
XX	
DR	WPI, 2004-168865/16.
DR	P-PSDB, ADL16359.
XX	
PT	Immunogenic composition for preparing a vaccine against a lethal
PT	infection of <i>Bacillus anthracis</i> in an animal, comprises an immunizing
PT	amount of a recombinant <i>B. anthracis</i> protective antigen protein and/or
XX	lethal factor protein.
XX	
PS	Disclosure; SEQ ID NO 23; 143pp; English.
XX	
CC	The present invention relates to immunogenic compositions useful for
CC	preparing a vaccine against a lethal infection of <i>Bacillus anthracis</i> in
CC	an animal. The compositions comprise an immunising amount of a
CC	recombinant <i>B. anthracis</i> protective antigen (rPA) protein and a
CC	recombinant <i>B. anthracis</i> lethal factor (rLF) protein. The composition and
CC	method are useful in protecting against anthrax or lethal infections
CC	caused by <i>B. anthracis</i> . The present sequence is pBP13 vector DNA for the
CC	expression of <i>Bacillus anthracis</i> 47 kDa N-terminal PA deletion mutant
CC	(PA47). This sequence is used in the invention.
XX	
SO	Sequence 1272 BP; 507 A; 172 C; 238 G; 355 T; 0 U; 0 Other;
Query Match	100.0%; Score 59; DB 12; Length 1272;
Best Local Similarity	100.0%; Pred. No. 2.6e-24;
Matches	59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	1 GGTGAAAGCGCGATAGCGGCGGTAAATCTAGTGCATTAGAAAGCACTAAACCGG 59
Db	564 GGTGAAAGCGCGATAGCGGCGGTAAATCTAGTGCATTAGAAAGCACTAAACCGG 622
RESULT 9	
AAD29119	
ID	.AAD29119 standard; DNA; 1278 BP.
AC	
XX	AAD29119;
XX	
DT	07-MAY-2002 (first entry)
XX	
DE	<i>Bacillus subtilis</i> protective antigen (PA) domain 1b+2+3 DNA.
XX	
KW	Immunogenic reagent; immune response; protective antigen; PA; vaccine;
XX	<i>Bacillus anthracis</i> infection; antibacterial; ds.
XX	
OS	<i>Bacillus subtilis</i> .
XX	
Key	Location/Qualifiers
PH	1..1278
FT	/*tag a
FT	/product= "Domain 1b+2+3"
FT	/note= "CDS does not include start and stop codon"
FT	/partial
XX	
PN	WO200204646-A1.
XX	
PD	17-JAN-2002.
XX	
PF	06-JUL-2001; 2001WO-GB003065.
XX	
PR	08-JUL-2000; 2000GB-00016702.
XX	
PA	(MINA ) UK SEC FOR DEFENCE.
XX	
PI	Williamson BD, Miller J, Walker ND, Baillie LMW, Holden PT;
PI	Flick-Smith HC, Bullfeint HL, Tiddall RW, Topping AW;
XX	
DR	WPI, 2002-171720/22.
DR	P-PSDB; AAE18287.
XX	



PT New immunogenic reagent having a polypeptide of the full length  
PT Protective antigen of Bacillus anthracis, useful for treating B.  
PT anthracis infection or in preparing a medicament for the prophylaxis or  
PT treatment of the infection.  
XX  
XX Example 5; Fig 3; 40pp; English.  
PS  
XX The present invention relates to an immunogenic reagent, which produces  
CC an immune response that is protective against Bacillus anthracis. The  
CC reagent comprises one or more polypeptides which together represent up to  
CC three domains of the full length Protective antigen (PA) of Bacillus  
CC anthracis or variants of these, and at least one of the domains comprises  
CC domain 1 or domain 4 of PA or its variant. The invention is used as a  
CC vaccine. The immunogenic reagent is useful in the preparation of a  
CC medicament for the prophylaxis or treatment of B. anthracis infection.  
CC The present sequence is Bacillus subtilis protective antigen domain  
CC 1b+2+3 DNA  
XX  
SQ Sequence 1278 BP; 489 A; 210 C; 245 G; 334 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 993 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1051  
RESULT 10  
ID AEB63722 standard; DNA; 1281 BP.  
XX AEB63722;  
AC  
XX 06-OCT-2005 (first entry)  
DT  
XX  
DE DNA encoding anthrax protective antigen domain D1b23.  
XX  
XX Antigen; bacillus anthracis infection; antibacterial; vaccine;  
KM protective antigen; PA; ds.  
XX  
XX Bacillus anthracis.  
OS  
XX WO2005068493-A1.  
PN  
XX 28-JUL-2005.  
PD  
XX 17-JAN-2005; 2005WO-GB000170.  
PF  
XX 17-JAN-2004; 2004GB-00001036.  
PR  
XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
PA  
XX Cutting SM;  
PI  
XX WPI; 2005-563956/57.  
DR  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
XX Claim 5; SEQ ID NO 10; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus baduui; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment

CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen domain D1b23.  
XX  
SQ Sequence 1281 BP; 492 A; 210 C; 244 G; 335 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 14; Length 1281;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 999 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1057  
RESULT 11  
ID ADL16350 standard; DNA; 1515 BP.  
XX ADL16350;  
AC  
XX 06-MAY-2004 (first entry)  
DT  
XX  
DE pBP107 expression vector DNA for expression of Lf-PA fusion protein.  
XX  
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;  
KM lethal factor; LF; anthrax; antibacterial; gene; fusion protein; ds.  
XX  
XX Bacillus anthracis.  
OS  
XX Synthetic.  
XX  
XX Key Location/Qualifiers  
FH 1..1515  
FT CDS /\*tag= a  
FT /\*product= "Lf-PA fusion protein"  
FT /partial  
FT /note= "No start codon"  
XX  
XX US2004028695-A1.  
PN  
XX  
XX 12-FEB-2004.  
PD  
XX  
XX 28-MAR-2003; 2003US-00402466.  
PF  
XX 12-APR-2002; 2002US-0372152P.  
PR  
XX (PARK/) PARK S.  
PA (GIRI/) GIRI L.  
PA  
XX Park S, Giri L;  
PI  
XX WPI; 2004-168865/16.  
DR P-PsDB; ADL16351.  
XX  
XX Immunogenic composition for preparing a vaccine against a lethal  
PT infection of Bacillus anthracis in an animal, comprises an immunizing  
PT amount of a recombinant B. anthracis protective antigen protein and/or  
PT lethal factor protein.  
XX  
XX Disclosure; SEQ ID NO 15; 143pp; English.  
PS



XX The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant *B. anthracis* protective antigen (rPA) protein and a  
CC recombinant *B. anthracis* lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by *B. anthracis*. The present sequence is pBP107 expression vector  
CC DNA for the expression of *Bacillus anthracis* LF-PA fusion protein. This  
CC sequence is used in the invention.

XX  
SQ Sequence 1515 BP; 632 A; 174 C; 287 G; 422 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 12; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 807 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 865

RESULT 12  
AD251325  
ID AD251325 standard; DNA; 1704 BP.  
XX  
AC AD251325;  
XX  
DT 30-JUN-2005 (first entry)  
XX  
DE Nucleotide sequence of a PA63 gene fragment.  
XX  
KM protective antigen protein; PA63; PA83; antibacterial; vaccine;  
KM prophylactic immunization; anthrax infection; gene; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1704  
FT /\*tag= a  
FT /partial  
FT /product= "PA63 fragment"  
FT /transl\_except= (pos:475..477, aa:Xaa)  
FT /note= "Xaa represents Asn, Phe, Ile, Gly"  
XX  
PN WO2005034841-A2.  
XX  
PD 21-APR-2005.  
XX  
PF 13-MAY-2004; 2004MO-US014971.  
XX  
PR 14-MAY-2003; 2003US-0470563P.  
XX  
PA (MERI ) MERCK & CO INC.  
XX  
PI Hegler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L;  
XX WPI; 2005-306231/31.  
XX DR P-PSDB; AD251326.  
XX  
XX Producing recombinant *Bacillus anthracis* Protective Antigen protein  
PT encoded by an expression vector having a nucleotide sequence being codon-  
PT optimized for expression in yeast, useful for manufacturing anthrax  
PT vaccines.  
XX  
PS Example 1; SEQ ID NO 47; 91pp; English.  
XX  
XX The specification describes a method for producing recombinant *Bacillus*  
CC anthracis protective antigen protein. The method comprises providing an  
CC expression vector having a polynucleotide encoding a *Bacillus anthracis*  
CC protective antigen protein which is codon-optimized for expression in  
CC yeast, transforming a yeast with the vector, fermenting the transformed  
CC yeast for the expression of the protein, and isolating the protein. The

CC protective antigen protein is PA63 or PA83. The method of the invention  
CC is useful for the produce of antigen protein, which is used for  
CC prophylactic immunization against anthrax infections. The present  
CC sequence encodes a PA63 fragment.

XX  
SQ Sequence 1704 BP; 663 A; 248 C; 328 G; 465 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 14; Length 1704;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 999 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1057

RESULT 13  
AEB63720  
ID AEB63720 standard; DNA; 1707 BP.  
XX  
AC AEB63720;  
XX  
DT 06-OCT-2005 (first entry)  
XX  
DE DNA encoding anthrax protective antigen PA63.  
XX  
KM Antigen; *Bacillus anthracis* infection; antibacterial; vaccine;  
KM protective antigen; PA; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
PN WO2005068493-A1.  
XX  
PD 28-JUL-2005.  
XX  
PF 17-JAN-2005; 2005MO-GB000170.  
XX  
PR 17-JAN-2004; 2004GB-00001036.  
XX  
PA (UNIL ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.  
XX  
PI Cutting SM;  
XX WPI; 2005-563956/57.  
XX  
XX New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.  
XX  
PS Disclosure; SEQ ID NO 8; 90pp; English.  
XX  
XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The *Bacillus* species spore is a spore from many species such  
CC as *Bacillus alvei*; *Bacillus badu*; *Bacillus brevis* and preferably a  
CC spore from *Bacillus subtilis*. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA63 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for



CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA  
CC encoding anthrax protective antigen PA63.  
XX  
SQ Sequence 1707 BP; 665 A; 248 C; 327 G; 467 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 14; Length 1707;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24; Mismatches 0; Gaps 0;  
Matches 59; Conservative 0; Indels 0; Gaps 0;  
Db 999 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 1057  
QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 59  
|||||  
ID ADL16356 standard; DNA; 1710 BP.  
AAZ56877  
XX AAZ56877;  
AC  
XX 25-APR-2000 (first entry)  
DT  
XX  
XX B. anthracis PA63 protein encoding DNA.  
DE  
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;  
KM tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; de.  
XX  
XX Bacillus anthracis.  
OS  
XX  
FH Key Location/Qualifiers  
FT 1..1710  
FT CDS /tag= a  
FT /product= "MAT-PA protein"  
XX  
XX WO200002522-A2.  
PN  
XX  
XX 20-JAN-2000.  
PD  
XX  
XX 09-JUL-1999; 99WO-US015568.  
PF  
XX  
XX 10-JUL-1998; 98US-0092416P.  
PR  
XX  
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.  
PA  
XX  
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;  
PI WPI; 2000-182165/16.  
DR P-PSDB; AAY56961.  
XX  
XX Recombinant DNA construct useful as vaccines for anthrax, in producing  
PT host cells for analyzing the drugs and agents inhibiting anthrax.  
PS  
XX  
XX Disclosure; Page 35; 35pp; English.  
XX  
XX The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis PA63 protein encoding DNA  
XX  
SQ Sequence 1710 BP; 666 A; 248 C; 329 G; 467 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 3; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 59  
|||||  
Db 1002 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 1060  
RESULT 15  
ADL16356  
ID ADL16356 standard; DNA; 1722 BP.  
ADL16356;  
XX  
XX 06-MAY-2004 (first entry)  
DT  
XX  
XX pBp11 vector DNA for expression of 64kDa PA deletion mutant (PA64).  
DE  
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;  
KM lethal factor; LF; anthrax; antibacterial; gene; mutant; de.  
XX  
XX Bacillus anthracis.  
OS  
XX Synthetic.  
OS  
XX  
FH Key Location/Qualifiers  
FT 1..1722  
FT CDS /tag= a  
FT /product= "PA deletion mutant protein (PA64)"  
FT /partial  
FT /note= "No start codon"  
XX  
XX US2004028695-A1.  
PN  
XX  
XX 12-FEB-2004.  
PD  
XX  
XX 28-MAR-2003; 2003US-00402466.  
PF  
XX  
XX 12-APR-2002; 2002US-0372152P.  
PR  
XX  
XX (PARK/) PARK S.  
PA (GIRI/) GIRI L.  
XX  
XX Park S, Giri L;  
PI WPI; 2004-168865/16.  
DR P-PSDB; ADL16357.  
XX  
XX Immunogenic composition for preparing a vaccine against a lethal  
PT infection of Bacillus anthracis in an animal, comprises an immunizing  
PT amount of a recombinant B. anthracis protective antigen protein and/or  
PT lethal factor protein.  
PS  
XX  
XX Disclosure; SEQ ID NO 21; 143pp; English.  
XX  
XX The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of Bacillus anthracis in  
CC an animal. The compositions comprise an immunizing amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (LF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is pBp11 vector DNA for the  
CC expression of Bacillus anthracis 64kDa N-terminal PA deletion mutant  
CC (PA64). This sequence is used in the invention.  
XX  
SQ Sequence 1722 BP; 673 A; 251 C; 330 G; 468 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 12; Length 1722;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Db 1014 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAAGAAAGCACTAAACCGG 1072



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RESULT 16
AAD29120
ID AAD29120 standard; DNA; 1785 BP.
XX
XX
AC AAD29120;
XX
XX 07-MAY-2002 (first entry)
XX
XX Bacillus subtilis protective antigen (PA) domain 1+2+3 DNA.
DE
XX
XX Immunogenic reagent; immune response; protective antigen; PA; vaccine;
KW Bacillus anthracis infection; antibacterial; ds.
XX
XX Bacillus subtilis.
OS
XX
XX Key Location/Qualifiers
FH CDS 1..1785
FT /*tag= a
FT /product= "Domain 1+2+3"
FT /note= "CDS does not include start and stop codon"
FT /partial

W0200204646-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-GB003065.
XX
XX 08-JUL-2000; 2000GB-00016702.
XX
XX (MINA ) UK SEC FOR DEFENCE.
XX
XX Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
PI Flick-Smith HC, Bullifent HL, Tibball RW, Topping AW;
XX
XX WPI; 2002-171720/22.
DR
XX P-PSDB; AAE18288.
XX
XX New immunogenic reagent having a polypeptide of the full length
PT Protective Antigen of Bacillus anthracis, useful for treating B.
PT anthracis infection or in preparing a medicament for the prophylaxis or
PT treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
PS
XX
XX The present invention relates to an immunogenic reagent, which produces
CC an immune response that is protective against Bacillus anthracis. The
CC reagent comprises one or more polypeptides which together represent up to
CC three domains of the full length Protective Antigen (PA) of Bacillus
CC anthracis or variants of these, and at least one of the domains comprises
CC domain 1 or domain 4 of PA or its variant. The invention is used as a
CC vaccine. The immunogenic reagent is useful in the preparation of a
CC medicament for the prophylaxis or treatment of B. anthracis infection.
CC The present sequence is Bacillus subtilis protective antigen domain 1+2+3
CC DNA
XX
XX
SQ Sequence 1785 BP; 686 A; 285 C; 333 G; 481 T; 0 U; 0 Other;
Query Match 100.0%; Score 59; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
DB 1500 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1558

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DT 06-MAY-2004 (first entry)
XX
XX pBP108 expression vector DNA for expression of LF-PA fusion protein.
DE
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
KW lethal factor; LF; anthrax; antibacterial; gene; fusion protein; ds.
XX
XX Bacillus anthracis.
OS
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
FH CDS 1..1974
FT /*tag= a
FT /product= "LF-PA fusion protein"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168865/16.
DR
XX P-PSDB; ADL16353.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
PT infection of Bacillus anthracis in an animal, comprises an immunizing
PT amount of a recombinant B. anthracis protective antigen protein and/or
PT lethal factor protein.
XX
XX Disclosure; SEQ ID NO 17; 143pp; English.
PS
XX
XX The present invention relates to immunogenic compositions useful for
CC preparing a vaccine against a lethal infection of Bacillus anthracis in
CC an animal. The compositions comprise an immunising amount of a
CC recombinant B. anthracis protective antigen (rPA) protein and a
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and
CC methods are useful in protecting against anthrax or lethal infections
CC caused by B. anthracis. The present sequence is pBP108 expression vector
CC DNA for the expression of Bacillus anthracis LF-PA fusion protein. This
CC sequence is used in the invention.
XX
XX
SQ Sequence 1974 BP; 822 A; 230 C; 372 G; 550 T; 0 U; 0 Other;
Query Match 100.0%; Score 59; DB 12; Length 1974;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
DB 1266 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1324

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RESULT 17
ADL16352
ID ADL16352 standard; DNA; 1974 BP.
XX
XX
XX ADL16352;
XX

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RESULT 18
AAQ70189
ID AAQ70189 standard; DNA; 2160 BP.
XX
XX
XX AAQ70189;
XX
XX 25-MAR-2003 (revised)
DT 04-APR-1995 (first entry)
XX
XX Sequence encoding modified protective antigen of Bacillus anthracis.
DE Anthrax; Bacillus anthracis; fusion protein; lethal factor;
XX

```



KW protective antigen; cell killing; targeting; targeting; pathogen;  
 KW intracellular; HIV; human immunodeficiency virus; toxin; ss.  
 XX Bacillus anthracis.  
 OS  
 XX Key Location/Qualifiers  
 FT CDS 1..2160  
 FT /\*tag= a  
 FT /product= "Modified anthrax protective antigen."  
 XX  
 XX MO9418332-A2.  
 XX  
 XX 18-AUG-1994.  
 XX  
 XX 14-FEB-1994; 94WO-US001624.  
 XX  
 XX 12-FEB-1993; 93US-00021601.  
 XX 25-JUN-1993; 93US-00082849.  
 XX  
 XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 XX Leppla SH, Klimpel K, Arora N, Singh Y, Nichols PJ,  
 XX MPI: 1994-279753/34.  
 XX P-PSDB; AAR60193.  
 XX  
 XX Nucleic acid encoding anthrax toxin fusion protein - useful for  
 PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
 PT infected cells.  
 XX  
 XX Example 6; Page 111-113; 124pp; English.  
 XX  
 XX The sequence encoding the protective antigen of Bacillus anthracis may be  
 CC used in the construction of a nucleic acid which encodes a fusion protein  
 CC comprising the anthrax protective antigen binding domain of the native  
 CC anthrax lethal factor and a sequence encoding an activity inducing domain  
 CC of a second protein. Such fusion proteins are useful for the specific  
 CC killing of tumour cells or the killing of cells infected with  
 CC intracellular pathogens, especially HIV, depending on the second  
 CC component. The protective antigen and other toxins require proteolytic  
 CC cleavage to acquire activity. Since some cells infected with an  
 CC intracellular pathogen possess an active protease with quite a narrow  
 CC substrate specificity e.g. HIV, the protease cleavage site found in the  
 CC native toxin is replaced with an intracellular pathogen specific protease  
 CC site (See AAR60184-88). The protease in cells that are infected with an  
 CC intracellular pathogen cleaves the modified toxin which is then rendered  
 CC active and kills the cell. This sequence encodes the Bacillus anthracis  
 CC protective antigen but the nucleotide originally at positions 482-523  
 CC have been replaced with the cassette described in AA070186, resulting in  
 CC replacement in the corresponding protein of amino acids 162-171 with the  
 CC HIV protease cleavable sequence described in AAR60186. (Updated on 25-MAR  
 CC -2003 to correct PN field.)  
 CC  
 XX  
 XX Sequence 2160 BP; 828 A; 321 C; 408 G; 603 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 100.0%; Score 59; DB 2; Length 2160;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTAGAAAGCGCGATGCGCGGTTATCTAGTATGATTCATTGAGAACGACTAAACCGG 59  
 DB 1452 GGTAGAAAGCGCGATGCGCGGTTATCTAGTATGATTCATTGAGAACGACTAAACCGG 1510  
 RESULT 19  
 AD251331  
 ID AD251331 standard; DNA; 2205 BP.  
 XX  
 XX AD251331;  
 XX  
 XX 30-JUN-2005 (first entry)  
 XX  
 XX Nucleotide sequence of a PA83 gene fragment.

XX  
 KW protective antigen protein; PA63; PA83; antibacterial; vaccine;  
 KW prophylactic immunization; anthrax infection; ss.  
 XX  
 XX Bacillus anthracis.  
 OS  
 XX MO2005034841-A2.  
 XX  
 XX 21-APR-2005.  
 XX  
 XX 13-MAY-2004; 2004WO-US014971.  
 XX  
 XX 14-MAY-2003; 2003US-0470563P.  
 XX  
 XX (MERI ) MERCK & CO INC.  
 XX  
 XX Heppler R, Jansen K, Kelly R, Kurtz M, Losada MC, Schultz L,  
 XX MPI: 2005-306231/31.  
 XX P-PSDB; AD251332.  
 XX  
 XX Example 6; SEQ ID NO 53; 91pp; English.  
 XX  
 XX The specification describes a method for producing recombinant Bacillus  
 CC anthracis protective antigen protein. The method comprises providing an  
 CC expression vector having a polynucleotide encoding a Bacillus anthracis  
 CC protective antigen protein which is codon-optimized for expression in  
 CC yeast, transforming a yeast with the vector, fermenting the transformed  
 CC yeast for the expression of the protein, and isolating the protein. The  
 CC protective antigen protein is PA63 or PA83. The method of the invention  
 CC is useful for the produce of antigen protein, which is used for  
 CC prophylactic immunization against anthrax infections. The present  
 CC sequence encodes a PA83 fragment.  
 XX  
 XX Sequence 2205 BP; 857 A; 322 C; 415 G; 611 T; 0 U; 0 Other;  
 SQ  
 XX  
 XX Query Match 100.0%; Score 59; DB 14; Length 2205;  
 XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GGTAGAAAGCGCGATGCGCGGTTATCTAGTATGATTCATTGAGAACGACTAAACCGG 59  
 DB 1500 GGTAGAAAGCGCGATGCGCGGTTATCTAGTATGATTCATTGAGAACGACTAAACCGG 1558  
 RESULT 20  
 AAD29121  
 ID AAD29121 standard; DNA; 2208 BP.  
 XX  
 XX AAD29121;  
 XX  
 XX 07-MAY-2002 (first entry)  
 XX  
 XX Bacillus subtilis protective antigen (PA) domain 1+2+3+4 DNA.  
 XX  
 XX Immunogenic reagent; immune response; protective antigen; PA; vaccine;  
 KW Bacillus anthracis infection; antibacterial; ds.  
 XX  
 XX Bacillus subtilis.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 FT CDS 1..2208  
 FT /\*tag= a  
 FT /product= "Domain 1+2+3+4"  
 FT /transl\_except= (pos:853..855, aa:Gln)  
 FT /note= "CDS does not include start codon"  
 FT /partial  
 XX



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PN WO200204646-A1.
XX
XX 17-JAN-2002.
XX
XX 06-JUL-2001; 2001WO-GB003065.
XX
XX 08-JUL-2000; 2000GB-00016702.
XX
XX (MINA ) UK SEC FOR DEFENCE.
XX
XX Williamson ED, Miller J, Walker NJ, Baillie LMJ, Holden PT;
XX Flick-Smith HC, Bullifent HL, Tibball RW, Topping AW;
XX
XX WPI; 2002-171720/22.
XX
XX P-PSDB; AAE18289.
XX
XX New immunogenic reagent having a polypeptide of the full length
XX Protective Antigen of Bacillus anthracis, useful for treating B.
XX anthracis infection or in preparing a medicament for the prophylaxis or
XX treatment of the infection.
XX
XX Example 5; Fig 3; 40pp; English.
XX
XX The present invention relates to an immunogenic reagent, which produces
XX an immune response that is protective against Bacillus anthracis. The
XX reagent comprises one or more polypeptides which together represent up to
XX three domains of the full length Protective Antigen (PA) of Bacillus
XX anthracis or variants of these, and at least one of the domains comprises
XX domain 1 or domain 4 of PA or its variant. The invention is used as a
XX vaccine. The immunogenic reagent is useful in the preparation of a
XX medicament for the prophylaxis or treatment of B. anthracis infection.
XX The present sequence is Bacillus subtilis protective antigen domain
XX 1+2+3+4 DNA
XX
XX Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 6; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGTAGAAAAGCGGATAGCGCGGTTAATCTTAGATCCATTAGAAAAGACTAAACCGG 59
DB 1500 GGTAGAAAAGCGGATAGCGCGGTTAATCTTAGATCCATTAGAAAAGACTAAACCGG 1558

```

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PA (HARD ) HARVARD COLLEGE.
XX
XX Collier RJ, Sellman BR;
XX
XX WPI; 2002-017725/02.
XX
XX P-PSDB; AAM51483.
XX
XX Protecting humans against anthrax using mutant B groups (anthrax
XX protective antigens) of the pore-forming binary A-B toxin of Bacillus
XX anthracis.
XX
XX Disclosure; Fig 14; 77pp; English.
XX
XX The invention relates to antibacterial agents comprising mutant forms of
XX pore-forming toxins (AAM52113 and AAM51484-AAM51500), especially mutants
XX in the B moiety of the pore-forming binary A-B anthrax toxin, where the B
XX moiety is anthrax protective antigen (PA) and using these mutants or
XX compositions of them for protecting against Bacillus anthracis infections
XX in humans, especially as vaccines. The present sequence is that of the
XX anthrax PA encoding DNA
XX
XX Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 6; Length 2208;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 1 GGTAGAAAAGCGGATAGCGCGGTTAATCTTAGATCCATTAGAAAAGACTAAACCGG 59
DB 1500 GGTAGAAAAGCGGATAGCGCGGTTAATCTTAGATCCATTAGAAAAGACTAAACCGG 1558

```

```

RESULT 22
ADL16343
XX ID ADL16343 standard; DNA; 2208 BP.
XX
XX ADL16343;
XX
XX 06-MAY-2004 (first entry)
XX
XX Bacillus anthracis wild-type rPA DNA #1.
XX
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX lethal factor; LF; anthrax; antibacterial; gene; ds.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1..2208
XX /*tag= a
XX /*product= "rPA protein"
XX /*partial
XX /*note= "No start codon"
XX
XX US2004028695-A1.
XX
XX 12-FEB-2004.
XX
XX 28-MAR-2003; 2003US-00402466.
XX
XX 12-APR-2002; 2002US-0372152P.
XX
XX (PARK/) PARK S.
XX PA (GIRI/) GIRI L.
XX
XX Park S, Giri L;
XX
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16344.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen protein and/or

```



PT lethal factor protein.  
XX  
PS Disclosure; SEQ ID NO 8; 143pp; English.  
XX  
CC The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunising amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a  
CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is *Bacillus anthracis* wild-  
CC type rPA DNA used in the invention.  
XX  
SQ Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 12; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTTAGAAAGCACTAAACCGG 59  
DB 1500 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTTAGAAAGCACTAAACCGG 1558  
RESULT 23  
ADL16346  
ID ADL16346 standard; DNA; 2208 BP.  
XX  
AC ADL16346;  
XX  
DT 06-MAY-2004 (first entry)  
XX  
DE *Bacillus anthracis* PA DNA from pBP105 vector.  
XX  
KM Immunogenic; vaccine; lethal infection; protective antigen; PA;  
KM lethal factor; LF; anthrax; antibacterial; gene; ds.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2208  
FT /\*tag= a  
FT /product= "PA protein"  
FT /partial  
FT /note= "No start codon"  
XX  
PN US2004028695-A1.  
XX  
PD 12-FEB-2004.  
XX  
PF 28-MAR-2003; 2003US-00402466.  
XX  
PR 12-APR-2002; 2002US-0372152P.  
XX  
PA (PARK/) PARK S.  
PA (GIRI/) GIRI L.  
XX  
PI Park S, Giri L;  
XX  
PS WPI; 2004-168865/16.  
DR P-PSDB; ADL16348.  
XX  
PT Immunogenic composition for preparing a vaccine against a lethal  
PT infection of *Bacillus anthracis* in an animal, comprises an immunizing  
PT amount of a recombinant B. anthracis protective antigen protein and/or  
PT lethal factor protein.  
XX  
PS Disclosure; SEQ ID NO 11; 143pp; English.  
XX  
CC The present invention relates to immunogenic compositions useful for  
CC preparing a vaccine against a lethal infection of *Bacillus anthracis* in  
CC an animal. The compositions comprise an immunising amount of a  
CC recombinant B. anthracis protective antigen (rPA) protein and a

CC recombinant B. anthracis lethal factor (rLF) protein. The composition and  
CC methods are useful in protecting against anthrax or lethal infections  
CC caused by B. anthracis. The present sequence is *Bacillus anthracis* PA DNA  
CC from pBP105 vector used in the invention.  
XX  
SQ Sequence 2208 BP; 859 A; 323 C; 414 G; 612 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 12; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTTAGAAAGCACTAAACCGG 59  
DB 1500 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTTAGAAAGCACTAAACCGG 1558  
RESULT 24  
ADM05484  
ID ADM05484 standard; DNA; 2208 BP.  
XX  
AC ADM05484;  
XX  
DT 07-APR-2005 (first entry)  
XX  
DE B. anthracis wild-type protective antigen, DNA.  
XX  
KM Protein engineering; *Bacillus anthracis* infection; protective antigen;  
KM toxin; bacterial infection; vaccine; antibacterial; ds; gene.  
XX  
OS *Bacillus anthracis*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..2208  
FT /\*tag= a  
FT /product= "Protective antigen"  
FT /partial  
FT /note= "No start codon shown"  
XX  
PN WO2005004791-A2.  
XX  
PD 20-JAN-2005.  
XX  
PF 10-NOV-2003; 2003WO-US035733.  
XX  
PR 08-NOV-2002; 2002US-0424987P.  
XX  
PA (HARD ) HARVARD COLLEGE.  
PA (UYOK-) UNIV OKLAHOMA.  
XX  
PI Collier RJ, Ballard JD, Tweten R, Mourez M;  
XX  
PS WPI; 2005-091963/10.  
DR P-PSDB; ADM05483.  
XX  
PT New B moiety of pore-forming binary A-B toxin or its fragment, where the  
PT moiety has a mutation that inhibits its pore-forming ability, useful for  
PT preventing or treating bacterial infection, e.g. anthrax.  
XX  
PS Disclosure; SEQ ID NO 22; 129pp; English.  
XX  
CC The invention relates to a B moiety of pore-forming binary A-B toxin or  
CC its fragment, where the moiety has a mutation that inhibits its pore-  
CC forming ability and is selected from S382, N399, and N422 of the *Bacillus*  
CC anthracis protective antigen (PA) appearing as ADM05483. Also included  
CC are a vaccine composition comprising the mutant B moiety or its fragment  
CC (and a carrier), preventing or treating a bacterial infection in a mammal  
CC by administering the vaccine to the mammal, a nucleic acid encoding the  
CC mutant B moiety, a vector comprising the nucleic acid and a purified  
CC antibody that specifically binds a B moiety, but fails to bind a  
CC naturally occurring B moiety. The B moiety is selected from *Clostridium*  
CC difficile, *C. perfringens*, *C. spiroforme*, *C. botulinum*, and *Bacillus*  
CC cereus. The mutation inhibits the pore-forming ability of the toxin in  
CC vivo. The B moiety and vaccine composition are useful for preventing or



CC creating a bacterial infection, e.g. anthrax. The present sequence  
CC encodes the wild-type PA protein.

XX  
SQ Sequence 2208 BP; 859 A; 322 C; 415 G; 612 T; 0 U; 0 Other;

Query Match 100.0%; Score 59; DB 14; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGTATCATCTAGAAAGACTAAACCGG 59  
DB 1500 GGTAGAAAGCGGATAGCGGGCTTAATCTAGTATCATCTAGAAAGACTAAACCGG 1558

## RESULT 25

AEB63729  
ID AEB63729 standard; DNA; 2208 BP.

AC AEB63729;

DT 06-OCT-2005 (first entry)

DE DNA encoding anthrax protective antigen, PA63.

KW Antigen; bacillus anthracis infection; antibacterial; vaccine;

KW protective antigen; PA; ds; gene.

OS Bacillus anthracis.

XX WO2005068493-A1.

XX 28-JUL-2005.

XX 17-JAN-2005; 2005WO-GB000170.

XX 17-JAN-2004; 2004GB-00001036.

XX (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.

XX Cutting SM;

XX WPI; 2005-563956/57.

PT New non-pathogenic spore comprising an antigenic fragment of anthrax  
PT protective antigen, useful as an anthrax vaccine or for manufacturing an  
PT anthrax vaccine.

PS Disclosure; SEQ ID NO 17; 90pp; English.

XX The present invention relates to a non-pathogenic spore comprising an  
CC antigenic fragment of anthrax protective antigen. Also given is a  
CC pharmaceutical composition comprising a non-pathogenic spore comprising  
CC at least an antigenic fragment of anthrax protective antigen in  
CC association with a pharmaceutical carrier and/or excipient; and methods  
CC of inducing immunity to anthrax in a mammal susceptible to anthrax  
CC infection. The Bacillus species spore is a spore from many species such  
CC as Bacillus alvei; Bacillus bedius; Bacillus brevis and preferably a  
CC spore from Bacillus subtilis. The spore comprises an antigenic fragment  
CC of anthrax protective antigen in the form of a protein attached to the  
CC proteinaceous coat of the spore. It comprises an antigenic fragment of  
CC anthrax protective antigen encoded in the form of DNA which is adapted to  
CC be expressed when the spore germinates. The antigenic fragment is one or  
CC more of: PA63 which comprises a sequence of SEQ ID NO: 6; PA63 which  
CC comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen  
CC which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen  
CC which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen  
CC which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the  
CC protective antigen which has a sequence of SEQ ID NO: 4; and Domain D1b23  
CC which is a sequence of SEQ ID NO: 10. The composition further comprises  
CC an adjuvant that potentiates an antigen-specific immune response. The  
CC composition (including the spore) is useful as an anthrax vaccine or for  
CC manufacturing an anthrax vaccine. The composition and method are used for  
CC inducing an immune response against anthrax. The present sequence is DNA

CC encoding anthrax protective antigen, PA63.

XX  
SQ Sequence 2208 BP; 859 A; 321 C; 414 G; 614 T; 0 U; 0 Other;

Query Match 100.0%; Score 59; DB 14; Length 2208;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGTATCATCTAGAAAGACTAAACCGG 59  
DB 1500 GGTAGAAAGCGGATAGCGGGCTTAATCTAGTATCATCTAGAAAGACTAAACCGG 1558

## RESULT 26

AAZ56875  
ID AAZ56875 standard; DNA; 2211 BP.

AC AAZ56875;

DT 25-APR-2000 (first entry)

DE B. anthracis MAT-PA protein encoding DNA.

KW Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;

KW tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; ds.

OS Bacillus anthracis.

XX Key Location/Qualifiers

FX CDS 1..2211

FT /\*tag= a

FT /product= "MAT-PA protein"

XX WO200002522-A2.

XX 20-JAN-2000.

XX 09-JUL-1999; 99WO-US015568.

XX 10-JUL-1998; 98US-0092416P.

XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.

XX WPI; 2000-182165/16.

XX P-PSDB; AAY56959.

PT Recombinant DNA construct useful as vaccines for anthrax, in producing  
PT host cells for analyzing the drugs and agents inhibiting anthrax.

PS Disclosure; Page 34; 35pp; English.

XX The invention provides a recombinant DNA construct that comprises a  
CC vector and at least one nucleic acid (or its fragment) encoding a  
CC combination of Bacillus anthracis proteins, selected from protective  
CC antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA  
CC with its secretory signals replaced with those of tissue plasminogen  
CC activator) and PA63 (63 KDa PA). The construct is useful as a DNA vaccine  
CC for anthrax and in producing infectious alpha virus particles. These  
CC particles, expressing the B. anthracis proteins are useful also as  
CC vaccines for anthrax. Host cells transformed with the construct are  
CC useful for analyzing the effectiveness of drugs and agents that inhibit  
CC anthrax or B. anthracis proteins. The present sequence represents a B.  
CC anthracis MAT-PA protein encoding DNA

XX Sequence 2211 BP; 860 A; 322 C; 416 G; 613 T; 0 U; 0 Other;

Query Match 100.0%; Score 59; DB 3; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGTATCATCTAGAAAGACTAAACCGG 59



Db 1503 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTCATTAGAAACGACTAAACCGG 1561

## RESULT 27

ID ADY84835 standard; DNA; 2211 BP.

AC ADY84835;

DT 02-JUN-2005 (first entry)

DE Bacillus anthracis protective antigen coding sequence.

XX Bacillus anthracis infection; vaccine; antibacterial; protective antigen;

XX gene; ds.

OS Bacillus anthracis.

Key Location/Qualifiers

FT CDS 1..2211

FT /tag= a

FT /product= "Protective antigen"

PN WO2005026203-A2.

PD 24-MAR-2005.

PF 20-SEP-2004; 2004MO-US030616.

PR 18-SEP-2003; 2003US-0504504P.

PR 18-SEP-2003; 2003US-0504505P.

XX (USNA ) US SEC OF NAVY.

XX Kopecko DJ, Osorio M, Bhattacharya S, Giri CP, Blake M;

XX WPI; 2005-233481/24.

PT New attenuated bacterium capable of expressing a heterologous protein,

PT which is under the control of a promoter, useful as a vaccine against

PT Bacillus anthracis infection, or for treating Bacillus anthracis

PT infection.

PS Claim 10; SEQ ID NO 9; 83pp; English.

CC The invention provides an attenuated bacterium which is capable of

CC expressing a heterologous protein. The expression of the heterologous

CC protein is under the control of a promoter selected from 8 fully defined

CC sequences ADY84827-ADY84834. The attenuated bacterium is preferably

CC Salmonella typhi or Salmonella typhimurium. The heterologous protein

CC comprises an antigenic sequence derived from a virus, bacterium, fungus,

CC yeast or parasite, and is especially a protective antigen (PA) of

CC Bacillus anthracis. A claimed live attenuated vaccine for immunization

CC against anthrax comprises an attenuated galactose epimerase-less mutant

CC strain of S. typhi (e.g. strain Ty21a) carrying a Bacillus anthracis PA,

CC especially a wild-type PA or its immunogenic fragment. The PA is

CC preferably encoded by a low-copy plasmid such as pGS2. The plasmid

CC promotes expression of the PA by a ntb promoter or by a Sec signal

CC sequence. The vaccine is used in a claimed method of immunizing a

CC susceptible host against B. anthracis disease. The present sequence is

CC the B. anthracis PA coding sequence (wild-type).

XX Sequence 2211 BP; 860 A; 323 C; 415 G; 613 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 59; DB 14; Length 2211;

XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;

XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTCATTAGAAACGACTAAACCGG 59

DB 1503 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTCATTAGAAACGACTAAACCGG 1561

## RESULT 28

ID ADV96726 standard; DNA; 2220 BP.

AC ADV96726;

DT 24-FEB-2005 (first entry)

DE Gene of the invention SEQ ID NO:12.

XX antineoplastic; chemotherapy; toxin; tumor; cytostatic; ds; gene.

XX Unidentified.

Key Location/Qualifiers

FT CDS 1..2220

FT /tag= a

PN CN1513878-A.

PD 21-JUL-2004.

PF 13-JUN-2003; 2003CN-00143142.

PR 13-JUN-2003; 2003CN-00143142.

XX (MIJU/) MI J.

XX Mi J;

XX WPI; 2004-710658/70.

DR P-PsDB; ADV96725.

PT Antitumor medicine containing recombination bacterial toxin protein

PT complex substance.

PS Claim 2; SEQ ID NO 12; 29pp; Chinese.

CC The invention relates to a novel antineoplastic medicine containing the

CC recombinant bacteriotoxin protein composition TPCB whose key components

CC are recombinant proteins IP33 and LP14. Under the action of a particular

CC enzyme generated by tumor cells, the non-toxic protein can be changed

CC into toxic protein to directly kill tumor cells specifically. The present

CC sequence encodes a protein of the invention.

XX Sequence 2220 BP; 860 A; 326 C; 419 G; 615 T; 0 U; 0 Other;

XX Query Match 100.0%; Score 59; DB 13; Length 2220;

XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;

XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTCATTAGAAACGACTAAACCGG 59

DB 1512 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTCATTAGAAACGACTAAACCGG 1570

RESULT 29

ADY840459

ID ADY840459 standard; DNA; 2235 BP.

AC ADY840459;

DT 18-NOV-2004 (first entry)

DE Bacillus anthracis protective antigen double mutant DNA seqid 3.

XX antibacterial; vaccine; protective antigen; PA; proteolytic degradation;

XX B. anthracis toxin; B. anthracis infection; passive immunization;

XX inhalation anthrax; cutaneous anthrax; gastrointestinal anthrax; mutant;

XX gene; ds.

XX Bacillus anthracis.



```
OS Synthetic.
XX Key Location/Qualifiers
FH CDS 88..2235
FT /*tag= a
FT /product= "Bacillus anthracis protective antigen double
FT mutant"
XX US2004171121-A1.
XX 02-SEP-2004.
XX 08-AUG-2003; 2003US-00638006.
XX 09-AUG-2002; 2002US-040285P.
XX (LEPP/) LEPPILA S H.
XX (ROSO/) ROSOVITZ M J.
XX (HSUS/) HSU S D.
XX Leppila SH, Rosovitz MJ, Hsu SD;
XX WPI; 2004-625107/60.
XX P-PSDB; ADR40457.
XX
XX Novel Bacillus anthracis protective antigen having mutations conferring
XX enhanced resistance to proteolytic degradation compared to wild type
XX antigen, useful for inducing antibodies having neutralizing activity
XX anthrax toxin.
XX
XX Example 5; SEQ ID NO 3; 30pp; English.
XX
XX The invention describes a recombinant Bacillus anthracis protective
XX antigen (PA), modified to incorporate one or more mutations comprising an
XX amino acid deletion or substitution in a flexible, exposed, or loop
XX segment of the PA protein, where the one or more mutations confers
XX enhanced resistance to proteolytic degradation compared to wild type PA.
XX A pharmaceutical composition (I) comprising PA and physiologically
XX acceptable carrier or a composition (II) comprising a synthetic construct
XX encoding PA and a carrier is useful for inducing serum antibodies that
XX have neutralising activity for a B.anthraxis toxin which involves
XX administering (i) to a mammal (human), sufficient to elicit production of
XX the antibodies. The antibodies protect the mammal against the infection.
XX (i) is useful for vaccinating a human against B.anthraxis infection. An
XX anti-PA-antibody containing composition is useful for passively
XX immunising a mammal against the toxic effect of B.anthraxis. PA is useful
XX as vaccines to induce serum antibodies which are useful to prevent, treat
XX or reduced the severity of infections caused by B.anthraxis, such as
XX inhalation anthrax, cutaneous anthrax and/or gastrointestinal anthrax. PA
XX exhibits enhanced stability to proteolytic degradation that is increased
XX by at least 25% compared to proteolytic stability of wild-type PA under
XX comparable conditions. This sequence encodes an exemplary double
XX protective antigen (PA) mutant comprising deletion of residues 162-167
XX and residues 304-317 and substitutions S168I and S319G.
XX
XX Sequence 2235 BP; 873 A; 325 C; 416 G; 621 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 13; Length 2235;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
XX 1527 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1585
XX
XX RESULT 30
XX ADL16354
XX ID ADL16354 standard; DNA; 2289 BP.
XX AC ADL16354;
XX XX
XX 06-MAY-2004 (first entry)
```

```
XX
XX pBP109 expression vector DNA for expression of LF-PA fusion protein.
DE
XX Immunogenic; vaccine; lethal infection; protective antigen; PA;
XX lethal factor; LF; anthrax; antibacterial; gene; fusion protein; ds.
XX
XX Bacillus anthracis.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH CDS 1..2289
FT /*tag= a
FT /product= "LF-PA fusion protein"
FT /partial
FT /note= "No start codon"
XX
XX US2004028695-A1.
XX 12-FEB-2004.
XX 28-MAR-2003; 2003US-00402466.
XX 12-APR-2002; 2002US-0372152P.
XX (PARK/) PARK S.
XX (GIRI/) GIRI L.
XX Park S, Giri L;
XX WPI; 2004-168865/16.
XX P-PSDB; ADL16355.
XX
XX Immunogenic composition for preparing a vaccine against a lethal
XX infection of Bacillus anthracis in an animal, comprises an immunizing
XX amount of a recombinant B. anthracis protective antigen and/or
XX lethal factor protein.
XX
XX Disclosure; SEQ ID NO 19; 143pp; English.
XX
XX The present invention relates to immunogenic compositions useful for
XX preparing a vaccine against a lethal infection of Bacillus anthracis in
XX an animal. The compositions comprise an immunising amount of a
XX recombinant B. anthracis protective antigen (rPA) protein and a
XX recombinant B. anthracis lethal factor (rLF) protein. The composition and
XX methods are useful in protecting against anthrax or lethal infections
XX caused by B. anthracis. The present sequence is pBP109 expression vector
XX DNA for the expression of Bacillus anthracis LF-PA fusion protein. This
XX sequence is used in the invention.
XX
XX Sequence 2289 BP; 946 A; 270 C; 423 G; 650 T; 0 U; 0 Other;
XX
XX Query Match 100.0%; Score 59; DB 12; Length 2289;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
XX 1581 GGTGAAAAGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1639
XX
XX RESULT 31
XX AA256876
XX ID AA256876 standard; DNA; 2292 BP.
XX AC AA256876;
XX XX
XX 25-APR-2000 (first entry)
XX
XX B. anthracis TPA-PA protein encoding DNA.
XX
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;
XX tlasue plasmidogen activator; PA63; vaccine; anthrax; antibacterial; ds.
XX
```



```
OS Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1..2292
XX /*tag= a
XX /*product= "TPA-PA protein"
XX
XX WO200002522-A2.
XX
XX 20-JAN-2000.
XX
XX 09-JUL-1999; 99WO-US015568.
XX
XX 10-JUL-1998; 98US-0092416P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;
XX
XX WPI; 2000-182165/16.
XX
XX P-PSDB; AAY56960.
XX
XX Recombinant DNA construct useful as vaccines for anthrax, in producing
XX host cells for analyzing the drugs and agents inhibiting anthrax.
XX
XX Disclosure; Page 32; 35pp; English.
XX
XX The invention provides a recombinant DNA construct that comprises a
XX vector and at least one nucleic acid (or its fragment) encoding a
XX combination of Bacillus anthracis proteins, selected from protective
XX antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA
XX with its secretory signals replaced with those of tissue plasminogen
XX activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine
XX for anthrax and in producing infectious alpha virus particles. These
XX particles, expressing the B. anthracis proteins are useful also as
XX vaccines for anthrax. Host cells transformed with the construct are
XX useful for analyzing the effectiveness of drugs and agents that inhibit
XX anthrax or B. anthracis proteins. The present sequence represents a B.
XX anthracis TPA-PA protein encoding DNA
XX
XX Sequence 2292 BP; 874 A; 337 C; 446 G; 635 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 59; DB 3; Length 2292;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATTCATTAGAAACGACTAAACCGG 59
DB 1584 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATTCATTAGAAACGACTAAACCGG 1642
RESULT 32
AAZ56874
ID AAZ56874 standard; DNA; 2295 BP.
XX
XX AAZ56874;
XX
XX 25-APR-2000 (first entry)
XX
XX B. anthracis protective antigen (PA) protein encoding DNA.
XX
XX Bacillus anthracis protein; protective antigen; PA; MAT-PA; TPA-PA;
XX tissue plasminogen activator; PA63; vaccine; anthrax; antibacterial; de.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1..2295
XX /*tag= a
XX /*product= "PA protein"
XX
XX WO200002522-A2.
XX
```

```
PD 20-JAN-2000.
XX
XX 09-JUL-1999; 99WO-US015568.
XX
XX 10-JUL-1998; 98US-0092416P.
XX
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Parker MD, Smith JF, Welkos SL;
XX
XX WPI; 2000-182165/16.
XX
XX P-PSDB; AAY56958.
XX
XX Recombinant DNA construct useful as vaccines for anthrax, in producing
XX host cells for analyzing the drugs and agents inhibiting anthrax.
XX
XX Disclosure; Page 33; 35pp; English.
XX
XX The invention provides a recombinant DNA construct that comprises a
XX vector and at least one nucleic acid (or its fragment) encoding a
XX combination of Bacillus anthracis proteins, selected from protective
XX antigen (PA), MAT-PA (PA with its secretory signals removed), TPA-PA (PA
XX with its secretory signals replaced with those of tissue plasminogen
XX activator) and PA63 (63 kDa PA). The construct is useful as a DNA vaccine
XX for anthrax and in producing infectious alpha virus particles. These
XX particles, expressing the B. anthracis proteins are useful also as
XX vaccines for anthrax. Host cells transformed with the construct are
XX useful for analyzing the effectiveness of drugs and agents that inhibit
XX anthrax or B. anthracis proteins. The present sequence represents a B.
XX anthracis PA protein encoding DNA
XX
XX Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;
SQ
Query Match 100.0%; Score 59; DB 3; Length 2295;
Best Local Similarity 100.0%; Pred. No. 2.6e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATTCATTAGAAACGACTAAACCGG 59
DB 1587 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATTCATTAGAAACGACTAAACCGG 1645
RESULT 33
AAC86016
ID AAC86016 standard; CDNA; 2295 BP.
XX
XX AAC86016;
XX
XX 29-AUG-2001 (first entry)
XX
XX Wild type B. anthracis protective antigen coding sequence.
XX
XX Lethal factor; LF; immunogen; LF4; protective antigen; PA; DNA vaccine;
XX humoral; cell-mediated; immune memory response; ss.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX sig_peptide 1..87
XX /*tag= a
XX mat_peptide 88..2295
XX /*tag= b
XX /*product= "PA"
XX misc_RNA 610..2295
XX /*tag= C
XX /*product= "Encodes PCPA peptide"
XX
XX WO200145639-A2.
XX
XX 28-JUN-2001.
XX
XX 21-DEC-2000; 2000WO-US034912.
XX
```



PR 22-DEC-1999; 99US-0171459P.  
XX (OHIS ) UNIV OHIO STATE RES FOUND.  
PA (GALL/) GALLOWAY D R.  
PA (MATE/) MATECZUN A J.  
XX  
PI Galloway DR, Mateczun AJ;  
XX WPI; 2001-408540/43.  
DR P-PSDB; AAB47306.  
XX  
XX  
PT Protecting animal against lethal infection with Bacillus anthracis, by  
PT administering wildtype or mutated form of Bacillus anthracis lethal  
PT factor protein or its fragment or a nucleic acid encoding the mutated  
PT protein.  
XX  
XX  
PS Claim 25; Fig 2; 33pp; English.  
XX  
CC This sequence encodes the B. anthracis protective antigen (PA). An  
CC immunogenic fragment of PA, pCPA, can be used to produce an immune  
CC response which protects an animal against lethal injection with Bacillus  
CC anthracis. DNA encoding the B. anthracis PA can be used in conjunction  
CC with DNA encoding the lethal factor (Lf) in a DNA vaccine. Using a DNA  
CC vaccine which encodes the mutated Lf protein or fragment alone or in  
CC combination with a DNA encoding the PA protein or its fragment, both  
CC components (humoral and cell-mediated) of the immune system are  
CC stimulated, which results in longer term immune memory response. The  
CC combined use of a mutated Lf and PA gene or their fragments results in a  
CC higher level of immune response, as judged by overall serum antibody  
CC titers for Lf and PA antigens, than the use of either Lf or PA genes in  
CC separate immunizations  
XX  
SQ Sequence 2295 BP; 892 A; 333 C; 433 G; 637 T; 0 U; 0 Other;

Query Match 100.0%; Score 59; DB 4; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 GGTGAAGAGCGGATAGCGCGGTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
DB 1587 GGTGAAGAGCGGATAGCGCGGTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 34

ADM29247  
ID ADM29247 standard; DNA; 2295 BP.

AC ADW29247;

DT 24-MAR-2005 (first entry)

DE B. anthracis DNA encoding protective antigen, PA.

KM Protective antigen; bacillus anthracis infection; vaccine; infection; ds;  
KM antibacterial.

OS Bacillus anthracis.

XX Key Location/Qualifiers

FT CDS 1..2295

FT /\*tag= a

FT /product= "Protective antigen"

PN W0200500884-A1.

PD 06-JAN-2005.

PF 04-JUN-2004; 2004WO-US017736.

PR 05-JUN-2003; 2003US-0476598P.

PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX

PI Schneerson R, Leppla S, Robbline JB, Shiloach J, Kubler-Kiehl J;  
PI Liu D, Majadly F;  
XX WPI; 2005-066555/07.  
DR P-PSDB; ADM29248.  
XX  
XX  
PT Immunogenic conjugate, useful for inhibiting or treating infection and/or  
PT disease caused by Bacillus anthracis or other bacilli, comprises Bacillus  
PT capsular poly-gamma-glutamic acid polypeptide covalently linked to  
PT carrier.  
XX  
XX  
PS Disclosure; SEQ ID NO 2; 66pp; English.

CC The invention relates to an immunogenic conjugate comprising a Bacillus  
CC capsular poly-gamma-glutamic acid (gammaPGA) polypeptide covalently  
CC linked to a carrier, where the conjugate elicits an immune response in a  
CC subject. Also included are a composition comprising the conjugate and a  
CC pharmaceutically acceptable carrier (for use in eliciting an immune  
CC response against Bacillus antigenic epitope, preferably Bacillus  
CC anthracis antigenic epitope in a subject) and an isolated antibody that  
CC binds to the Bacillus capsular gammaPGA polypeptide (that recognizes  
CC antigenic epitopes on both the Bacillus capsular gammaPGA polypeptide,  
CC or that binds Bacillus anthracis capsular gammaPGA). The carrier may  
CC comprise recombinant B. anthracis protective antigen. The composition and  
CC conjugate are useful for eliciting an immune response against a Bacillus  
CC antigenic epitope in a subject and for inhibiting or treating infection  
CC and/or disease caused by B. anthracis or other bacilli. The immune  
CC response comprises opsonophagocytic activity. The composition is useful  
CC for active immunization for preventing B. anthracis infections and for  
CC preparation of immune antibodies. The present sequence encodes Bacillus  
CC anthracis protective antigen, PA.  
XX

SQ Sequence 2295 BP; 892 A; 334 C; 432 G; 637 T; 0 U; 0 Other;  
Query Match 100.0%; Score 59; DB 14; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DY 1 GGTGAAGAGCGGATAGCGCGGTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
DB 1587 GGTGAAGAGCGGATAGCGCGGTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 35

AE63728  
ID AEB63728 standard; DNA; 2295 BP.

AC AEB63728;

DT 06-OCT-2005 (first entry)

DE DNA encoding full length anthrax protective antigen, PA83.

KM Antigen; bacillus anthracis infection; antibacterial; vaccine;  
KM protective antigen; PA; ds; gene.

OS Bacillus anthracis.

XX Key Location/Qualifiers

FT CDS 1..2295

FT /\*tag= a

FT /product= "Protective antigen"

PN W02005068493-A1.

PD 17-JAN-2005; 2005WO-GB000170.

PR 17-JAN-2004; 2004GB-00001036.

PA (UNLO ) ROYAL HOLLOWAY & BEDFORD NEW COLLEGE.

PI Cutting SM;

XX WPI; 2005-563956/57.

XX New non-pathogenic spore comprising an antigenic fragment of anthrax



PT	protective antigen, useful as an anthrax vaccine or for manufacturing an
PT	anthrax vaccine.
PS	Claim 5; SEQ ID NO 16; 90bp; English.
XX	The present invention relates to a non-pathogenic spore comprising an
CC	antigenic fragment of anthrax protective antigen. Also given is a
CC	pharmaceutical composition comprising a non-pathogenic spore comprising
CC	at least an antigenic fragment of anthrax protective antigen in
CC	association with a pharmaceutical carrier and/or excipient; and methods
CC	of inducing immunity to anthrax in a mammal susceptible to anthrax
CC	infection. The Bacillus species spore is a spore from many species such
CC	as Bacillus alvei; Bacillus badarius; Bacillus brevis and preferably a
CC	spore from Bacillus subtilis. The spore comprises an antigenic fragment
CC	of anthrax protective antigen in the form of a protein attached to the
CC	proteolaceous coat of the spore. It comprises an antigenic fragment of
CC	anthrax protective antigen encoded in the form of DNA which is adapted to
CC	be expressed when the spore germinates. The antigenic fragment is one or
CC	more of: PA83 which comprises a sequence of SEQ ID NO: 6; PA63 which
CC	comprises a sequence of SEQ ID NO: 7; Domain 1 of the protective antigen
CC	which has a sequence of SEQ ID NO: 1; Domain 2 of the protective antigen
CC	which has a sequence of SEQ ID NO: 2; Domain 3 of the protective antigen
CC	which has a sequence of SEQ ID NO: 3; Domain 4 (residues 595-735) of the
CC	protective antigen which has a sequence of SEQ ID NO: 4; and Domain Dnb23
CC	which is a sequence of SEQ ID NO: 10. The composition further comprises
CC	an adjuvant that potentiates an antigen-specific immune response. The
CC	composition (including the spore) is useful as an anthrax vaccine or for
CC	manufacturing an anthrax vaccine. The composition and method are used for
CC	inducing an immune response against anthrax. The present sequence is DNA
CC	encoding full length anthrax protective antigen, PA83.
XX	Sequence 2295 BP; 892 A; 332 C; 432 G; 639 T; 0 U; 0 Other;
SQ	
Query Match	100.0%; Score 59; DB 14; Length 2295;
Best Local Similarity	100.0%; Pred. No. 2.6e-24;
Matches	59; Conservative 0; Mismatches 0; Indels 0; Gaps 0
Oy	1 GGTAGAAAGGCGGATAGCGGCGGTTAATCTTAGTGATTCATTAGAAACGACTTAAACCGG 59
Db	1587 GGTAGAAAGGCGGATAGCGGCGGTTAATCTTAGTGATTCATTAGAAACGACTTAAACCGG 1645
RESULT 36	
ADBE5871	
ID	ADBE5871 standard; DNA; 2605 BP.
XX	ADBE5871;
AC	
XX	29-JAN-2004 (first entry)
DT	
XX	Bacillus anthracis PA antigen encoding sequence.
DE	
XX	Antibacterial; Vaccine; immune response; Bacillus anthracis; ds.
KW	
XX	Bacillus anthracis.
OS	
XX	Key Location/Qualifiers
FH	3..2600
FT	/+tag= a
FT	
XX	WO2003087378-A1.
PN	
XX	23-OCT-2003.
PD	
XX	11-APR-2003; 2003WO-GB001553.
PF	
XX	11-APR-2002; 2002US-0371416P.
XX	(POMD-) POWDERJECT RES LTD.
XX	Schmaljohn C, Fuller J;
PI	
XX	WPI; 2003-877105/81.
DR	

Query Match	Best Local Similarity	Score 59; DB 10; Length 2605;
Matches 59; Conservative	100.0%; Pred. No. 2.6e-24;	Mismatches 0; Indels 0; Gaps 0
Db	1760 GGTAGAAAGCGGATAGCGCGCGTTATCTGATGATTCATTAGAAACGACTAAACCGG 59	
Result 37	AEb20797	
ID	AEb20797 standard; DNA; 2605 BP.	
XX	AEb20797;	
XX	08-SBP-2005 (first entry)	
XX	Bacillus anthracis Protective Antigen (PA) gene, SEQ ID NO:3.	
XX	Nucleic acid vaccine; Bacillus anthracis infection; Protective Antigen;	
XX	gene; ds.	
XX	Bacillus anthracis.	
XX	Location/Qualifiers	
XX	3..2603	
XX	/*tag= a	
XX	/product= "Translated sequence shown in Fig 1A-O"	
XX	/note= "No start or stop codon given. Xaa corresponds to	
XX	in-frame stop codon"	
XX	/transl_except= (pos:15..17,aa:Xaa)	
XX	/transl_except= (pos:63..65,aa:Xaa)	
XX	/transl_except= (pos:81..83,aa:Xaa)	
XX	/transl_except= (pos:141..143,aa:Xaa)	
XX	/transl_except= (pos:147..149,aa:Xaa)	
XX	/transl_except= (pos:2465..2468,aa:Xaa)	
XX	/transl_except= (pos:2481..2483,aa:Xaa)	
XX	/transl_except= (pos:2556..2558,aa:Xaa)	
XX	/transl_except= (pos:2568..2570,aa:Xaa)	
XX	/transl_except= (pos:2586..2588,aa:Xaa)	
XX	/transl_except= (pos:2598..2600,aa:Xaa)	
XX	/transl_except= (pos:2604..2605,aa:Pro)	
XX	174..2468	
XX	/*tag= c	
XX	/product= "Bacillus anthracis Protective Antigen"	
XX	174..245	
XX	/*tag= b	
XX	246..2465	
XX	/*tag= d	
XX	/product= "Mature Protective Antigen"	
XX	US2005148529-A1.	
XX	07-UTL-2005.	



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XX 05-JAN-2004; 2004US-00751103.
PF 05-JAN-2004; 2004US-00751103.
PR 05-JAN-2004; 2004US-00751103.
XX (POWD-) POWDERJECT VACCINES INC.
XX Schmaljohn CS, Fuller JT;
XX WPI; 2005-478100/48.
XX P-PSDB; AEB20798, AEB20803.
XX
XX New polynucleotide vaccine composition comprising a nucleic acid sequence
PT that encodes a Bacillus anthracis antigen, useful for eliciting an immune
PT response against B. anthracis in a subject.
XX
XX Example 1; SEQ ID NO 3; 40pp; English.
XX
XX The invention relates to a polynucleotide vaccine composition comprising
CC a Bacillus anthracis antigen-encoding nucleic acid which is operatively
CC linked to a promoter for expression of the antigen in a mammalian cell.
CC The invention also relates to use of the vaccine composition of the
CC invention for eliciting an immune response in an individual. Preferably,
CC the antigen encoded by the polynucleotide vaccine is obtained or derived
CC from the Bacillus anthracis Protective Antigen (PA), a non-toxic factor
CC responsible for binding to cell membranes which is known to confer active
CC protection against anthrax. The encoded Bacillus anthracis antigen may
CC also be linked to a leader signal peptide (such as the tissue plasminogen
CC activator (TPA) signal peptide) which permits its secretion. The vaccine
CC composition may additionally comprise an adjuvant component such as a CpG
CC sequence, a nucleic acid encoding a polypeptide adjuvant, a lipid, a non-
CC protein hormone or a vitamin. The polynucleotide vaccine composition of
CC the invention can be administered directly into skin or muscle tissue,
CC preferably in particulate form, and is useful for inducing a protective
CC immune response against Bacillus anthracis infection. The present
CC sequence represents the complete nucleotide sequence encoding the
CC Bacillus anthracis Protective Antigen, used in the construction of a
CC Bacillus anthracis polynucleotide vaccine in an example of the invention.
XX
XX Sequence 2605 BP; 1016 A; 362 C; 465 G; 762 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 59; DB 14; Length 2605;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTGAAAAGCGCGATAGCGCGGTTAATCTTAGTATCATTGAAACGACTAAACCGG 59
Db 1760 GGTGAAAAGCGCGATAGCGCGGTTAATCTTAGTATCATTGAAACGACTAAACCGG 1818
XX
XX RESULT 38
XX AAQ70184
XX ID AAQ70184 standard; DNA; 2709 BP.
XX
XX AC AAQ70184;
XX
XX DT 25-MAR-2003 (revised)
XX DT 04-APR-1995 (first entry)
XX
XX PA(1-725) -----Human CD4 fusion protein coding sequence.
XX
XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;
XX protective antigen; cell killing; targeting; targeting; pathogen;
XX intracellular; HIV; human immunodeficiency virus; toxin; Pseudomonas;
XX exotoxin; ss.
XX
XX Bacillus anthracis.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..2709
XX FT /tag= a
XX FT /product= "Anthrax fusion protein."

```

```

XX MO9418332-A2.
XX 18-AUG-1994.
XX
XX 14-FEB-1994; 94WO-US001624.
XX
XX 12-FEB-1993; 93US-00021601.
XX 25-JUN-1993; 93US-00082849.
XX
XX (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
XX Leppia SH, Klimpel K, Aroza N, Singh Y, Nichols PJ;
XX WPI; 1994-279753/34.
XX P-PSDB; AAR60183.
XX
XX Nucleic acid encoding anthrax toxin fusion protein - useful for
PT targeting toxin to specific cells, eg for killing tumour cells or HIV-
PT infected cells.
XX
XX Disclosure; Page 97-100; 124pp; English.
XX
XX This sequence encodes a fusion protein comprising amino acid residues 1-
CC 725 of the anthrax protective antigen protein and a sequence encoding
CC residues 1-178 of human CD4, the portion which binds to gp120 on HIV
CC infected cells. Such fusion proteins may be useful for the specific
CC killing of tumour cells or the killing of cells infected with
CC intracellular pathogens, especially HIV, depending on their components.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 2709 BP; 1006 A; 444 C; 551 G; 708 T; 0 U; 0 Other;
SQ
XX
XX Query Match 100.0%; Score 59; DB 2; Length 2709;
XX Best Local Similarity 100.0%; Pred. No. 2.6e-24;
XX Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 1 GGTGAAAAGCGCGATAGCGCGGTTAATCTTAGTATCATTGAAACGACTAAACCGG 59
Db 1500 GGTGAAAAGCGCGATAGCGCGGTTAATCTTAGTATCATTGAAACGACTAAACCGG 1558
XX
XX RESULT 39
XX AAQ70180
XX ID AAQ70180 standard; DNA; 4235 BP.
XX
XX AC AAQ70180;
XX
XX DT 25-MAR-2003 (revised)
XX DT 03-APR-1995 (first entry)
XX
XX Sequence encoding protective antigen of Bacillus anthracis.
XX
XX Anthrax; Bacillus anthracis; fusion protein; lethal factor;
XX protective antigen; cell killing; targeting; targeting; pathogen;
XX intracellular; HIV; human immunodeficiency virus; toxin; ss.
XX
XX Bacillus anthracis.
XX
XX Key Location/Qualifiers
XX CDS 1891..4098
XX FT /tag= a
XX FT /product= "Anthrax protective antigen."
XX
XX MO9418332-A2.
XX 18-AUG-1994.
XX
XX 14-FEB-1994; 94WO-US001624.
XX
XX 12-FEB-1993; 93US-00021601.
XX 25-JUN-1993; 93US-00082849.
XX

```



PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.  
 XX  
 PI Leppla SM, Klimpel K, Arora N, Singh Y, Nichols PJ;  
 XX  
 DR WPI; 1994-279753/34.  
 DR P-PSDB; ABR60179.  
 XX  
 PT Nucleic acid encoding anthrax toxin fusion protein - useful for  
 PT targeting toxin to specific cells, eg for killing tumour cells or HIV-  
 PT infected cells.  
 XX  
 PS Disclosure; Page 78-81; 124pp; English.  
 XX  
 CC The sequence encoding the protective antigen of Bacillus anthracis may be  
 CC used in the construction of a nucleic acid which encodes a fusion protein  
 CC comprising the anthrax protective antigen binding domain of the native  
 CC anthrax lethal factor and a sequence encoding an activity inducing domain  
 CC of a second protein. The fusion proteins are useful for the specific  
 CC killing of tumour cells or the killing of cells infected with  
 CC intracellular pathogens, especially HIV. (Updated on 25-MAR-2003 to  
 CC correct PN field.)  
 CC  
 XX  
 SQ Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 59; DB 2; Length 4235;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GGTAGAAAAGCGGATAGCGCGGTTAATCCTAGATGATCATTAGAAAGACTAAACCGG 59  
 DB 3390 GGTAGAAAAGCGGATAGCGCGGTTAATCCTAGATGATCATTAGAAAGACTAAACCGG 3448

RESULT 40  
 ACF58207  
 ID ACF58207 strand; DNA; 4235 BP.  
 XX  
 AC ACF58207;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE B. anthracis protective antigen (PA) encoding DNA.  
 XX  
 KW Molecular modeling; antibacterial; protozoacide; fungicide; vaccine;  
 KW protective antigen; PA; gene; ds.  
 XX  
 OS Bacillus anthracis.  
 XX  
 PN WO2003087129-A2.  
 XX  
 PD 23-OCT-2003.  
 XX  
 PF 08-APR-2003; 2003WO-US010851.  
 XX  
 PR 08-APR-2002; 2002US-0371250P.  
 PR 08-APR-2002; 2002US-0371256P.  
 PR 17-APR-2002; 2002US-0373668P.  
 XX  
 XX (PLEX-) PLEXUS VACCINE INC.  
 XX  
 PI Katritch V, Bordner A, Deans RJ, Sumner M;  
 XX  
 DR WPI; 2003-853938/79.  
 DR P-PSDB; ABR39189.  
 XX  
 PT Identifying immunogenic peptides representative of a structural element  
 PT of a target protein comprising detecting an epitope corresponding to the  
 PT molecular model of the three dimensional structure of the epitope in the  
 PT target protein.  
 XX  
 PS Example 1; Page 106-108; 0pp; English.  
 XX  
 CC The invention relates to identifying an immunogenic peptide

CC representative of a structural element of a target protein. The method  
 CC involves detecting in a molecular model of a chimeric polypeptide  
 CC comprising a selected epitope linked to a scaffold protein, an epitope  
 CC having a three dimensional conformation corresponding to the molecular  
 CC model of the three dimensional structure of the epitope in the target  
 CC protein. The methods of the invention are useful for identifying  
 CC immunogenic peptides of a target protein having a known three dimensional  
 CC structure, or of a target protein having a known amino acid sequence but  
 CC unknown three dimensional structure. The immunogenic peptides are useful  
 CC as vaccines for stimulating an immune response in a subject against  
 CC infectious microorganisms including protozoan (Entamoeba histolytica),  
 CC yeast (Candida albicans) or bacterium (Shigella flexneri, Yersinia  
 CC pestis, Serratia marcescens or Bacillus anthracis). The present sequence  
 CC represents a B. anthracis protective antigen (PA) DNA (GenBank Accession  
 CC No. 143280), where the antigen can be used as a target protein  
 XX  
 SQ Sequence 4235 BP; 1624 A; 568 C; 708 G; 1335 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 59; DB 10; Length 4235;  
 Best Local Similarity 100.0%; Pred. No. 2.6e-24;  
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 1 GGTAGAAAAGCGGATAGCGCGGTTAATCCTAGATGATCATTAGAAAGACTAAACCGG 59  
 DB 3390 GGTAGAAAAGCGGATAGCGCGGTTAATCCTAGATGATCATTAGAAAGACTAAACCGG 3448

Search completed: April 11, 2006, 16:27:13  
 Job time : 100.203 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 23.9474 Seconds  
(without alignments)  
4379.433 Million cell updates/sec

Title: US-10-712-654-24

Perfect score: 59

Sequence: 1 ggtagaagcgcgatagcg.....atagaacgactaacgcg 59

Scoring table:

OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888760828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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Issued Patents NA:\*

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3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgm2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/PCRTUS\_COMB.seq:\*  
7: /cgm2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgm2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgm2\_6/ptodata/1/ina/backfiles.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	No.	Score	Query Match Length	ID	Description
1	59	100.0	867	US-09-273-839A-7	Sequence 7, Appli
2	59	100.0	1710	US-09-350-729A-4	Sequence 4, Appli
3	59	100.0	2160	US-08-082-849B-30	Sequence 30, Appli
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5	59	100.0	2211	US-09-350-729A-2	Sequence 2, Appli
6	59	100.0	2292	US-09-350-729A-3	Sequence 3, Appli
7	59	100.0	2295	US-09-350-729A-1	Sequence 1, Appli
8	59	100.0	2709	US-08-021-601-11	Sequence 11, Appli
9	59	100.0	2709	PCT-US94-01624-11	Sequence 11, Appli
10	59	100.0	2709	US-08-082-849B-11	Sequence 11, Appli
11	59	100.0	4235	US-08-021-601-3	Sequence 3, Appli
12	59	100.0	4235	US-08-082-849B-3	Sequence 3, Appli
13	59	100.0	4235	PCT-US94-01624-3	Sequence 3, Appli
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16	16	27.1	601	US-09-949-016-103879	Sequence 103879,
17	16	27.1	601	US-09-949-016-160246	Sequence 160246,
18	16	27.1	601	US-09-949-016-160290	Sequence 160290,
19	16	27.1	603	US-09-328-352-2710	Sequence 2710, Ap
20	16	27.1	912	US-09-489-039A-5410	Sequence 5410, Ap
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22	16	27.1	78649	US-09-949-016-14620	Sequence 14620, A
23	16	27.1	78649	US-09-949-016-16227	Sequence 16227, A
24	16	27.1	78649	US-09-949-016-16228	Sequence 16228, A

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27	15	25.4	713	3	US-08-781-986A-1022	Sequence 1022, Ap
28	15	25.4	1929	3	US-09-248-796A-2003	Sequence 2003, Ap
29	15	25.4	7110	3	US-09-653-730-26	Sequence 26, Appli
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34	14	23.7	601	3	US-09-949-016-163810	Sequence 163810,
35	14	23.7	601	3	US-09-949-016-163818	Sequence 163818,
36	14	23.7	601	3	US-09-949-016-163819	Sequence 163819,
37	14	23.7	601	3	US-09-949-016-163820	Sequence 163820,
38	14	23.7	601	3	US-09-949-016-163820	Sequence 163820,
39	14	23.7	601	3	US-09-949-016-185590	Sequence 185590,
40	14	23.7	606	3	US-09-949-016-201562	Sequence 201562,
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42	14	23.7	795	3	US-09-543-691A-2914	Sequence 2914, Ap
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46	14	23.7	1350	3	US-09-252-991A-336	Sequence 336, App
47	14	23.7	1389	3	US-08-956-171E-325	Sequence 325, App
48	14	23.7	1495	3	US-08-781-986A-325	Sequence 325, App
49	14	23.7	2073	3	US-09-354-123-9	Sequence 9, Appli
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51	14	23.7	6185	3	US-08-609-230A-8	Sequence 8, Appli
52	14	23.7	6185	3	US-09-453-702B-140	Sequence 140, App
53	14	23.7	6527	3	US-10-114-170-140	Sequence 140, App
54	14	23.7	7143	3	US-09-492-308A-3	Sequence 3, Appli
55	14	23.7	10350	2	US-09-381-862-4	Sequence 4, Appli
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69	14	23.7	94847	3	US-09-949-016-12414	Sequence 12414, A
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87	13	22.0	423	3	US-09-489-039A-1265	Sequence 1265, App
88	13	22.0	444	3	US-09-540-236-851	Sequence 851, App
89	13	22.0	444	3	US-09-248-796A-4269	Sequence 4269, App
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91	13	22.0	447	3	US-09-270-767-16990	Sequence 16990, App
92	13	22.0	459	3	US-09-270-767-6712	Sequence 6712, App
93	13	22.0	459	3	US-09-270-767-6712	Sequence 21994, A
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95	13	22.0	464	2	US-08-196-178-2	Sequence 2, Appli
96	13	22.0	490	2	US-08-488-961-1	Sequence 1, Appli
97	13	22.0	490	3	US-08-973-297-1	Sequence 1, Appli



C 98	13	22.0	490	3	US-09-632-957-1	Sequence 1, Appl1	171	13	22.0	1155	3	US-09-248-796A-5987	Sequence 5987, Ap
C 99	13	22.0	490	6	PCT-US96-06511-1	Sequence 1, Appl1	172	13	22.0	1164	3	US-09-489-039A-5069	Sequence 5069, Ap
C 100	13	22.0	507	2	US-08-488-961-11	Sequence 11, Appl	173	13	22.0	1182	3	US-09-107-532A-743	Sequence 743, App
C 101	13	22.0	507	3	US-08-973-297-11	Sequence 11, Appl	174	13	22.0	1183	3	US-09-799-451-763	Sequence 763, App
C 102	13	22.0	507	3	US-09-632-957-11	Sequence 11, Appl	175	13	22.0	1185	3	US-09-248-766A-4548	Sequence 4548, Ap
C 103	13	22.0	507	6	PCT-US96-06511-11	Sequence 11, Appl	176	13	22.0	1198	3	US-09-319-989-1	Sequence 1, Appl1
C 104	13	22.0	547	3	US-09-270-767-4766	Sequence 4766, Ap	177	13	22.0	1211	2	US-08-196-178-1	Sequence 1, Appl1
C 105	13	22.0	547	3	US-09-270-767-20048	Sequence 20048, A	178	13	22.0	1239	3	US-09-107-532A-1131	Sequence 1, Appl1
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C 107	13	22.0	571	3	US-09-270-767-26475	Sequence 26475, A	180	13	22.0	1342	3	US-08-976-259-66	Sequence 66, Appl
C 108	13	22.0	600	3	US-09-328-352-987	Sequence 987, App	181	13	22.0	1342	3	US-09-956-004-66	Sequence 66, Appl
C 109	13	22.0	601	3	US-09-949-016-18060	Sequence 18060, A	182	13	22.0	1377	3	US-09-540-226-1393	Sequence 1393, Ap
C 110	13	22.0	601	3	US-09-949-016-30572	Sequence 30572, A	183	13	22.0	1455	3	US-09-489-039A-2361	Sequence 2361, Ap
C 111	13	22.0	601	3	US-09-949-016-30573	Sequence 30573, A	184	13	22.0	1497	2	US-08-488-961-5	Sequence 5, Appl1
C 112	13	22.0	601	3	US-09-949-016-30574	Sequence 30574, A	185	13	22.0	1497	3	US-08-973-297-5	Sequence 5, Appl1
C 113	13	22.0	601	3	US-09-949-016-31104	Sequence 31104, A	186	13	22.0	1497	3	US-09-632-957-5	Sequence 5, Appl1
C 114	13	22.0	601	3	US-09-949-016-44812	Sequence 44812, A	187	13	22.0	1497	6	PCT-US96-06511-5	Sequence 23, Appl
C 115	13	22.0	601	3	US-09-949-016-64268	Sequence 64268, A	188	13	22.0	1572	2	US-08-353-400-23	Sequence 5, Appl1
C 116	13	22.0	601	3	US-09-949-016-105070	Sequence 105070, A	189	13	22.0	1581	2	US-08-898-780A-1	Sequence 1, Appl1
C 117	13	22.0	601	3	US-09-949-016-105071	Sequence 105071, A	190	13	22.0	1581	2	US-09-270-917-1	Sequence 1, Appl1
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C 119	13	22.0	601	3	US-09-949-016-142011	Sequence 142011, A	192	13	22.0	1601	2	US-08-722-001-7	Sequence 7, Appl1
C 120	13	22.0	601	3	US-09-949-016-148873	Sequence 148873, A	193	13	22.0	1639	2	US-08-334-688-5	Sequence 5, Appl1
C 121	13	22.0	601	3	US-09-949-016-150046	Sequence 150046, A	194	13	22.0	1639	2	US-08-228-932-5	Sequence 5, Appl1
C 122	13	22.0	601	3	US-09-949-016-150047	Sequence 150047, A	195	13	22.0	1639	2	US-08-468-939-5	Sequence 5, Appl1
C 123	13	22.0	601	3	US-09-949-016-150048	Sequence 150048, A	196	13	22.0	1639	2	US-08-406-855A-5	Sequence 5, Appl1
C 124	13	22.0	601	3	US-09-949-016-150048	Sequence 150048, A	197	13	22.0	1639	2	US-08-722-190-5	Sequence 5, Appl1
C 125	13	22.0	601	3	US-09-949-016-155682	Sequence 155682, A	198	13	22.0	1639	2	US-08-244-354-5	Sequence 5, Appl1
C 126	13	22.0	601	3	US-09-949-016-155683	Sequence 155683, A	199	13	22.0	1639	3	US-09-206-899-5	Sequence 5, Appl1
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C 129	13	22.0	618	3	US-09-949-016-197087	Sequence 197087, A	202	13	22.0	1639	3	US-09-444-793-5	Sequence 5, Appl1
C 130	13	22.0	619	3	US-09-107-532A-2221	Sequence 2221, Ap	203	13	22.0	1639	6	PCT-US95-0403-5	Sequence 5, Appl1
C 131	13	22.0	624	3	US-09-270-767-12365	Sequence 12365, A	204	13	22.0	1647	3	US-09-489-039A-1331	Sequence 1331, Ap
C 132	13	22.0	624	3	US-09-270-767-25423	Sequence 25423, A	205	13	22.0	1672	3	US-09-270-767-10975	Sequence 10975, A
C 133	13	22.0	624	3	US-09-252-991A-5230	Sequence 5230, Ap	206	13	22.0	1714	3	US-08-961-083-3	Sequence 3, Appl1
C 134	13	22.0	650	3	US-09-669-751-140	Sequence 140, App	207	13	22.0	1714	3	US-09-536-784-3	Sequence 3, Appl1
C 135	13	22.0	666	2	US-08-196-178-3	Sequence 6991, Ap	208	13	22.0	1714	3	US-09-765-271-3	Sequence 3, Appl1
C 136	13	22.0	666	2	US-08-196-178-3	Sequence 3921, Ap	209	13	22.0	1714	3	US-09-765-272A-3	Sequence 3, Appl1
C 137	13	22.0	714	3	US-09-172-952-9	Sequence 9, Appl1	210	13	22.0	1743	3	US-09-252-991A-13609	Sequence 13609, A
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C 139	13	22.0	750	3	US-09-252-991A-2257	Sequence 2257, Ap	212	13	22.0	1753	3	US-09-620-312D-645	Sequence 645, App
C 140	13	22.0	822	3	US-09-134-000C-212	Sequence 212, App	213	13	22.0	1775	3	US-09-270-767-10082	Sequence 8, Appl1
C 141	13	22.0	827	3	US-09-270-767-11310	Sequence 11310, A	214	13	22.0	1800	3	US-09-080-983-8	Sequence 8, Appl1
C 142	13	22.0	835	3	US-08-961-083-93	Sequence 93, Appl1	215	13	22.0	1800	3	US-09-613-486-8	Sequence 13501, A
C 143	13	22.0	835	3	US-09-536-784-93	Sequence 93, Appl1	216	13	22.0	1839	3	US-09-252-991A-13501	Sequence 1, Appl1
C 144	13	22.0	835	3	US-09-765-271-93	Sequence 93, Appl1	217	13	22.0	1848	2	US-08-278-042C-1	Sequence 6720, Ap
C 145	13	22.0	835	3	US-09-423-439-47	Sequence 47, Appl1	218	13	22.0	1848	2	US-09-248-796A-6730	Sequence 1, Appl1
C 146	13	22.0	864	3	US-09-423-439-47	Sequence 6233, Ap	219	13	22.0	1868	2	US-08-392-367B-1	Sequence 15950, A
C 147	13	22.0	864	3	US-09-489-039A-6332	Sequence 1174, Ap	220	13	22.0	1868	3	US-08-893-467A-1	Sequence 15950, A
C 148	13	22.0	876	3	US-09-252-991A-1174	Sequence 5709, Ap	221	13	22.0	1923	3	US-09-252-991A-15950	Sequence 1864, Ap
C 149	13	22.0	879	3	US-09-489-039A-5709	Sequence 5709, Ap	222	13	22.0	1926	3	US-09-328-352-1864	Sequence 5825, Ap
C 150	13	22.0	885	3	US-09-489-039A-6124	Sequence 6124, Ap	223	13	22.0	1926	3	US-09-248-796A-5825	Sequence 2435, Ap
C 151	13	22.0	891	3	US-09-543-681A-493	Sequence 493, App	224	13	22.0	1950	3	US-09-252-991A-5425	Sequence 1600, Ap
C 152	13	22.0	909	3	US-09-134-000C-1284	Sequence 1284, Ap	225	13	22.0	1976	3	US-10-104-001-1680	Sequence 26, Appl
C 153	13	22.0	918	3	US-09-270-767-2827	Sequence 2827, Ap	226	13	22.0	1987	2	US-08-722-001-26	Sequence 11487, A
C 154	13	22.0	918	3	US-09-270-767-18109	Sequence 18109, A	227	13	22.0	1997	2	US-09-270-767-11487	Sequence 27, Appl
C 155	13	22.0	939	3	US-09-107-532A-2715	Sequence 2715, Ap	228	13	22.0	1997	2	US-08-722-001-27	Sequence 11, Appl
C 156	13	22.0	951	3	US-09-248-796A-6531	Sequence 6531, Ap	229	13	22.0	2004	2	US-08-722-001-11	Sequence 31, Appl
C 157	13	22.0	972	3	US-09-134-000C-2130	Sequence 2130, Ap	230	13	22.0	2025	3	US-09-423-439-37	Sequence 37, Appl
C 158	13	22.0	972	3	US-09-902-540C-9173	Sequence 9173, Ap	231	13	22.0	2025	3	US-09-423-439-37	Sequence 4399, Ap
C 159	13	22.0	1001	3	US-09-641-638-522	Sequence 522, App	232	13	22.0	2046	3	US-09-489-039A-6592	Sequence 2516, Ap
C 160	13	22.0	1001	3	US-10-170-097-552	Sequence 522, App	233	13	22.0	2046	3	US-09-543-681A-5516	Sequence 4516, Ap
C 161	13	22.0	1014	3	US-09-252-991A-13690	Sequence 13690, A	234	13	22.0	2229	3	US-09-489-039A-7991	Sequence 2791, Ap
C 162	13	22.0	1020	3	US-09-543-681A-897	Sequence 897, App	235	13	22.0	2290	3	US-09-916-434-1368	Sequence 1368, Ap
C 163	13	22.0	1023	3	US-09-328-352-3184	Sequence 3184, Ap	236	13	22.0	2334	3	US-08-936-165A-406	Sequence 206, App
C 164	13	22.0	1023	3	US-09-134-000C-3121	Sequence 3121, Ap	237	13	22.0	2436	3	US-09-710-279-4398	Sequence 4398, Ap
C 165	13	22.0	1026	3	US-09-134-001C-813	Sequence 813, App	238	13	22.0	2484	3	US-09-252-991A-1388	Sequence 1388, Ap
C 166	13	22.0	1026	3	US-09-134-000C-2906	Sequence 2906, Ap	239	13	22.0	2514	3	US-09-144-914-3	Sequence 3, Appl1
C 167	13	22.0	1038	3	US-09-489-039A-5062	Sequence 5062, Ap	240	13	22.0	2536	3	US-09-919-039-5	Sequence 5, Appl1
C 168	13	22.0	1092	3	US-09-489-039A-8481	Sequence 8481, Ap	241	13	22.0	2682	2	US-08-867-941-7	Sequence 7, Appl1
C 169	13	22.0	1104	3	US-09-328-352-3536	Sequence 3536, Ap	242	13	22.0	2682	2	US-09-074-658-7	Sequence 7, Appl1
C 170	13	22.0	1136	3	US-08-860-820-1	Sequence 1, Appl1	243	13	22.0	2846	3	US-09-613-182-5	Sequence 5, Appl1



244	13	22.0	3078	3	US-09-543-681A-2940	Sequence 2940, Ap	317	13	22.0	78157	3	US-09-949-016-16466	Sequence 16466, A
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247	13	22.0	3126	3	US-08-929-329-2	Sequence 2, Appli	320	13	22.0	83516	3	US-09-949-016-15378	Sequence 15378, A
248	13	22.0	3217	3	US-09-710-279-4051	Sequence 4051, Ap	321	13	22.0	87594	3	US-09-949-016-12135	Sequence 12135, A
249	13	22.0	3310	3	US-09-799-451-780	Sequence 780, App	322	13	22.0	87594	3	US-09-949-016-16139	Sequence 16139, A
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252	13	22.0	3640	3	US-09-221-017B-1047	Sequence 1047, Ap	325	13	22.0	95318	3	US-09-949-016-11784	Sequence 11784, A
253	13	22.0	3671	2	US-08-176-620A-5	Sequence 5, Appli	326	13	22.0	95318	3	US-09-949-016-13998	Sequence 13998, A
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C 394	12	20.3	72	2	US-08-433-585-66	Sequence 66, Appl
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C 528	12	20.3	601	3	US-09-949-016-63409	Sequence 63409, A
C 529	12	20.3	601	3	US-09-949-016-63410	Sequence 63410, A
C 530	12	20.3	601	3	US-09-949-016-63411	Sequence 63411, A
C 531	12	20.3	601	3	US-09-949-016-71329	Sequence 71329, A
C 532	12	20.3	601	3	US-09-949-016-71330	Sequence 71330, A
C 533	12	20.3	601	3	US-09-949-016-71330	Sequence 71330, A
C 534	12	20.3	601	3	US-09-949-016-71394	Sequence 71394, A
C 535	12	20.3	601	3	US-09-949-016-71617	Sequence 71617, A



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C 537	12	20.3	601	3	US-09-949-016-71763	Sequence 71763, A	C 610	12	20.3	601	3	US-09-949-016-176979	Sequence 176979, A
C 538	12	20.3	601	3	US-09-949-016-71836	Sequence 71836, A	C 611	12	20.3	601	3	US-09-949-016-177894	Sequence 177894, A
C 539	12	20.3	601	3	US-09-949-016-71909	Sequence 71909, A	C 612	12	20.3	601	3	US-09-949-016-178475	Sequence 178475, A
C 540	12	20.3	601	3	US-09-949-016-71982	Sequence 71982, A	C 613	12	20.3	601	3	US-09-949-016-182837	Sequence 182837, A
C 541	12	20.3	601	3	US-09-949-016-72055	Sequence 72055, A	C 614	12	20.3	601	3	US-09-949-016-182881	Sequence 182881, A
C 542	12	20.3	601	3	US-09-949-016-72128	Sequence 72128, A	C 615	12	20.3	601	3	US-09-949-016-182882	Sequence 182882, A
C 543	12	20.3	601	3	US-09-949-016-72201	Sequence 72201, A	C 616	12	20.3	601	3	US-09-949-016-187042	Sequence 187042, A
C 544	12	20.3	601	3	US-09-949-016-72274	Sequence 72274, A	C 617	12	20.3	601	3	US-09-949-016-187237	Sequence 187237, A
C 545	12	20.3	601	3	US-09-949-016-77124	Sequence 77124, A	C 618	12	20.3	601	3	US-09-949-016-187238	Sequence 187238, A
C 546	12	20.3	601	3	US-09-949-016-77125	Sequence 77125, A	C 619	12	20.3	601	3	US-09-949-016-187239	Sequence 187239, A
C 547	12	20.3	601	3	US-09-949-016-83405	Sequence 83405, A	C 620	12	20.3	601	3	US-09-949-016-194801	Sequence 194801, A
C 548	12	20.3	601	3	US-09-949-016-83406	Sequence 83406, A	C 621	12	20.3	601	3	US-09-949-016-194801	Sequence 194801, A
C 549	12	20.3	601	3	US-09-949-016-83406	Sequence 83406, A	C 622	12	20.3	601	3	US-09-949-016-195488	Sequence 195488, A
C 550	12	20.3	601	3	US-09-949-016-86174	Sequence 86174, A	C 623	12	20.3	601	3	US-09-949-016-195488	Sequence 195488, A
C 551	12	20.3	601	3	US-09-949-016-86175	Sequence 86175, A	C 624	12	20.3	601	3	US-09-949-016-196682	Sequence 196682, A
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C 553	12	20.3	601	3	US-09-949-016-86365	Sequence 86365, A	C 626	12	20.3	601	3	US-09-949-016-198933	Sequence 198933, A
C 554	12	20.3	601	3	US-09-949-016-86366	Sequence 86366, A	C 627	12	20.3	601	3	US-09-949-016-198934	Sequence 198934, A
C 555	12	20.3	601	3	US-09-949-016-86570	Sequence 86570, A	C 628	12	20.3	601	3	US-09-949-016-199630	Sequence 199630, A
C 556	12	20.3	601	3	US-09-949-016-87571	Sequence 87571, A	C 629	12	20.3	601	3	US-09-949-016-199740	Sequence 199740, A
C 557	12	20.3	601	3	US-09-949-016-87572	Sequence 87572, A	C 630	12	20.3	601	3	US-09-949-016-200370	Sequence 200370, A
C 558	12	20.3	601	3	US-09-949-016-87573	Sequence 87573, A	C 631	12	20.3	601	3	US-09-949-016-204053	Sequence 204053, A
C 559	12	20.3	601	3	US-09-949-016-90139	Sequence 90139, A	C 632	12	20.3	601	3	US-09-949-016-205700	Sequence 205700, A
C 560	12	20.3	601	3	US-09-949-016-90140	Sequence 90140, A	C 633	12	20.3	601	3	US-09-949-016-205701	Sequence 205701, A
C 561	12	20.3	601	3	US-09-949-016-90165	Sequence 90165, A	C 634	12	20.3	601	3	US-09-949-002-447	Sequence 447, App
C 562	12	20.3	601	3	US-09-949-016-90166	Sequence 90166, A	C 635	12	20.3	601	3	US-09-949-002-4926	Sequence 4926, App
C 563	12	20.3	601	3	US-09-949-016-91860	Sequence 91860, A	C 636	12	20.3	601	3	US-09-949-002-6167	Sequence 6167, App
C 564	12	20.3	601	3	US-09-949-016-91869	Sequence 91869, A	C 637	12	20.3	601	3	US-09-949-002-6176	Sequence 6176, App
C 565	12	20.3	601	3	US-09-949-016-93806	Sequence 93806, A	C 638	12	20.3	601	3	US-09-949-002-9711	Sequence 9711, App
C 566	12	20.3	601	3	US-09-949-016-104858	Sequence 104858, A	C 639	12	20.3	601	3	US-09-949-002-10231	Sequence 10231, App
C 567	12	20.3	601	3	US-09-949-016-104865	Sequence 104865, A	C 640	12	20.3	601	3	US-09-949-002-10240	Sequence 10240, App
C 568	12	20.3	601	3	US-09-949-016-108797	Sequence 108797, A	C 641	12	20.3	605	3	US-09-270-767-1929	Sequence 4929, App
C 569	12	20.3	601	3	US-09-949-016-112357	Sequence 112357, A	C 642	12	20.3	605	3	US-09-270-767-20211	Sequence 20211, App
C 570	12	20.3	601	3	US-09-949-016-117145	Sequence 117145, A	C 643	12	20.3	609	3	US-09-543-681A-2420	Sequence 2420, App
C 571	12	20.3	601	3	US-09-949-016-117146	Sequence 117146, A	C 644	12	20.3	612	3	US-09-540-236-1905	Sequence 1905, App
C 572	12	20.3	601	3	US-09-949-016-117845	Sequence 117845, A	C 645	12	20.3	612	3	US-09-248-796A-1573	Sequence 1573, App
C 573	12	20.3	601	3	US-09-949-016-120500	Sequence 120500, A	C 646	12	20.3	621	3	US-09-248-796A-2780	Sequence 2780, App
C 574	12	20.3	601	3	US-09-949-016-120916	Sequence 120916, A	C 647	12	20.3	624	3	US-09-248-796A-3312	Sequence 3312, App
C 575	12	20.3	601	3	US-09-949-016-121419	Sequence 121419, A	C 648	12	20.3	628	3	US-09-328-111-367	Sequence 367, App
C 576	12	20.3	601	3	US-09-949-016-124854	Sequence 124854, A	C 649	12	20.3	630	6	PCT-US94-01149-21	Sequence 21, App1
C 577	12	20.3	601	3	US-09-949-016-124995	Sequence 124995, A	C 650	12	20.3	650	3	US-09-221-0178-647	Sequence 647, App
C 578	12	20.3	601	3	US-09-949-016-131051	Sequence 131051, A	C 651	12	20.3	653	3	US-09-385-982-90	Sequence 90, App1
C 579	12	20.3	601	3	US-09-949-016-133634	Sequence 133634, A	C 652	12	20.3	654	3	US-09-636-215-645	Sequence 645, App
C 580	12	20.3	601	3	US-09-949-016-133887	Sequence 133887, A	C 653	12	20.3	654	3	US-09-685-166A-645	Sequence 645, App
C 581	12	20.3	601	3	US-09-949-016-135014	Sequence 135014, A	C 654	12	20.3	654	3	US-09-679-143-645	Sequence 645, App
C 582	12	20.3	601	3	US-09-949-016-136677	Sequence 136677, A	C 655	12	20.3	654	3	US-09-759-143-645	Sequence 645, App
C 583	12	20.3	601	3	US-09-949-016-136678	Sequence 136678, A	C 656	12	20.3	654	3	US-09-651-236-645	Sequence 645, App
C 584	12	20.3	601	3	US-09-949-016-136779	Sequence 136779, A	C 657	12	20.3	654	3	US-09-657-279-645	Sequence 645, App
C 585	12	20.3	601	3	US-09-949-016-139246	Sequence 139246, A	C 658	12	20.3	654	3	US-10-012-896-645	Sequence 645, App
C 586	12	20.3	601	3	US-09-949-016-140848	Sequence 140848, A	C 659	12	20.3	670	6	PCT-US94-01149-5	Sequence 5, App11
C 587	12	20.3	601	3	US-09-949-016-140940	Sequence 140940, A	C 660	12	20.3	672	3	US-09-270-767-9247	Sequence 9247, App
C 588	12	20.3	601	3	US-09-949-016-141300	Sequence 141300, A	C 661	12	20.3	672	3	US-09-270-767-24529	Sequence 24529, App
C 589	12	20.3	601	3	US-09-949-016-141301	Sequence 141301, A	C 662	12	20.3	678	3	US-09-533-659-5747	Sequence 5747, App
C 590	12	20.3	601	3	US-09-949-016-142043	Sequence 142043, A	C 663	12	20.3	680	3	US-09-071-035-119	Sequence 119, App
C 591	12	20.3	601	3	US-09-949-016-143723	Sequence 143723, A	C 664	12	20.3	680	3	US-10-206-576-119	Sequence 119, App1
C 592	12	20.3	601	3	US-09-949-016-143724	Sequence 143724, A	C 665	12	20.3	681	6	PCT-US94-01149-25	Sequence 25, App1
C 593	12	20.3	601	3	US-09-949-016-144655	Sequence 144655, A	C 666	12	20.3	687	3	US-09-267-177-24	Sequence 24, App1
C 594	12	20.3	601	3	US-09-949-016-147848	Sequence 147848, A	C 667	12	20.3	693	3	US-09-267-177-24	Sequence 24, App1
C 595	12	20.3	601	3	US-09-949-016-147849	Sequence 147849, A	C 668	12	20.3	700	3	US-09-735-271-164	Sequence 164, App
C 596	12	20.3	601	3	US-09-949-016-148907	Sequence 148907, A	C 669	12	20.3	700	3	US-09-735-271-165	Sequence 165, App
C 597	12	20.3	601	3	US-09-949-016-149401	Sequence 149401, A	C 670	12	20.3	700	3	US-09-735-271-165	Sequence 165, App
C 598	12	20.3	601	3	US-09-949-016-149852	Sequence 149852, A	C 671	12	20.3	704	3	US-09-533-659-4393	Sequence 4393, App
C 599	12	20.3	601	3	US-09-949-016-150962	Sequence 150962, A	C 672	12	20.3	708	3	US-09-489-039A-5401	Sequence 5401, App
C 600	12	20.3	601	3	US-09-949-016-153420	Sequence 153420, A	C 673	12	20.3	710	3	US-08-998-616-597	Sequence 597, App
C 601	12	20.3	601	3	US-09-949-016-168259	Sequence 168259, A	C 674	12	20.3	713	3	US-09-270-767-3965	Sequence 3965, App
C 602	12	20.3	601	3	US-09-949-016-168845	Sequence 168845, A	C 675	12	20.3	717	6	PCT-US94-01149-23	Sequence 23, App1
C 603	12	20.3	601	3	US-09-949-016-168894	Sequence 168894, A	C 676	12	20.3	717	6	PCT-US94-01149-23	Sequence 23, App1
C 604	12	20.3	601	3	US-09-949-016-168895	Sequence 168895, A	C 677	12	20.3	724	3	US-09-976-594-433	Sequence 433, App
C 605	12	20.3	601	3	US-09-949-016-168914	Sequence 168914, A	C 678	12	20.3	729	6	PCT-US94-01149-17	Sequence 17, App1
C 606	12	20.3	601	3	US-09-949-016-168915	Sequence 168915, A	C 679	12	20.3	739	6	PCT-US94-01149-17	Sequence 17, App1
C 607	12	20.3	601	3	US-09-949-016-168916	Sequence 168916, A	C 680	12	20.3	736	3	US-09-270-767-13119	Sequence 13119, App
C 608	12	20.3	601	3	US-09-949-016-169508	Sequence 169508, A	C 681	12	20.3	747	3	US-09-107-532A-2345	Sequence 2345, App



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C 684	12	20.3	756	3	US-09-248-796A-3699	Sequence 3699, Ap
C 685	12	20.3	756	3	US-09-248-796A-3778	Sequence 3778, Ap
C 686	12	20.3	759	3	US-09-902-540-5086	Sequence 5086, Ap
C 687	12	20.3	771	3	US-09-107-532A-418	Sequence 418, App
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C 690	12	20.3	795	3	US-08-956-171E-474	Sequence 474, App
C 691	12	20.3	795	3	US-08-781-986A-474	Sequence 481, App
C 692	12	20.3	795	3	US-09-107-433-481	Sequence 481, App
C 693	12	20.3	801	3	US-09-134-000C-866	Sequence 866, App
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C 695	12	20.3	804	3	US-09-003-570-21	Sequence 21, Appl
C 696	12	20.3	804	3	US-09-864-541A-21	Sequence 4017, Ap
C 697	12	20.3	807	3	US-09-328-352-4017	Sequence 19, Appl
C 698	12	20.3	810	6	PCT-US94-01149-19	Sequence 117, App
C 699	12	20.3	813	3	US-09-071-035-117	Sequence 117, App
C 700	12	20.3	813	3	US-10-206-576-117	Sequence 1552, Ap
C 701	12	20.3	834	3	US-09-134-001C-1552	Sequence 7, Appli
C 702	12	20.3	837	3	US-09-288-339-7	Sequence 524, App
C 703	12	20.3	850	3	US-08-998-416-524	Sequence 3814, Ap
C 704	12	20.3	857	3	US-09-533-559-3814	Sequence 12, Appl
C 705	12	20.3	858	3	US-09-334-938-12	Sequence 7, Appli
C 706	12	20.3	863	3	US-09-513-775B-7	Sequence 791, App
C 707	12	20.3	864	3	US-09-248-796A-791	Sequence 9, Appli
C 708	12	20.3	867	3	US-09-513-775B-9	Sequence 5283, Ap
C 709	12	20.3	868	3	US-09-533-559-5283	Sequence 8468, Ap
C 710	12	20.3	876	3	US-09-902-540-8468	Sequence 494, App
C 711	12	20.3	879	3	US-08-998-416-494	Sequence 16, Appl
C 712	12	20.3	885	3	US-09-090-793-16	Sequence 16, Appl
C 713	12	20.3	885	3	US-09-231-899-16	Sequence 4070, Ap
C 714	12	20.3	894	3	US-09-543-681A-4070	Sequence 4070, Ap
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C 716	12	20.3	904	3	US-09-270-767-10624	Sequence 10624, A
C 717	12	20.3	912	6	PCT-US94-01149-31	Sequence 31, Appl
C 718	12	20.3	924	6	PCT-US94-01149-15	Sequence 15, Appl
C 719	12	20.3	927	3	US-09-107-532A-3369	Sequence 2369, Ap
C 720	12	20.3	927	3	US-09-489-039A-423	Sequence 423, App
C 721	12	20.3	930	3	US-09-248-796A-3114	Sequence 3114, Ap
C 722	12	20.3	937	3	US-09-270-767-15165	Sequence 15165, A
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C 724	12	20.3	947	3	US-09-221-017B-637	Sequence 637, App
C 725	12	20.3	948	3	US-09-724-623-60	Sequence 60, Appl
C 726	12	20.3	951	3	US-09-270-767-28427	Sequence 28427, A
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C 728	12	20.3	954	3	US-09-107-532A-1942	Sequence 1942, Ap
C 729	12	20.3	966	3	US-09-134-000C-1927	Sequence 1927, Ap
C 730	12	20.3	966	3	US-09-270-767-243	Sequence 243, App
C 731	12	20.3	966	3	US-09-270-767-15525	Sequence 15525, A
C 732	12	20.3	978	3	US-09-489-039A-1168	Sequence 1168, Ap
C 733	12	20.3	993	3	US-09-248-796A-1980	Sequence 1980, Ap
C 734	12	20.3	1020	3	US-09-489-039A-1488	Sequence 1488, Ap
C 735	12	20.3	1026	3	US-09-489-039A-1454	Sequence 1454, Ap
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C 738	12	20.3	1032	2	US-08-553-633A-3	Sequence 3, Appli
C 739	12	20.3	1040	3	US-09-270-767-13785	Sequence 13785, A
C 740	12	20.3	1047	3	US-09-107-532A-1767	Sequence 1767, A
C 741	12	20.3	1068	3	US-09-134-001C-743	Sequence 743, App
C 742	12	20.3	1068	3	US-09-489-039A-2382	Sequence 2382, Ap
C 743	12	20.3	1068	3	US-09-134-000C-1479	Sequence 1479, Ap
C 744	12	20.3	1069	3	US-09-614-912-203	Sequence 203, App
C 745	12	20.3	1083	3	US-09-134-001C-1847	Sequence 1847, Ap
C 746	12	20.3	1086	3	US-09-107-532A-2836	Sequence 2836, Ap
C 747	12	20.3	1086	3	US-09-543-681A-3138	Sequence 3138, Ap
C 748	12	20.3	1086	3	US-09-248-796A-2530	Sequence 2530, Ap
C 749	12	20.3	1089	3	US-09-248-796A-5777	Sequence 5777, Ap
C 750	12	20.3	1098	3	US-09-257-179-24	Sequence 24, Appl
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C 752	12	20.3	1128	3	US-09-755-630B-246	Sequence 246, App
C 753	12	20.3	1128	3	US-09-755-630B-250	Sequence 250, App
C 754	12	20.3	1128	3	US-09-755-630B-254	Sequence 254, App
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C 685	12	20.3	756	3	US-09-248-796A-3778	Sequence 3778, Ap
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C 687	12	20.3	771	3	US-09-107-532A-418	Sequence 418, App
C 688	12	20.3	786	3	US-09-270-767-13368	Sequence 13368, A
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C 690	12	20.3	795	3	US-08-956-171E-474	Sequence 474, App
C 691	12	20.3	795	3	US-08-781-986A-474	Sequence 481, App
C 692	12	20.3	795	3	US-09-107-433-481	Sequence 481, App
C 693	12	20.3	801	3	US-09-134-000C-866	Sequence 866, App
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C 699	12	20.3	813	3	US-09-071-035-117	Sequence 117, App
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C 702	12	20.3	837	3	US-09-288-339-7	Sequence 524, App
C 703	12	20.3	850	3	US-08-998-416-524	Sequence 3814, Ap
C 704	12	20.3	857	3	US-09-533-559-3814	Sequence 12, Appl
C 705	12	20.3	858	3	US-09-334-938-12	Sequence 7, Appli
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C 998 12 20.3 1959 3 US-08-996-441B-43 Sequence 43, Appl  
C 999 12 20.3 1959 3 US-08-996-441B-45 Sequence 45, Appl  
C1000 12 20.3 1959 3 US-08-996-441B-47 Sequence 47, Appl

## ALIGNMENTS

RESULT 1  
US-09-273-839A-7

Sequence 7, Application US/09273839A  
Patent No. 6329156  
GENERAL INFORMATION:  
APPLICANT: Ciriaco, Nick M  
APPLICANT: Jackson, Paul J  
APPLICANT: Lehnert, Bruce E  
TITLE OF INVENTION: Disruption of Anthrax Toxin Binding to Cell Surface  
FILE REFERENCE: S-89/662  
CURRENT APPLICATION NUMBER: US/09/273, 839A  
CURRENT FILING DATE: 1999-03-22  
NUMBER OF SEQ ID NOS: 12  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 867  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-273-839A-7

Query Match 100.0%; Score 59; DB 3; Length 867;  
Best Local Similarity 100.0%; Pred. No. 2.5e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGCGATAGCGCGGTTATCTTAGTGATTCATTGAAACGACTTAAACCGG 59  
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RESULT 2  
US-09-350-729A-4

Sequence 4, Application US/09350729A  
Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PUSKO, PETER  
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APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WEIKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES

FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350, 729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092, 416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 1710  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-350-729A-4

Query Match 100.0%; Score 59; DB 3; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 2.5e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTATCTTAGTGATTCATTGAAACGACTTAAACCGG 59  
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RESULT 3  
US-08-082-849B-30

Sequence 30, Application US/08082849B  
Patent No. 5677274  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Atora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and  
NUMBER OF SEQUENCES: 35  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Townsend and Townsend and Crew LLP  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94111-3834  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/082, 849B  
FILING DATE: 25-JUN-1993  
CLASSIFICATION: 514  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/021,601  
FILING DATE: 12-FEB-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-161-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 576-0200  
TELEFAX: (415) 576-0300  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2160 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURE:  
NAME/KEY: CDS



LOCATION: 1..2157  
OTHER INFORMATION: /product= "PAHIV#2"  
US-08-082-849B-30

Query Match 100.0%; Score 59; DB 2; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 1452 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1510

## RESULT 4

PCT-US94-01624-30  
Sequence 30, Application PC/TUS9401624  
GENERAL INFORMATION:  
APPLICANT: Leppla, Stephen H.  
APPLICANT: Klimpel, Kurt R.  
APPLICANT: Arora, Naveen  
APPLICANT: Singh, Yogendra  
APPLICANT: Nichols, Peter J.  
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND  
TITLE OF INVENTION: RELATED METHODS  
NUMBER OF SEQUENCES: 31  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW  
STREET: Steuart Street Tower, 20th Floor, One Market  
STREET: Plaza  
CITY: San Francisco  
STATE: CA  
COUNTRY: USA  
ZIP: 94105  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US94/01624  
FILING DATE: June 25, 1993  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Weber, Kenneth A.  
REGISTRATION NUMBER: 31,677  
REFERENCE/DOCKET NUMBER: 15280-115  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 543-9600  
TELEFAX: (415) 543-5043  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2160 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ORIGINAL SOURCE:  
ORGANISM: Bacillus anthracis  
FEATURES:  
NAME/KEY: CDS  
LOCATION: 1..2157  
OTHER INFORMATION: /product= "PAHIV#2"  
PCT-US94-01624-30

Query Match 100.0%; Score 59; DB 6; Length 2160;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 1452 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1510

RESULT 5  
US-09-350-729A-2  
Sequence 2, Application US/09350729A  
Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350,729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 2211  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-350-729A-2

Query Match 100.0%; Score 59; DB 3; Length 2211;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 1503 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1561

RESULT 6  
US-09-350-729A-3  
Sequence 3, Application US/09350729A  
Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT  
APPLICANT: PARKER, MICHAEL D.  
APPLICANT: SMITH, JONATHAN F.  
APPLICANT: WELKOS, SUSAN L.  
TITLE OF INVENTION: ANTHRAX VACCINES  
FILE REFERENCE: ARMY135  
CURRENT APPLICATION NUMBER: US/09/350,729A  
CURRENT FILING DATE: 2001-06-20  
PRIOR APPLICATION NUMBER: 60/092,416  
PRIOR FILING DATE: 1998-07-10  
NUMBER OF SEQ ID NOS: 8  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 3  
LENGTH: 2292  
TYPE: DNA  
ORGANISM: Bacillus anthracis  
US-09-350-729A-3

Query Match 100.0%; Score 59; DB 3; Length 2292;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59  
Db 1584 GGTGAAGGCGGATAGCGGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1642

RESULT 7  
US-09-350-729A-1  
Sequence 1, Application US/09350729A  
Patent No. 6770479  
GENERAL INFORMATION:  
APPLICANT: LEE, JOHN SCOTT



US-08-021-601-11

Query Match 100.0%; Score 59; DB 3; Length 2295;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1587 GGTAGAAAGCGGATAGCGCGGCTTAATCTAGTGATCATTAAGAAACGACTAAACCGG 1645

QY 1 GGTAGAAAGCGGATAGCGCGGCTTAATCTAGTGATCATTAAGAAACGACTAAACCGG 59

RESULT 8

US-08-021-601-11

Sequence 11, Application US/08021601

Patent No. 5591631

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Kimpel, Kurt R.

APPLICANT: Nichols, Peter J.

APPLICANT: Ariola, Naveen

APPLICANT: Singh, Yogendra

TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND

TITLE OF INVENTION: RELATED METHODS

NUMBER OF SEQUENCES: 12

CLASSIFICATION: 514

CORRESPONDENCE ADDRESS:

ADDRESSEE: Needle & Rosenberg, P.C.

STREET: 133 Carnegie Way, Suite 400

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,601

FILING DATE: 19930212

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414,057

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404/688-9880

TELEFAX: 404/688-9880

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 2709 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2709

US-08-021-601-11

Query Match 100.0%; Score 59; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DB 1500 GGTAGAAAGCGGATAGCGCGGCTTAATCTAGTGATCATTAAGAAACGACTAAACCGG 1558

QY 1 GGTAGAAAGCGGATAGCGCGGCTTAATCTAGTGATCATTAAGAAACGACTAAACCGG 59

RESULT 9

US-08-082-849B-11

Sequence 11, Application US/08082849B

Patent No. 5677274

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Kimpel, Kurt R.

APPLICANT: Ariola, Naveen

APPLICANT: Singh, Yogendra

APPLICANT: Nichols, Peter J.

TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and

TITLE OF INVENTION: Related Methods

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/082,849B

FILING DATE: 25-JUN-1993

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/021,601

FILING DATE: 12-FEB-1993

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 15280-161-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 2709 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Bacillus anthracis

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2709

OTHER INFORMATION: /product= "PA(1-725)-Human CD4

OTHER INFORMATION: residues (1-178)"

US-08-082-849B-11

Query Match 100.0%; Score 59; DB 2; Length 2709;  
Best Local Similarity 100.0%; Pred. No. 2.6e-25;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGCTTAATCTAGTGATCATTAAGAAACGACTAAACCGG 59



Db 1500 GGTAGAAAGCGGATAGCGGGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1558

RESULT 10

PCT-US94-01624-11

Sequence 11, Application PC/TUS9401624

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Klimpel, Kurt R.

APPLICANT: Arota, Naveen

APPLICANT: Singh, Yogendra

APPLICANT: Nichols, Peter J.

TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND

NUMBER OF SEQUENCES: 31

CORRESPONDENCE ADDRESS:

ADDRESSEE: TOWNSEND and TOWNSEND KHOURI and CREW

STREET: Stewart Street Tower, 20th Floor, One Market

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94105

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US94/01624

FILING DATE: June 25, 1993

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Weber, Kenneth A.

REGISTRATION NUMBER: 31,677

REFERENCE/DOCKET NUMBER: 15280-115

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 543-9600

TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 2709 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ORIGINAL SOURCE:

ORGANISM: Bacillus anthracis

FEATURE:

NAME/KEY: CDS

LOCATION: 1..2709

OTHER INFORMATION: /product= "PA(1-725)-----Human CD4

PCT-US94-01624-11

Query Match 100.0%; Score 59; DB 6; Length 2709;

Best Local Similarity 100.0%; Pred. No. 2.6e-25;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 1500 GGTAGAAAGCGGATAGCGGGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 1558

RESULT 11

US-08-021-601-3

Sequence 3, Application US/08021601

Patient No. 5531631

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Klimpel, Kurt R.

APPLICANT: Nichols, Peter J.

APPLICANT: Arota, Naveen

APPLICANT: Singh, Yogendra

TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: Needle & Rosenberg, P.C.

STREET: 133 Carnegie Way, Suite 400

CITY: Atlanta

STATE: Georgia

COUNTRY: USA

ZIP: 30303

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/021,601

FILING DATE: 19930212

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Spratt, Gwendolyn D.

REGISTRATION NUMBER: 36,016

REFERENCE/DOCKET NUMBER: 1414.057

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404/688-0770

TELEFAX: 404/688-9880

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 4235 base pairs

TYPE: NUCLEIC ACID

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

ORIGINAL SOURCE:

ORGANISM: Bacillus anthracis

FEATURE:

NAME/KEY: CDS

LOCATION: 1891..4095

US-08-021-601-3

Query Match 100.0%; Score 59; DB 2; Length 4235;

Best Local Similarity 100.0%; Pred. No. 2.6e-25;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 3390 GGTAGAAAGCGGATAGCGGGGTTAATCTAGTATCCATTAGAAACGACTAAACCGG 3448

RESULT 12

US-08-082-849B-3

Sequence 3, Application US/08082849B

Patient No. 5677274

GENERAL INFORMATION:

APPLICANT: Leppla, Stephen H.

APPLICANT: Klimpel, Kurt R.

APPLICANT: Arota, Naveen

APPLICANT: Singh, Yogendra

APPLICANT: Nichols, Peter J.

TITLE OF INVENTION: Anthrax Toxin Fusion Proteins and

NUMBER OF SEQUENCES: 35

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk



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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/082,849B
FILING DATE: 25-JUN-1993
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/021,601
FILING DATE: 12-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-161-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: CDS
LOCATION: 1891..4095
OTHER INFORMATION: /product= "Protective Antigen"
US-08-082-849B-3

Query Match      100.0%; Score 59; DB 2; Length 4235;
Best Local Similarity 100.0%; Pred. No. 2.6e-25;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTAGAAAGCACTAAACCGG 59
DB      3390 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTAGAAAGCACTAAACCGG 3448

RESULT 13
PCT-US94-01624-3
Sequence 3, Application PC/TUS9401624
GENERAL INFORMATION:
APPLICANT: Leppla, Stephen H.
APPLICANT: Klimpel, Kurt R.
APPLICANT: Ayora, Naveen
APPLICANT: Singh, Yogendra
APPLICANT: Nichols, Peter J.
TITLE OF INVENTION: ANTHRAX TOXIN FUSION PROTEINS AND
TITLE OF INVENTION: RELATED METHODS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSES: TOWNSEND and TOWNSEND KHOURI and CREW
STREET: Stewart Street Tower, 20th Floor, One Market
STREET: Plaza
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILING DATE: June 25, 1993
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
```

```
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 15280-115
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9500
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 4235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bacillus anthracis
FEATURE:
NAME/KEY: CDS
LOCATION: 1891..4095
OTHER INFORMATION: /product= "Protective Antigen"
PCT-US94-01624-3

Query Match      100.0%; Score 59; DB 6; Length 4235;
Best Local Similarity 100.0%; Pred. No. 2.6e-25;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1  GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTAGAAAGCACTAAACCGG 59
DB      3390 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTGCATTAGAAAGCACTAAACCGG 3448

RESULT 14
US-09-134-000C-1428
Sequence 1428, Application US/09134000C
Patent No. 6617156
GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 032796-032
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/055,778
PRIOR FILING DATE: 1997-08-15
NUMBER OF SEQ ID NOS: 6812
SOFTWARE: Patent version 3.1
SEQ ID NO 1428
LENGTH: 573
TYPE: DNA
ORGANISM: Enterococcus faecalis
US-09-134-000C-1428

Query Match      30.5%; Score 18; DB 3; Length 573;
Best Local Similarity 100.0%; Pred. No. 0.43;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      34 TGATCCATTAGAAAGCAC 51
DB      30 TGATCCATTAGAAAGCAC 47

RESULT 15
US-09-949-016-103835
Sequence 103835, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
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; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 103835  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-103835

Query Match 27.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
Db 215 GTGATCCATTAGAAAC 230

RESULT 16  
US-09-949-016-103879  
; Sequence 103879, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 103879  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-103879

Query Match 27.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
Db 215 GTGATCCATTAGAAAC 230

RESULT 17  
US-09-949-016-160246  
; Sequence 160246, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 160246  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-160246

Query Match 27.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
Db 215 GTGATCCATTAGAAAC 230

RESULT 18  
US-09-949-016-160290  
; Sequence 160290, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 160290  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-160290

Query Match 27.1%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
Db 215 GTGATCCATTAGAAAC 230

RESULT 19  
US-09-328-352-2710/c  
; Sequence 2710, Application US/09328352  
; Patent No. 6562958  
; GENERAL INFORMATION:  
; APPLICANT: Gary L. Breton et al.  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER  
; FILE REFERENCE: GTC99-03PA  
; CURRENT APPLICATION NUMBER: US/09/328,352  
; PRIOR FILING DATE: 1999-06-04  
; NUMBER OF SEQ ID NOS: 8252  
; SEQ ID NO 2710  
; LENGTH: 603  
; TYPE: DNA  
; ORGANISM: Acinetobacter baumannii  
US-09-328-352-2710

Query Match 27.1%; Score 16; DB 3; Length 603;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 40 ATTGAAACGACTAA 55  
|||||  
Db 570 ATTGAAACGACTAA 555

RESULT 20  
US-09-489-039A-5410/C  
; Sequence 5410, Application US/09489039A  
; Patent No. 6610836  
; GENERAL INFORMATION:  
; APPLICANT: Gary Breton et. al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 2709.2004001  
; CURRENT APPLICATION NUMBER: US/09/489,039A  
; PRIOR FILING DATE: 2000-01-27  
; PRIOR APPLICATION NUMBER: US 60/117,747  
; PRIOR FILING DATE: 1999-01-29  
; NUMBER OF SEQ ID NOS: 14342  
; SEQ ID NO 5410  
; LENGTH: 912  
; TYPE: DNA  
; ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-5410

Query Match 27.1%; Score 16; DB 3; Length 912;  
Best Local Similarity 100.0%; Pred. No. 6.7;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 AGCGGATAGCGCGG 23  
|||||  
Db 785 AGCGGATAGCGCGG 770

RESULT 21  
US-09-949-016-14619  
; Sequence 14619, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14619  
; LENGTH: 78649  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14619

Query Match 27.1%; Score 16; DB 3; Length 78649;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
|||||  
Db 53753 GTGATCCATTAGAAAC 53768

RESULT 22  
US-09-949-016-14620  
; Sequence 14620, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14620  
; LENGTH: 78649  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14620

Query Match 27.1%; Score 16; DB 3; Length 78649;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
|||||  
Db 53753 GTGATCCATTAGAAAC 53768

RESULT 23  
US-09-949-016-16227  
; Sequence 16227, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16227  
; LENGTH: 78649  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-16227

Query Match 27.1%; Score 16; DB 3; Length 78649;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 33 GTGATCCATTAGAAAC 48  
|||||  
Db 53753 GTGATCCATTAGAAAC 53768

RESULT 24  
US-09-949-016-16228  
; Sequence 16228, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307



CURRENT APPLICATION NUMBER: US/09/949,016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO: 16228  
LENGTH: 78649  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-16228

Query Match 27.1%; Score 16; DB 3; Length 78649;  
Best Local Similarity 100.0%; Pred. No. 7.1;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTGATCCATTGAAAC 48  
Db 53753 GTGATCCATTGAAAC 53768

RESULT 25  
US-09-621-976-2758  
Sequence 2758, Application US/09621976  
Patent No. 6639063  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J.B.  
APPLICANT: Jobert, S.  
APPLICANT: Giordano, J.Y.  
TITLE OF INVENTION: ESTs and Encoded Human Proteins.  
FILE REFERENCE: GENSET,054PR2  
CURRENT APPLICATION NUMBER: US/09/621,976  
CURRENT FILING DATE: 2000-07-21  
NUMBER OF SEQ ID NOS: 19335  
SOFTWARE: Patent.pm  
SEQ ID NO: 2758  
LENGTH: 476  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 39..356  
US-09-621-976-2758

Query Match 25.4%; Score 15; DB 3; Length 476;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 GTTAATCCTAGTGAT 37  
Db 323 GTTAATCCTAGTGAT 337

RESULT 26  
US-08-956-171E-1022/c  
Sequence 1022, Application US/08956171E  
Patent No. 6593114  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
Gil H. Choi  
Patrick S. Dillon  
Craig A. Rosen  
Steven C. Barash  
Michael R. Rannon  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5256  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue

CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/956,171E  
FILING DATE: 20-Oct-1997  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/009,861  
FILING DATE: January 5, 1996  
APPLICATION NUMBER: 08/781,986  
FILING DATE: January 3, 1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mark J. Hyman  
REGISTRATION NUMBER: 46,789  
REFERENCE/DOCKET NUMBER: PB248P1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (240) 314-1224  
TELEFAX: (301) 309-8439  
INFORMATION FOR SEQ ID NO: 1022:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 713 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 1022:  
US-08-956-171E-1022

Query Match 25.4%; Score 15; DB 3; Length 713;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTGATCCATTGAAA 47  
Db 224 GTGATCCATTGAAA 210

RESULT 27  
US-08-781-986A-1022/c  
Sequence 1022, Application US/08781986A  
Patent No. 6737248  
GENERAL INFORMATION:  
APPLICANT: Charles Kunsch  
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences  
NUMBER OF SEQUENCES: 5255  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: Maryland  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
COMPUTER: HP Vectra 486/33  
OPERATING SYSTEM: MSDOS version 6.2  
SOFTWARE: ASCII Text  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/781,986A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Benson, Bob  
REGISTRATION NUMBER: 30,446



```
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 1022:
SEQUENCE CHARACTERISTICS:
LENGTH: 713 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-781-986A-1022

Query Match      25.4%; Score 15; DB 3; Length 713;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 GTGATCCATTAGAAA 47
Db      224 GTGATCCATTAGAAA 210

RESULT 28
US-09-248-796A-2003
Sequence 2003, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:
APPLICANT: Keith Weinlock et al
TITLE OF INVENTION: NOCLETIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 2003
LENGTH: 1929
TYPE: DNA
ORGANISM: Candida albicans
US-09-248-796A-2003

Query Match      25.4%; Score 15; DB 3; Length 1929;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      36 ATCCATTAGAAACGA 50
Db      1616 ATCCATTAGAAACGA 1630

RESULT 29
US-09-653-730-26/c
Sequence 26, Application US/09653730
Patent No. 6855313
GENERAL INFORMATION:
APPLICANT: Whiteley, Marvin
APPLICANT: Lee, Kimberly
APPLICANT: Greenberg, E. P.
APPLICANT: Muh, Ute
TITLE OF INVENTION: QUORUM SENSING SIGNALING IN BACTERIA
FILE REFERENCE: UIZ-038
CURRENT APPLICATION NUMBER: US/09/653,730
CURRENT FILING DATE: 2000-09-01
PRIOR APPLICATION NUMBER: 60/153,022
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 26
LENGTH: 7110
TYPE: DNA
ORGANISM: Pseudomonas aeruginosa
```

```
US-09-653-730-26

Query Match      25.4%; Score 15; DB 3; Length 7110;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCGGATAGCGGCGGT 24
Db      4141 GCGGATAGCGGCGGT 4127

RESULT 30
US-09-477-962-1/c
Sequence 1, Application US/09477962
Patent No. 6927286
GENERAL INFORMATION:
APPLICANT: SHEN, BEN
APPLICANT: DU, LIANGCHENG
APPLICANT: SANCHEZ, CESAR
APPLICANT: CHEN, MEI
APPLICANT: EDWARDS, DANIEL, J.
TITLE OF INVENTION: BLOOMYCIN GENE CLUSTER COMPONENTS AND THEIR USES
FILE REFERENCE: 407T-895820US
CURRENT APPLICATION NUMBER: US/09/477,962
CURRENT FILING DATE: 2000-01-05
PRIOR APPLICATION NUMBER: 60/115,435
PRIOR FILING DATE: 1999-01-06
PRIOR APPLICATION NUMBER: 60/118,848
PRIOR FILING DATE: 1999-02-05
NUMBER OF SEQ ID NOS: 133
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 1
LENGTH: 58857
TYPE: DNA
ORGANISM: Streptomyces verticillius
US-09-477-962-1

Query Match      25.4%; Score 15; DB 3; Length 58857;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      10 GCGGATAGCGGCGGT 24
Db      30756 GCGGATAGCGGCGGT 30742

RESULT 31
US-09-949-016-32942/c
Sequence 32942, Application US/09949016
Patent No. 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: 60/237,768
PRIOR FILING DATE: 2000-10-03
PRIOR APPLICATION NUMBER: 60/231,498
PRIOR FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 32942
LENGTH: 601
TYPE: DNA
ORGANISM: Human
US-09-949-016-32942

Query Match      23.7%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e+02;
```



Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 GATCATTAGAAC 48  
|||  
Db 224 GATCATTAGAAC 211

RESULT 32  
US-09-949-016-163808/c  
; Sequence 163808, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 163808  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-163808

Query Match 23.7%; Score 14; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AGTATCATTAGA 45  
|||  
Db 93 AGTATCATTAGA 80

RESULT 33  
US-09-949-016-163809/c  
; Sequence 163809, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 163809  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-163809

Query Match 23.7%; Score 14; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AGTATCATTAGA 45  
|||  
Db 277 AGTATCATTAGA 264

RESULT 34  
US-09-949-016-163810/c  
; Sequence 163810, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 163810  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-163810

Query Match 23.7%; Score 14; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AGTATCATTAGA 45  
|||  
Db 529 AGTATCATTAGA 516

RESULT 35  
US-09-949-016-163818/c  
; Sequence 163818, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CLO01307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 163818  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-163818

Query Match 23.7%; Score 14; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AGTATCATTAGA 45  
|||  
Db 93 AGTATCATTAGA 80

RESULT 36  
US-09-949-016-163819/c  
; Sequence 163819, Application US/09949016



```

; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163819
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-163819

Query Match      23.7%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      32 AGTGATCCATTAGA 45
DB      277 AGTGATCCATTAGA 264

RESULT 37
US-09-949-016-163820/C
; Sequence 163820, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 163820
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-163820

Query Match      23.7%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      32 AGTGATCCATTAGA 45
DB      529 AGTGATCCATTAGA 516

RESULT 38
US-09-949-016-185590/C
; Sequence 185590, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185590
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-185590

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Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB      224 GATCCATTAGAAAC 211

RESULT 39
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; Sequence 201562, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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US-09-949-016-201562

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Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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US-09-252-991A-310/C
; Sequence 310, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
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; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185590
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-185590

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Best Local Similarity 100.0%; Pred. No. 1e+02;
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QY      35 GATCCATTAGAAAC 48
DB      224 GATCCATTAGAAAC 211

RESULT 39
US-09-949-016-201562
; Sequence 201562, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
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; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-201562

Query Match      23.7%; Score 14; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGTAGAAAGCGCGA 14
DB      492 GGTAGAAAGCGCGA 505

RESULT 40
US-09-252-991A-310/C
; Sequence 310, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
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; PRIOR APPLICATION NUMBER: US 60/094,190  
; PRIOR FILING DATE: 1998-07-27  
; NUMBER OF SEQ ID NOS: 33142  
; SEQ ID NO 310  
; LENGTH: 606  
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; ORGANISM: Pseudomonas aeruginosa  
US-09-252-991A-310

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C 139	15	25.4	2167	6	US-10-094-749-416	Sequence 416, Ap	C 212	14	23.7	576	9	US-10-363-483A-11051	Sequence 31051, A
C 140	15	25.4	2193	7	US-10-437-963-89950	Sequence 89950, A	C 213	14	23.7	576	9	US-10-363-483A-11052	Sequence 31052, A
C 141	15	25.4	2331	8	US-10-751-736-56	Sequence 56, Appl	C 214	14	23.7	580	4	US-09-925-065A-944121	Sequence 944121, A
C 142	15	25.4	2483	8	US-10-723-860-6065	Sequence 6065, Ap	C 215	14	23.7	580	4	US-09-925-065A-944122	Sequence 944122, A
C 143	15	25.4	3189	7	US-10-169-103-3	Sequence 3, Appl1	C 216	14	23.7	581	4	US-09-925-065A-154797	Sequence 154868, A
C 144	15	25.4	3861	10	US-11-097-143-11083	Sequence 11083, A	C 217	14	23.7	585	6	US-10-027-632-214868	Sequence 214868, A
C 145	15	25.4	3984	10	US-11-097-143-38792	Sequence 38792, A	C 218	14	23.7	585	6	US-10-027-632-214868	Sequence 214868, A
C 146	15	25.4	5969	5	US-10-172-086-46	Sequence 46, Appl	C 219	14	23.7	587	8	US-10-425-115-183963	Sequence 183963, A
C 147	15	25.4	5969	7	US-10-240-589C-136	Sequence 136, Appl	C 220	14	23.7	594	7	US-10-437-963-982	Sequence 982, Appl
C 148	15	25.4	5969	7	US-10-311-507-84	Sequence 84, Appl	C 221	14	23.7	600	3	US-09-864-761-7451	Sequence 7451, Ap
C 149	15	25.4	5969	8	US-10-480-846-46	Sequence 46, Appl	C 222	14	23.7	600	3	US-10-972-079-33155	Sequence 33155, Ap
C 150	15	25.4	6373	6	US-10-311-455-1939	Sequence 1939, Ap	C 223	14	23.7	600	9	US-10-972-079-33156	Sequence 48975, A
C 151	15	25.4	7059	7	US-10-389-647-202	Sequence 202, Appl	C 224	14	23.7	600	9	US-10-972-079-33156	Sequence 48975, A
C 152	15	25.4	7110	10	US-11-014-621-26	Sequence 26, Appl	C 225	14	23.7	604	4	US-10-972-079-60438	Sequence 60438, A
C 153	15	25.4	9336	10	US-11-097-143-23266	Sequence 23266, A	C 226	14	23.7	604	4	US-09-925-065A-836448	Sequence 836448, A
C 154	15	25.4	9262	10	US-11-097-143-27394	Sequence 27394, A	C 227	14	23.7	604	4	US-09-925-065A-902732	Sequence 902732, A
C 155	15	25.4	12775	10	US-11-097-143-27394	Sequence 27394, A	C 228	14	23.7	605	4	US-09-925-065A-908708	Sequence 908708, A
C 156	15	25.4	26565	6	US-10-085-959-91	Sequence 91, Appl	C 229	14	23.7	605	4	US-10-363-345A-1489	Sequence 1489, Ap
C 157	15	25.4	168407	7	US-10-322-281-305	Sequence 305, Appl	C 230	14	23.7	612	8	US-10-363-345A-23389	Sequence 23389, Ap
C 158	14	23.7	25	7	US-10-719-956-358658	Sequence 358658, A	C 231	14	23.7	612	8	US-10-363-345A-23389	Sequence 23389, Ap
C 159	14	23.7	201	8	US-10-719-993-40067	Sequence 40067, A	C 232	14	23.7	612	8	US-10-363-345A-23390	Sequence 23390, A
C 160	14	23.7	232	8	US-10-425-115-80608	Sequence 80608, A	C 233	14	23.7	612	8	US-10-363-483A-1489	Sequence 1489, Ap
C 161	14	23.7	243	3	US-09-864-761-17974	Sequence 17974, A	C 234	14	23.7	612	9	US-10-363-483A-1490	Sequence 1490, Ap
C 162	14	23.7	262	3	US-09-922-293-2645	Sequence 2645, Ap	C 235	14	23.7	612	9	US-10-363-483A-23389	Sequence 23389, Ap
C 163	14	23.7	302	3	US-09-960-706-929	Sequence 929, Appl	C 236	14	23.7	612	9	US-10-363-483A-23390	Sequence 23390, A
C 164	14	23.7	302	3	US-09-873-319-609	Sequence 609, Appl	C 237	14	23.7	619	4	US-09-925-065A-163305	Sequence 163305, A
C 165	14	23.7	302	3	US-09-922-293-3697	Sequence 3697, Ap	C 238	14	23.7	619	4	US-09-925-065A-163305	Sequence 163305, A
C 166	14	23.7	317	7	US-10-424-599-81861	Sequence 81861, A	C 239	14	23.7	619	4	US-09-925-065A-643944	Sequence 643944, A
C 167	14	23.7	319	7	US-10-424-599-141604	Sequence 141604, A	C 240	14	23.7	620	4	US-09-925-065A-127951	Sequence 127951, A
C 168	14	23.7	372	8	US-10-425-115-81147	Sequence 81147, A	C 241	14	23.7	627	4	US-09-925-065A-127951	Sequence 127951, A
C 169	14	23.7	374	3	US-09-922-293-3711	Sequence 3711, Ap	C 242	14	23.7	627	4	US-09-925-065A-127952	Sequence 127952, A



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C 254	14	23.7	683	8	US-10-363-345A-36584	Sequence 36584, A	C 327	14	23.7	1072	8	US-10-363-345A-14552	Sequence 14552, A
C 255	14	23.7	683	9	US-10-363-483A-36563	Sequence 36563, A	C 328	14	23.7	1072	9	US-10-363-483A-14551	Sequence 14551, A
C 256	14	23.7	683	9	US-10-363-483A-36564	Sequence 36564, A	C 329	14	23.7	1072	9	US-10-363-483A-14552	Sequence 14552, A
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258	14	23.7	696	3	US-09-974-300-8310	Sequence 8310, Ap	C 331	14	23.7	1080	7	US-10-282-122A-27355	Sequence 27355, A
C 259	14	23.7	703	8	US-10-363-345A-37721	Sequence 37721, A	C 332	14	23.7	1080	8	US-10-761-849-6190	Sequence 6190, Ap
C 260	14	23.7	703	8	US-10-363-345A-37722	Sequence 37722, A	C 333	14	23.7	1080	10	US-11-097-143-10439	Sequence 10439, A
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C 262	14	23.7	709	8	US-10-363-483A-37722	Sequence 37722, A	C 335	14	23.7	1101	7	US-10-412-698A-1205	Sequence 1205, Ap
C 263	14	23.7	709	8	US-10-363-345A-11659	Sequence 11659, A	C 336	14	23.7	1141	8	US-10-363-345A-17993	Sequence 17993, A
C 264	14	23.7	709	8	US-10-363-345A-11660	Sequence 11660, A	C 337	14	23.7	1141	8	US-10-363-345A-17994	Sequence 17994, A
C 265	14	23.7	709	9	US-10-363-483A-11659	Sequence 11659, A	C 338	14	23.7	1141	9	US-10-363-483A-17993	Sequence 17993, A
C 266	14	23.7	709	9	US-10-363-483A-11660	Sequence 11660, A	C 339	14	23.7	1141	9	US-10-363-483A-17994	Sequence 17994, A
C 267	14	23.7	725	8	US-10-363-345A-24123	Sequence 24123, A	C 340	14	23.7	1229	8	US-10-363-483A-11189	Sequence 11189, A
C 268	14	23.7	725	8	US-10-363-345A-24124	Sequence 24124, A	C 341	14	23.7	1229	8	US-10-363-345A-11189	Sequence 11189, A
C 269	14	23.7	725	9	US-10-363-483A-24123	Sequence 24123, A	C 342	14	23.7	1229	9	US-10-363-483A-11190	Sequence 11190, A
C 270	14	23.7	725	9	US-10-363-483A-24124	Sequence 24124, A	C 343	14	23.7	1229	9	US-10-363-483A-11190	Sequence 11190, A
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C 272	14	23.7	731	7	US-10-437-963-42606	Sequence 42606, A	C 345	14	23.7	1252	7	US-10-620-945-1	Sequence 1, Appl1
C 273	14	23.7	733	8	US-10-363-345A-4009	Sequence 4009, Ap	C 346	14	23.7	1262	7	US-10-425-114-11535	Sequence 11535, A
C 274	14	23.7	733	8	US-10-363-345A-4010	Sequence 4010, Ap	C 347	14	23.7	1272	8	US-10-425-115-1973	Sequence 1973, Ap
C 275	14	23.7	733	9	US-10-363-483A-4009	Sequence 4009, Ap	C 348	14	23.7	1320	8	US-10-282-122A-38466	Sequence 38466, A
C 276	14	23.7	733	9	US-10-363-483A-4010	Sequence 4010, Ap	C 349	14	23.7	1320	8	US-10-714-792-779	Sequence 779, Ap
C 277	14	23.7	738	8	US-10-767-795-5546	Sequence 5546, Ap	C 350	14	23.7	1389	2	US-08-761-986A-325	Sequence 325, Ap
C 278	14	23.7	741	8	US-10-363-345A-18897	Sequence 18897, A	C 351	14	23.7	1389	3	US-10-329-624-125	Sequence 325, Ap
C 279	14	23.7	741	8	US-10-363-345A-18898	Sequence 18898, A	C 352	14	23.7	1413	3	US-09-815-242-6074	Sequence 6074, Ap
C 280	14	23.7	741	9	US-10-363-483A-18897	Sequence 18897, A	C 353	14	23.7	1413	6	US-10-369-493-14531	Sequence 24531, A
C 281	14	23.7	741	9	US-10-363-483A-18898	Sequence 18898, A	C 354	14	23.7	1413	6	US-10-282-122A-20779	Sequence 20779, A
C 282	14	23.7	764	8	US-10-363-345A-10703	Sequence 10703, A	C 355	14	23.7	1425	6	US-10-369-493-19560	Sequence 19560, A
C 283	14	23.7	764	8	US-10-363-345A-10704	Sequence 10704, A	C 356	14	23.7	1442	10	US-11-097-143-6083	Sequence 6083, Ap
C 284	14	23.7	764	8	US-10-363-345A-11349	Sequence 11349, A	C 357	14	23.7	1442	10	US-10-425-115-101904	Sequence 101904,
C 285	14	23.7	764	8	US-10-363-345A-11350	Sequence 11350, A	C 358	14	23.7	1478	8	US-10-363-345A-31209	Sequence 31209, A
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C 287	14	23.7	764	9	US-10-363-483A-10704	Sequence 10704, A	C 360	14	23.7	1478	9	US-10-363-483A-31209	Sequence 31209, A
C 288	14	23.7	764	9	US-10-363-483A-11349	Sequence 11349, A	C 361	14	23.7	1478	9	US-10-363-483A-31210	Sequence 31210, A
C 289	14	23.7	766	4	US-10-363-483A-11350	Sequence 11350, A	C 362	14	23.7	1519	3	US-09-822-830A-215	Sequence 215, Ap
C 290	14	23.7	766	4	US-09-925-065A-87375	Sequence 87375, A	C 363	14	23.7	1551	3	US-09-938-842A-3931	Sequence 3931, Ap
C 291	14	23.7	766	4	US-09-925-065A-87376	Sequence 87376, A	C 364	14	23.7	1551	3	US-09-938-842A-3931	Sequence 3931, Ap
C 292	14	23.7	766	4	US-09-925-065A-87377	Sequence 87377, A	C 365	14	23.7	1619	8	US-10-425-115-153675	Sequence 153675, A
C 293	14	23.7	772	8	US-10-363-345A-39219	Sequence 39219, A	C 366	14	23.7	1653	7	US-10-437-963-177479	Sequence 177479, A
C 294	14	23.7	772	8	US-10-363-345A-39220	Sequence 39220, A	C 367	14	23.7	1660	7	US-10-282-122A-22876	Sequence 22876, A
C 295	14	23.7	772	9	US-10-363-345A-39219	Sequence 39219, A	C 368	14	23.7	1698	8	US-10-335-977-1163	Sequence 1163, Ap
C 296	14	23.7	772	9	US-10-363-483A-39219	Sequence 39219, A	C 369	14	23.7	1708	8	US-10-723-660-8337	Sequence 8337, Ap
C 297	14	23.7	814	5	US-10-363-483A-39220	Sequence 39220, A	C 370	14	23.7	1731	6	US-10-425-114-17758	Sequence 7758, Ap
C 298	14	23.7	842	8	US-10-106-698-539	Sequence 539, Ap	C 371	14	23.7	1743	7	US-10-369-493-87149	Sequence 87149, A
C 299	14	23.7	842	8	US-10-363-345A-40099	Sequence 40099, A	C 372	14	23.7	1834	8	US-10-425-115-153673	Sequence 153673, A
C 300	14	23.7	842	8	US-10-363-345A-40100	Sequence 40100, A	C 373	14	23.7	1834	8	US-10-425-115-153673	Sequence 153673, A
C 301	14	23.7	842	9	US-10-363-483A-40099	Sequence 40099, A	C 374	14	23.7	1872	10	US-11-097-143-23072	Sequence 23072, A
C 302	14	23.7	852	7	US-10-363-483A-40100	Sequence 40100, A	C 375	14	23.7	1902	4	US-09-925-065A-862	Sequence 862, Ap
C 303	14	23.7	852	7	US-10-335-977-1161	Sequence 1161, Ap	C 376	14	23.7	2000	7	US-10-260-338-1129	Sequence 1129, A
C 304	14	23.7	860	8	US-10-363-345A-15125	Sequence 15125, A	C 377	14	23.7	2073	7	US-10-388-796-3	Sequence 3, Appl1
C 305	14	23.7	860	8	US-10-363-345A-15126	Sequence 15126, A	C 378	14	23.7	2262	7	US-10-424-599-15552	Sequence 15552, A
C 306	14	23.7	860	9	US-10-363-483A-15125	Sequence 15125, A	C 379	14	23.7	2298	8	US-10-424-599-15552	Sequence 15552, A
C 307	14	23.7	864	7	US-10-363-483A-15126	Sequence 15126, A	C 380	14	23.7	2492	8	US-10-424-599-15552	Sequence 15552, A
C 308	14	23.7	927	7	US-10-282-122A-35410	Sequence 35410, A	C 381	14	23.7	2499	10	US-11-097-143-42655	Sequence 42655, A
C 309	14	23.7	929	6	US-10-282-122A-10034	Sequence 10034, A	C 382	14	23.7	2549	10	US-11-097-143-31189	Sequence 31189, A
C 310	14	23.7	930	7	US-10-356-631-1	Sequence 1, Appl1	C 383	14	23.7	2760	3	US-09-938-842A-1588	Sequence 1588, Ap
C 311	14	23.7	930	7	US-10-282-122A-39657	Sequence 39657, A	C 384	14	23.7	2760	3	US-09-938-842A-1588	Sequence 1588, Ap
C 312	14	23.7	933	7	US-10-282-122A-39704	Sequence 39704, A	C 385	14	23.7	2760	3	US-09-938-842A-1588	Sequence 1588, Ap
C 313	14	23.7	933	7	US-10-335-977-1162	Sequence 1162, Ap	C 386	14	23.7	2761	9	US-10-450-763-70513	Sequence 70513, A
C 314	14	23.7	941	7	US-10-857-625-286	Sequence 286, Ap	C 387	14	23.7	2887	10	US-11-097-143-40804	Sequence 40804, A
C 315	14	23.7	949	8	US-10-767-701-80	Sequence 80, Appl	C 388	14	23.7	3063	5	US-10-027-632-115186	Sequence 115186,
					US-10-363-345A-30459	Sequence 30459, A							



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390	14	23.7	3187	5	US-10-270-333-25	Sequence 25, Appl	C 463	13	22.0	25	9	US-10-843-527-33392	Sequence 53392, A
391	14	23.7	3187	10	US-11-097-143-10438	Sequence 10438, A	C 464	13	22.0	25	9	US-10-843-527-184785	Sequence 184785, A
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C 393	14	23.7	3566	10	US-11-097-143-38645	Sequence 38645, A	C 466	13	22.0	25	10	US-11-036-117-27728	Sequence 27728, A
C 394	14	23.7	3765	6	US-10-369-493-45818	Sequence 45818, A	C 467	13	22.0	25	10	US-11-036-117-169616	Sequence 169616, A
C 395	14	23.7	4572	10	US-11-097-143-33358	Sequence 33358, A	C 468	13	22.0	25	10	US-11-036-117-172206	Sequence 172206, A
C 396	14	23.7	4731	10	US-11-097-143-36314	Sequence 26314, A	C 469	13	22.0	25	10	US-11-036-117-209698	Sequence 209698, A
C 397	14	23.7	5076	10	US-11-097-143-40654	Sequence 40654, A	C 470	13	22.0	25	10	US-11-036-117-367391	Sequence 367391, A
C 398	14	23.7	5244	6	US-10-473-126-166	Sequence 166, App	C 471	13	22.0	25	10	US-10-032-585-3034	Sequence 3034, Ap
C 399	14	23.7	5304	6	US-10-240-453-230	Sequence 230, App	C 472	13	22.0	50	6	US-10-032-585-3034	Sequence 3837, Ap
C 400	14	23.7	5455	10	US-11-097-143-23071	Sequence 23071, A	C 473	13	22.0	64	7	US-10-282-122A-3819	Sequence 3819, Ap
C 401	14	23.7	5572	6	US-10-311-455-788	Sequence 788, App	C 474	13	22.0	66	7	US-10-282-122A-3819	Sequence 17727, Ap
C 402	14	23.7	5777	8	US-10-610-351A-19	Sequence 19, Appl	C 475	13	22.0	78	6	US-10-029-136-17727	Sequence 23, Appl
C 403	14	23.7	5777	8	US-10-715-872-141	Sequence 141, App	C 476	13	22.0	100	9	US-10-507-129-23	Sequence 61654, A
C 404	14	23.7	5912	10	US-11-097-143-22483	Sequence 22483, A	C 477	13	22.0	115	7	US-10-424-599-61564	Sequence 122066, A
C 405	14	23.7	6185	5	US-10-114-170-140	Sequence 140, App	C 478	13	22.0	133	8	US-10-425-115-123066	Sequence 472213, A
C 406	14	23.7	6283	6	US-10-311-455-808	Sequence 808, App	C 479	13	22.0	135	4	US-09-925-065A-472213	Sequence 3747, Ap
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C 408	14	23.7	6526	6	US-10-311-455-2210	Sequence 2210, Ap	C 481	13	22.0	146	3	US-10-282-122A-3879	Sequence 53635, A
C 409	14	23.7	6527	6	US-10-356-631-3	Sequence 3, Appli	C 482	13	22.0	148	7	US-10-424-599-53635	Sequence 3789, Ap
C 410	14	23.7	6948	6	US-10-311-455-1382	Sequence 1382, Ap	C 483	13	22.0	152	3	US-09-815-242-3789	Sequence 184, App
C 411	14	23.7	6948	6	US-10-221-613-180	Sequence 190, App	C 484	13	22.0	152	6	US-10-242-355-184	Sequence 3867, Ap
C 412	14	23.7	7131	7	US-10-221-613-324	Sequence 324, App	C 485	13	22.0	152	7	US-10-282-122A-3887	Sequence 3818, Ap
C 413	14	23.7	8244	6	US-10-311-455-966	Sequence 966, App	C 486	13	22.0	173	8	US-10-425-115-38188	Sequence 2647, Ap
C 414	14	23.7	8244	7	US-10-221-714A-118	Sequence 118, App	C 487	13	22.0	177	7	US-10-437-993-24882	Sequence 24882, A
C 415	14	23.7	8244	7	US-10-433-793-62	Sequence 62, Appl	C 488	13	22.0	195	7	US-10-437-993-24882	Sequence 15809, A
C 416	14	23.7	8855	8	US-10-857-625-51	Sequence 51, Appl	C 489	13	22.0	201	7	US-10-741-601-15809	Sequence 10829, A
C 417	14	23.7	10925	10	US-11-097-143-38644	Sequence 38644, A	C 490	13	22.0	201	8	US-10-719-993-10829	Sequence 53339, A
C 418	14	23.7	13815	10	US-11-097-143-5422	Sequence 5422, A	C 491	13	22.0	201	8	US-10-719-993-53239	Sequence 53797, A
C 419	14	23.7	17841	10	US-11-097-143-4543	Sequence 4543, App	C 492	13	22.0	201	8	US-10-741-600-53197	Sequence 53195, A
C 420	14	23.7	21890	10	US-11-097-143-21220	Sequence 21220, A	C 493	13	22.0	201	8	US-10-741-600-53197	Sequence 53195, A
C 421	14	23.7	23205	3	US-09-997-722-145	Sequence 145, App	C 494	13	22.0	203	8	US-10-425-115-88081	Sequence 88081, A
C 422	14	23.7	23732	10	US-11-097-143-42694	Sequence 42694, A	C 495	13	22.0	208	5	US-10-062-727-88081	Sequence 837, App
C 423	14	23.7	26047	5	US-10-087-192-558	Sequence 558, App	C 496	13	22.0	210	3	US-09-960-352-15066	Sequence 15066, A
C 424	14	23.7	28690	3	US-09-070-927A-138	Sequence 138, App	C 497	13	22.0	232	4	US-09-925-065A-583055	Sequence 583055, A
C 425	14	23.7	29793	3	US-09-973-451-38	Sequence 38, Appl	C 498	13	22.0	255	7	US-10-437-963-60431	Sequence 60431, A
C 426	14	23.7	29793	10	US-11-058-995-38	Sequence 38, Appl	C 499	13	22.0	268	3	US-09-815-242-3744	Sequence 3744, Ap
C 427	14	23.7	30069	7	US-10-389-886-3	Sequence 3, Appli	C 500	13	22.0	268	7	US-10-282-122A-3875	Sequence 3875, Ap
C 428	14	23.7	32987	7	US-10-322-281-366	Sequence 366, Appl	C 501	13	22.0	270	3	US-09-815-242-3725	Sequence 3725, Ap
C 429	14	23.7	74234	5	US-10-087-192-1120	Sequence 1120, Ap	C 502	13	22.0	270	7	US-10-282-122A-3860	Sequence 3860, Ap
C 430	14	23.7	122279	9	US-10-756-149-3596	Sequence 3596, Ap	C 503	13	22.0	270	8	US-10-425-115-29433	Sequence 29433, A
C 431	14	23.7	163350	9	US-10-469-052-3	Sequence 3, Appli	C 504	13	22.0	273	7	US-10-282-122A-9855	Sequence 9855, Ap
C 432	14	23.7	164702	8	US-10-484-577-658	Sequence 658, App	C 505	13	22.0	281	8	US-10-425-115-49994	Sequence 49994, A
C 433	14	23.7	168153	9	US-10-756-149-1933	Sequence 1933, Ap	C 506	13	22.0	282	7	US-10-437-963-16650	Sequence 16650, A
C 434	14	23.7	168174	7	US-10-071-411-63	Sequence 63, Appl	C 507	13	22.0	296	7	US-10-437-963-91411	Sequence 91411, A
C 435	14	23.7	168174	8	US-10-914-799-63	Sequence 63, Appl	C 508	13	22.0	296	8	US-10-674-124A-1564	Sequence 1564, Ap
C 436	14	23.7	168273	7	US-10-071-411-2	Sequence 2, Appli	C 509	13	22.0	298	6	US-10-287-274-242	Sequence 242, App
C 437	14	23.7	168273	8	US-10-914-799-2	Sequence 2, Appli	C 510	13	22.0	298	8	US-10-425-115-11384	Sequence 11384, A
C 438	14	23.7	175590	3	US-09-911-077A-113	Sequence 13, Appl	C 511	13	22.0	298	8	US-10-425-115-33502	Sequence 33502, A
C 439	14	23.7	175590	8	US-10-724-806-113	Sequence 113, Appl	C 512	13	22.0	300	9	US-10-450-763-3965	Sequence 3965, Ap
C 440	14	23.7	188794	7	US-10-322-696-112	Sequence 112, App	C 513	13	22.0	303	7	US-10-425-114-2809	Sequence 2809, Ap
C 441	14	23.7	204621	5	US-10-087-192-958	Sequence 958, App	C 514	13	22.0	303	8	US-10-425-115-18846	Sequence 18846, A
C 442	14	23.7	238484	5	US-10-087-192-544	Sequence 544, App	C 515	13	22.0	319	3	US-09-815-242-3706	Sequence 3706, Ap
C 443	14	23.7	290367	8	US-10-719-993-6887	Sequence 6887, Ap	C 516	13	22.0	319	3	US-09-815-242-3708	Sequence 3708, Ap
C 444	14	23.7	495269	7	US-10-398-221-8	Sequence 8, Appli	C 517	13	22.0	319	7	US-10-282-122A-3849	Sequence 3849, Ap
C 445	14	23.7	580073	6	US-10-205-220-1	Sequence 1, Appli	C 518	13	22.0	319	7	US-10-282-122A-3851	Sequence 3851, Ap
C 446	14	23.7	2140405	6	US-10-027-632-76212	Sequence 76212, A	C 519	13	22.0	321	7	US-10-424-599-72840	Sequence 72840, A
C 447	14	23.7	2140405	6	US-10-027-632-76212	Sequence 76212, A	C 520	13	22.0	321	4	US-09-925-065A-592820	Sequence 592820, A
C 448	14	23.7	3011208	7	US-10-398-221-2058	Sequence 2058, Ap	C 521	13	22.0	324	6	US-10-243-555-310	Sequence 310, App
C 449	14	23.7	3186778	5	US-10-027-632-174961	Sequence 174961, A	C 522	13	22.0	325	7	US-10-424-599-141273	Sequence 141273, A
C 450	14	23.7	3186778	6	US-10-027-632-174961	Sequence 174961, A	C 523	13	22.0	332	7	US-10-424-599-101778	Sequence 101778, A
C 451	13	22.0	21	8	US-10-751-736-26217	Sequence 26217, A	C 524	13	22.0	337	8	US-10-425-115-76337	Sequence 76337, A
C 452	13	22.0	21	8	US-10-751-736-26220	Sequence 26220, A	C 525	13	22.0	337	8	US-10-357-930-11896	Sequence 11896, A
C 453	13	22.0	21	8	US-10-751-736-26220	Sequence 26220, A	C 526	13	22.0	337	8	US-10-425-115-162987	Sequence 162987, A
C 454	13	22.0	25	7	US-10-719-956-49471	Sequence 49471, A	C 527	13	22.0	352	8	US-10-425-115-162987	Sequence 9979, Ap
C 455	13	22.0	25	7	US-10-719-956-152032	Sequence 152032, A	C 528	13	22.0	355	3	US-10-425-115-16575	Sequence 116575, A
C 456	13	22.0	25	8	US-10-719-900-22008	Sequence 22008, A	C 529	13	22.0	355	8	US-10-425-115-3764	Sequence 3764, Ap
C 457	13	22.0	25	8	US-10-719-900-37101	Sequence 37101, A	C 530	13	22.0	356	7	US-10-282-122A-3895	Sequence 3895, Ap
C 458	13	22.0	25	8	US-10-719-900-68328	Sequence 68328, A	C 531	13	22.0	357	7	US-10-437-963-94334	Sequence 94334, A
C 459	13	22.0	25	8	US-10-719-900-106131	Sequence 106131, A	C 532	13	22.0	360	7	US-10-437-963-44187	Sequence 44187, A
C 460	13	22.0	25	8	US-10-719-900-330071	Sequence 330071, A	C 533	13	22.0	372	7	US-10-242-535A-40201	Sequence 40201, A
C 461	13	22.0	25	8	US-10-719-900-689347	Sequence 689347, A	C 534	13	22.0	372	7	US-10-085-783A-40201	Sequence 40201, A



C 535	13	22.0	375	7	US-10-282-122A-28109	Sequence 28109, A	608	13	22.0	506	5	US-10-027-632-287474	Sequence 287474, A
C 536	13	22.0	375	8	US-10-425-115-50233	Sequence 50233, A	609	13	22.0	506	6	US-10-027-632-287474	Sequence 287474, A
C 537	13	22.0	377	8	US-10-437-963-19779	Sequence 19779, A	610	13	22.0	506	7	US-10-424-599-113700	Sequence 113700, A
C 538	13	22.0	377	9	US-10-779-543-10920	Sequence 10920, A	611	13	22.0	508	8	US-10-363-345A-34357	Sequence 34357, A
C 539	13	22.0	383	8	US-10-425-115-86624	Sequence 86624, A	612	13	22.0	508	8	US-10-363-345A-34358	Sequence 34358, A
C 540	13	22.0	388	3	US-09-815-242-3593	Sequence 3593, Ap	613	13	22.0	508	9	US-10-363-345A-34357	Sequence 34357, A
C 541	13	22.0	388	7	US-10-282-122A-2818	Sequence 3818, Ap	614	13	22.0	508	9	US-10-363-483A-34358	Sequence 34358, A
C 542	13	22.0	389	3	US-09-815-242-3704	Sequence 3704, Ap	615	13	22.0	510	8	US-10-363-483A-34358	Sequence 34358, A
C 543	13	22.0	389	3	US-09-815-242-3709	Sequence 3709, Ap	616	13	22.0	510	8	US-10-363-483A-34358	Sequence 34358, A
C 544	13	22.0	389	3	US-09-815-242-3710	Sequence 3710, Ap	617	13	22.0	510	8	US-10-363-483A-34358	Sequence 34358, A
C 545	13	22.0	389	7	US-10-282-122A-3848	Sequence 3848, Ap	618	13	22.0	510	9	US-10-363-483A-34358	Sequence 34358, A
C 546	13	22.0	389	7	US-10-282-122A-3850	Sequence 3850, Ap	619	13	22.0	514	4	US-09-925-065A-402248	Sequence 402248, A
C 547	13	22.0	389	7	US-10-282-122A-3852	Sequence 3852, Ap	620	13	22.0	514	4	US-10-425-115-154498	Sequence 154498, A
C 548	13	22.0	391	6	US-10-242-355-992	Sequence 992, Ap	621	13	22.0	519	8	US-10-363-345A-36687	Sequence 36687, A
C 549	13	22.0	391	6	US-10-357-930-47714	Sequence 47714, A	622	13	22.0	519	8	US-10-363-345A-36687	Sequence 36687, A
C 550	13	22.0	396	8	US-10-425-115-103791	Sequence 103791, A	623	13	22.0	519	8	US-10-363-345A-36687	Sequence 36687, A
C 551	13	22.0	397	9	US-10-779-543-10102	Sequence 10102, A	624	13	22.0	519	9	US-10-363-483A-36687	Sequence 36687, A
C 552	13	22.0	400	7	US-10-424-599-27503	Sequence 27503, A	625	13	22.0	519	9	US-10-363-483A-36688	Sequence 36688, A
C 553	13	22.0	404	4	US-09-925-065A-584646	Sequence 584646, A	626	13	22.0	520	4	US-09-925-065A-510384	Sequence 510384, A
C 554	13	22.0	405	4	US-09-925-065A-588290	Sequence 588290, A	627	13	22.0	520	4	US-09-925-065A-366770	Sequence 366770, A
C 555	13	22.0	410	8	US-10-425-115-133928	Sequence 133928, A	628	13	22.0	520	4	US-09-925-065A-366775	Sequence 366775, A
C 556	13	22.0	411	3	US-09-983-965-3749	Sequence 3749, Ap	629	13	22.0	520	4	US-09-925-065A-366776	Sequence 366776, A
C 557	13	22.0	411	3	US-10-282-122A-16062	Sequence 16062, A	630	13	22.0	521	5	US-10-066-543-3395	Sequence 3395, Ap
C 558	13	22.0	412	7	US-10-424-599-32263	Sequence 32263, A	631	13	22.0	523	4	US-09-925-065A-622865	Sequence 622865, A
C 559	13	22.0	418	4	US-09-925-065A-628645	Sequence 628645, A	632	13	22.0	523	4	US-09-925-065A-622865	Sequence 622865, A
C 560	13	22.0	418	7	US-10-424-599-136329	Sequence 136329, A	633	13	22.0	525	4	US-09-925-065A-510384	Sequence 510384, A
C 561	13	22.0	420	8	US-10-696-639-1243	Sequence 1243, Ap	634	13	22.0	525	4	US-09-925-065A-510384	Sequence 510384, A
C 562	13	22.0	421	7	US-10-425-114-23506	Sequence 23506, A	635	13	22.0	525	4	US-09-925-065A-510385	Sequence 510385, A
C 563	13	22.0	422	3	US-09-770-423-330	Sequence 330, Ap	636	13	22.0	525	6	US-10-029-386-6312	Sequence 6312, Ap
C 564	13	22.0	423	6	US-10-333-282-16	Sequence 16, Ap	637	13	22.0	526	4	US-09-925-065A-565710	Sequence 565710, A
C 565	13	22.0	425	3	US-09-983-965-4506	Sequence 4506, Ap	638	13	22.0	526	4	US-09-925-065A-565711	Sequence 565711, A
C 566	13	22.0	427	7	US-10-424-599-140562	Sequence 140562, A	639	13	22.0	526	4	US-10-363-345A-6077	Sequence 6077, Ap
C 567	13	22.0	429	6	US-10-443-502-17	Sequence 17, Ap	640	13	22.0	527	8	US-10-363-345A-6077	Sequence 6077, Ap
C 568	13	22.0	431	8	US-10-425-115-15356	Sequence 15356, A	641	13	22.0	527	8	US-10-363-345A-6078	Sequence 6078, Ap
C 569	13	22.0	433	8	US-10-425-115-91381	Sequence 91381, A	642	13	22.0	527	9	US-10-363-483A-6077	Sequence 6077, Ap
C 570	13	22.0	433	8	US-10-425-115-182902	Sequence 182902, A	643	13	22.0	527	9	US-10-363-483A-6078	Sequence 6078, Ap
C 571	13	22.0	442	5	US-10-027-632-49079	Sequence 49079, A	644	13	22.0	528	7	US-10-767-701-77994	Sequence 77994, A
C 572	13	22.0	442	6	US-10-027-632-49079	Sequence 49079, A	645	13	22.0	530	7	US-10-021-323-10053	Sequence 10053, A
C 573	13	22.0	446	7	US-10-437-963-62434	Sequence 62434, A	646	13	22.0	530	8	US-10-363-345A-33133	Sequence 33133, A
C 574	13	22.0	450	7	US-10-767-701-13577	Sequence 13577, A	647	13	22.0	530	8	US-10-363-345A-33134	Sequence 33134, A
C 575	13	22.0	455	8	US-10-425-115-11634	Sequence 11634, A	648	13	22.0	530	9	US-10-363-483A-33133	Sequence 33133, A
C 576	13	22.0	456	8	US-09-954-456-1430	Sequence 1430, Ap	649	13	22.0	530	9	US-10-363-483A-33134	Sequence 33134, A
C 577	13	22.0	460	6	US-10-843-641A-4457	Sequence 4457, Ap	650	13	22.0	532	5	US-10-027-632-103693	Sequence 103693, A
C 578	13	22.0	460	6	US-10-366-791-29	Sequence 29, Ap	651	13	22.0	532	5	US-10-027-632-103693	Sequence 103693, A
C 579	13	22.0	460	7	US-10-742-220-29	Sequence 29, Ap	652	13	22.0	533	5	US-10-027-632-80162	Sequence 80162, A
C 580	13	22.0	467	5	US-10-027-632-86886	Sequence 86886, A	653	13	22.0	533	5	US-10-027-632-109610	Sequence 109610, A
C 581	13	22.0	467	5	US-10-027-632-178962	Sequence 178962, A	654	13	22.0	533	6	US-10-027-632-80162	Sequence 80162, A
C 582	13	22.0	467	5	US-10-027-632-316494	Sequence 316494, A	655	13	22.0	533	6	US-10-027-632-109610	Sequence 109610, A
C 583	13	22.0	467	6	US-10-027-632-86886	Sequence 86886, A	656	13	22.0	533	6	US-10-363-345A-36621	Sequence 36621, A
C 584	13	22.0	467	6	US-10-027-632-178962	Sequence 178962, A	657	13	22.0	533	8	US-10-363-345A-36622	Sequence 36622, A
C 585	13	22.0	467	6	US-10-027-632-316494	Sequence 316494, A	658	13	22.0	533	9	US-10-363-483A-36621	Sequence 36621, A
C 586	13	22.0	470	5	US-10-027-632-126005	Sequence 126005, A	659	13	22.0	533	9	US-10-363-483A-36622	Sequence 36622, A
C 587	13	22.0	470	6	US-10-027-632-126005	Sequence 126005, A	660	13	22.0	534	4	US-09-925-065A-599976	Sequence 599976, A
C 588	13	22.0	472	8	US-10-914-037-194	Sequence 194, Ap	661	13	22.0	534	8	US-10-363-345A-39755	Sequence 39755, A
C 589	13	22.0	473	5	US-10-027-632-64356	Sequence 64356, A	662	13	22.0	534	8	US-10-363-345A-39756	Sequence 39756, A
C 590	13	22.0	473	6	US-10-027-632-64356	Sequence 64356, A	663	13	22.0	534	9	US-10-363-483A-39755	Sequence 39755, A
C 591	13	22.0	473	8	US-10-357-930-52500	Sequence 52500, A	664	13	22.0	534	9	US-10-363-483A-39756	Sequence 39756, A
C 592	13	22.0	482	3	US-09-864-761-11693	Sequence 11693, A	665	13	22.0	535	8	US-10-363-345A-2345	Sequence 2345, Ap
C 593	13	22.0	485	3	US-09-864-761-10044	Sequence 10044, A	666	13	22.0	535	8	US-10-363-345A-2346	Sequence 2346, Ap
C 594	13	22.0	487	7	US-09-867-701-6228	Sequence 6228, Ap	667	13	22.0	535	9	US-10-363-483A-2345	Sequence 2345, Ap
C 595	13	22.0	487	7	US-10-242-535A-7369	Sequence 7369, Ap	668	13	22.0	535	9	US-10-363-483A-2346	Sequence 2346, Ap
C 596	13	22.0	487	7	US-10-085-783A-7369	Sequence 7369, Ap	669	13	22.0	537	8	US-10-363-345A-3325	Sequence 3325, Ap
C 597	13	22.0	489	7	US-10-282-122A-33668	Sequence 33668, A	670	13	22.0	537	8	US-10-363-345A-3326	Sequence 3326, Ap
C 598	13	22.0	495	3	US-09-815-242-3782	Sequence 3782, Ap	671	13	22.0	537	9	US-10-363-483A-3325	Sequence 3325, Ap
C 599	13	22.0	495	7	US-10-282-122A-3875	Sequence 3875, Ap	672	13	22.0	537	9	US-10-363-483A-3326	Sequence 3326, Ap
C 600	13	22.0	497	3	US-09-918-995-35085	Sequence 35085, A	673	13	22.0	538	7	US-10-425-114-1163	Sequence 1163, Ap
C 601	13	22.0	497	5	US-10-066-543-1738	Sequence 1738, Ap	674	13	22.0	538	8	US-10-363-345A-23545	Sequence 23545, A
C 602	13	22.0	499	3	US-09-918-995-1586	Sequence 1586, Ap	675	13	22.0	538	8	US-10-363-345A-23545	Sequence 23545, A
C 603	13	22.0	501	4	US-09-925-065A-479701	Sequence 479701, A	676	13	22.0	538	9	US-10-363-483A-23545	Sequence 23545, A
C 604	13	22.0	505	8	US-10-363-345A-2065	Sequence 2065, Ap	677	13	22.0	538	9	US-10-363-483A-23546	Sequence 23546, A
C 605	13	22.0	505	8	US-10-363-345A-2066	Sequence 2066, Ap	678	13	22.0	542	4	US-09-925-065A-366772	Sequence 366772, A
C 606	13	22.0	505	9	US-10-363-483A-2065	Sequence 2065, Ap	679	13	22.0	542	4	US-09-925-065A-366774	Sequence 366774, A
C 607	13	22.0	505	9	US-10-363-483A-2066	Sequence 2066, Ap	680	13	22.0	542	4	US-09-925-065A-366777	Sequence 366777, A



681	13	22.0	542	7	US-10-717-897-66	Sequence 66, Appl	754	13	22.0	575	4	US-09-925-065A-304991	Sequence 304991,
682	13	22.0	543	4	US-09-925-065A-178013	Sequence 178013,	755	13	22.0	576	7	US-10-425-114-12592	Sequence 12592, A
683	13	22.0	543	6	US-10-091-007-129	Sequence 129, App	756	13	22.0	576	5	US-10-425-115-159370	Sequence 159370,
684	13	22.0	545	4	US-09-925-065A-762388	Sequence 762388,	757	13	22.0	578	5	US-10-027-632-50739	Sequence 50739, A
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686	13	22.0	545	8	US-10-363-345A-6330	Sequence 6330, Ap	759	13	22.0	578	6	US-10-027-632-50739	Sequence 50739, A
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689	13	22.0	546	6	US-10-029-386-7577	Sequence 7577, Ap	762	13	22.0	578	8	US-10-363-345A-23072	Sequence 23072, A
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C 832	13	22.0	604	4	US-09-925-065A-769857	Sequence 769857,	C 905	13	22.0	633	8	US-10-363-345A-26184	Sequence 26184, A
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C 837	13	22.0	604	6	US-10-027-632-223187	Sequence 223187,	C 910	13	22.0	635	5	US-10-027-632-211684	Sequence 211684,
C 838	13	22.0	604	8	US-10-363-345A-33705	Sequence 33705, A	C 911	13	22.0	636	6	US-10-027-632-211684	Sequence 211684,
C 839	13	22.0	604	8	US-10-363-345A-33706	Sequence 33706, A	C 912	13	22.0	636	6	US-10-369-493-28169	Sequence 28169, A
C 840	13	22.0	604	9	US-10-363-483A-33705	Sequence 33705, A	C 913	13	22.0	636	6	US-10-369-493-10978	Sequence 10978, A
C 841	13	22.0	604	9	US-10-363-483A-33706	Sequence 33706, A	C 914	13	22.0	637	8	US-10-363-345A-21795	Sequence 21795, A
C 842	13	22.0	605	4	US-09-925-065A-439871	Sequence 439871,	C 915	13	22.0	637	8	US-10-363-345A-21796	Sequence 21796, A
C 843	13	22.0	605	4	US-09-925-065A-849255	Sequence 849255,	C 916	13	22.0	637	9	US-10-363-483A-21795	Sequence 21795, A
C 844	13	22.0	608	4	US-09-925-065A-328848	Sequence 328848,	C 917	13	22.0	638	8	US-10-363-483A-21796	Sequence 21796, A
C 845	13	22.0	608	8	US-10-363-345A-18365	Sequence 18365, A	C 918	13	22.0	638	8	US-10-363-345A-8999	Sequence 8999, Ap
C 846	13	22.0	608	9	US-10-363-483A-18365	Sequence 18365, A	C 919	13	22.0	638	9	US-10-363-483A-8999	Sequence 8999, Ap
C 847	13	22.0	608	9	US-10-363-483A-18365	Sequence 18365, A	C 920	13	22.0	638	9	US-10-363-483A-8999	Sequence 8999, Ap
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C 850	13	22.0	610	4	US-09-925-065A-767735	Sequence 767735,	C 923	13	22.0	643	4	US-09-925-065A-591456	Sequence 591456,
C 851	13	22.0	610	8	US-10-363-345A-4363	Sequence 4363, Ap	C 924	13	22.0	643	4	US-09-925-065A-781049	Sequence 781049,
C 852	13	22.0	610	8	US-10-363-345A-4364	Sequence 4364, Ap	C 925	13	22.0	643	8	US-10-363-345A-35959	Sequence 35959, A
C 853	13	22.0	610	9	US-10-363-483A-4363	Sequence 4363, Ap	C 926	13	22.0	647	8	US-10-363-345A-35960	Sequence 35960, A
C 854	13	22.0	612	6	US-10-027-632-115297	Sequence 115297,	C 927	13	22.0	647	9	US-10-363-483A-35960	Sequence 35960, A
C 855	13	22.0	612	6	US-10-027-632-115297	Sequence 115297,	C 928	13	22.0	647	9	US-10-363-483A-35960	Sequence 35960, A
C 856	13	22.0	614	5	US-09-925-065A-798952	Sequence 798952,	C 929	13	22.0	650	5	US-10-255-536-140	Sequence 140, App
C 857	13	22.0	614	5	US-10-027-632-177012	Sequence 177012,	C 930	13	22.0	650	5	US-10-255-536-140	Sequence 140, App
C 858	13	22.0	614	5	US-10-027-632-177012	Sequence 177012,	C 931	13	22.0	650	5	US-10-487-901-7147	Sequence 7147, Ap
C 859	13	22.0	614	6	US-10-027-632-177012	Sequence 177012,	C 932	13	22.0	651	5	US-10-027-632-110095	Sequence 110095,
C 860	13	22.0	616	6	US-09-925-065A-515811	Sequence 515811,	C 933	13	22.0	651	6	US-10-027-632-110095	Sequence 110095,
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C 862	13	22.0	617	4	US-09-925-065A-767932	Sequence 767932,	C 935	13	22.0	654	8	US-10-363-345A-3432	Sequence 3432, Ap
C 863	13	22.0	618	7	US-10-335-977-4305	Sequence 4305, Ap	C 936	13	22.0	654	9	US-10-363-483A-3431	Sequence 3431, Ap
C 864	13	22.0	619	8	US-10-363-345A-2075	Sequence 2075, Ap	C 937	13	22.0	654	9	US-10-363-483A-3432	Sequence 3432, Ap
C 865	13	22.0	619	8	US-10-363-345A-2076	Sequence 2076, Ap	C 938	13	22.0	656	4	US-09-925-065A-291917	Sequence 291917,
C 866	13	22.0	619	8	US-10-363-345A-4789	Sequence 4789, Ap	C 939	13	22.0	657	4	US-09-925-065A-254022	Sequence 254022,
C 867	13	22.0	619	8	US-10-363-345A-4790	Sequence 4790, Ap	C 940	13	22.0	657	4	US-09-925-065A-902953	Sequence 902953,
C 868	13	22.0	619	9	US-10-363-483A-2075	Sequence 2075, Ap	C 941	13	22.0	657	8	US-10-425-115-47673	Sequence 47673, A
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C 870	13	22.0	619	9	US-10-363-483A-4789	Sequence 4789, Ap	C 943	13	22.0	660	4	US-09-925-065A-634796	Sequence 634796,
C 871	13	22.0	619	9	US-10-363-483A-4790	Sequence 4790, Ap	C 944	13	22.0	663	5	US-10-027-632-255923	Sequence 255923,
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C 873	13	22.0	620	7	US-10-424-599-122887	Sequence 122887,	C 946	13	22.0	665	5	US-10-027-632-102525	Sequence 102525,
C 874	13	22.0	621	7	US-10-437-963-58847	Sequence 58847, A	C 947	13	22.0	665	6	US-10-027-632-102525	Sequence 102525,
C 875	13	22.0	621	8	US-10-425-115-29540	Sequence 29540, A	C 948	13	22.0	669	7	US-10-437-963-10555	Sequence 10555, A
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C 878	13	22.0	622	8	US-10-363-345A-7347	Sequence 7347, Ap	C 951	13	22.0	673	4	US-09-925-065A-41992	Sequence 41992, A
C 879	13	22.0	622	8	US-10-363-345A-7348	Sequence 7348, Ap	C 952	13	22.0	673	8	US-10-363-345A-6659	Sequence 6659, Ap
C 880	13	22.0	622	9	US-10-363-483A-7347	Sequence 7347, Ap	C 953	13	22.0	673	8	US-10-363-345A-6660	Sequence 6660, Ap
C 881	13	22.0	622	9	US-10-363-483A-7348	Sequence 7348, Ap	C 954	13	22.0	673	9	US-10-363-483A-6659	Sequence 6659, Ap
C 882	13	22.0	622	9	US-10-363-483A-15645	Sequence 15645, A	C 955	13	22.0	674	9	US-10-363-483A-6660	Sequence 6660, Ap
C 883	13	22.0	623	8	US-10-363-345A-15646	Sequence 15646, A	C 956	13	22.0	674	4	US-09-925-065A-233399	Sequence 233399,
C 884	13	22.0	623	9	US-10-363-483A-15646	Sequence 15645, A	C 957	13	22.0	674	4	US-09-925-065A-233400	Sequence 233400,
C 885	13	22.0	623	9	US-10-363-483A-15646	Sequence 15645, A	C 958	13	22.0	675	5	US-10-027-632-290914	Sequence 290914,
C 886	13	22.0	624	5	US-10-027-632-28783	Sequence 28783, A	C 959	13	22.0	675	5	US-10-027-632-290915	Sequence 290915,
C 887	13	22.0	624	6	US-10-027-632-28783	Sequence 28783, A	C 960	13	22.0	675	6	US-10-027-632-290915	Sequence 290915,
C 888	13	22.0	625	8	US-10-363-345A-20855	Sequence 20855, A	C 961	13	22.0	676	6	US-10-027-632-290915	Sequence 290915,
C 889	13	22.0	625	8	US-10-363-345A-20856	Sequence 20856, A	C 962	13	22.0	676	8	US-10-425-115-147571	Sequence 147571,
C 890	13	22.0	625	8	US-10-363-345A-33269	Sequence 33269, A	C 963	13	22.0	677	8	US-10-363-345A-1015	Sequence 1015, Ap
C 891	13	22.0	625	8	US-10-363-345A-33270	Sequence 33270, A	C 964	13	22.0	677	8	US-10-363-345A-1016	Sequence 1016, Ap
C 892	13	22.0	625	9	US-10-363-483A-20855	Sequence 20855, A	C 965	13	22.0	677	9	US-10-363-483A-1015	Sequence 1015, Ap
C 893	13	22.0	625	9	US-10-363-483A-20856	Sequence 20856, A	C 966	13	22.0	677	9	US-10-363-483A-1016	Sequence 1016, Ap
C 894	13	22.0	625	9	US-10-363-483A-33269	Sequence 33269, A	C 967	13	22.0	678	7	US-10-126-103-2	Sequence 2, Appl1
C 895	13	22.0	625	9	US-10-363-483A-33270	Sequence 33270, A	C 968	13	22.0	680	9	US-10-487-901-11107	Sequence 1107, Ap
C 896	13	22.0	626	4	US-09-925-065A-524549	Sequence 524549,	C 969	13	22.0	682	4	US-09-925-065A-748100	Sequence 748100,
C 897	13	22.0	626	7	US-10-767-701-7890	Sequence 7890, Ap	C 970	13	22.0	683	4	US-09-925-065A-833475	Sequence 833475,
C 898	13	22.0	627	4	US-09-925-065A-463831	Sequence 463831,	C 971	13	22.0	683	4	US-09-925-065A-833475	Sequence 833475,
C 899	13	22.0	630	5	US-10-027-632-288267	Sequence 288267,	C 972	13	22.0	683	5	US-10-027-632-26288	Sequence 26288, A



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c 973 13 22.0 683 6 US-10-027-632-26288 Sequence 26288, A
c 974 13 22.0 684 3 US-09-974-300-7518 Sequence 7518, Ap
c 975 13 22.0 684 8 US-10-363-345A-1137 Sequence 1137, Ap
c 976 13 22.0 684 8 US-10-363-345A-1138 Sequence 1138, Ap
c 977 13 22.0 684 9 US-10-363-483A-1137 Sequence 1137, Ap
c 978 13 22.0 684 9 US-10-363-483A-1138 Sequence 1138, Ap
c 979 13 22.0 691 4 US-09-925-065A-928659 Sequence 928659,
c 980 13 22.0 692 8 US-10-363-345A-21313 Sequence 21313, A
c 981 13 22.0 692 8 US-10-363-345A-21314 Sequence 21314, A
c 982 13 22.0 692 8 US-10-363-483A-21313 Sequence 21313, A
c 983 13 22.0 692 9 US-10-363-483A-21314 Sequence 21314, A
c 984 13 22.0 693 5 US-10-027-632-131942 Sequence 131942,
c 985 13 22.0 693 5 US-10-027-632-131943 Sequence 131943,
c 986 13 22.0 693 5 US-10-027-632-131944 Sequence 131944,
c 987 13 22.0 693 5 US-10-027-632-131945 Sequence 131945,
c 988 13 22.0 693 6 US-10-027-632-131942 Sequence 131942,
c 989 13 22.0 693 6 US-10-027-632-131943 Sequence 131943,
c 990 13 22.0 693 6 US-10-027-632-131944 Sequence 131944,
c 991 13 22.0 693 6 US-10-027-632-131945 Sequence 131945,
c 992 13 22.0 693 7 US-10-425-114-14391 Sequence 14391, A
c 993 13 22.0 700 8 US-10-363-345A-32571 Sequence 32571, A
c 994 13 22.0 700 8 US-10-363-345A-32572 Sequence 32572, A
c 995 13 22.0 700 9 US-10-363-483A-32571 Sequence 32571, A
c 996 13 22.0 700 9 US-10-363-483A-32572 Sequence 32572, A
c 997 13 22.0 703 7 US-10-424-559-138589 Sequence 138589,
c 998 13 22.0 705 7 US-10-437-963-62895 Sequence 62895, A
c 999 13 22.0 705 8 US-10-425-115-96663 Sequence 96663, A
c1000 13 22.0 714 3 US-09-557-736-9 Sequence 9, Appli

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## ALIGNMENTS

```

RESULT 1
US-10-442-502-15
; Sequence 15, Application US/10442502
; Publication No. US20040009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSKHO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-442-502-15

Query Match          100.0%; Score 59; DB 6; Length 318;
Best Local Similarity 100.0%; Pred. No. 1,1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 59
Db 39 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 97

RESULT 2
US-10-402-466A-25
; Sequence 25, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:

```

```

; APPLICANT: Park, Sukjoon
; APPLICANT: Gili, Iallan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 25
; LENGTH: 723
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pbp15 for a PA deletion mutant PA27.
US-10-402-466A-25

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Query Match          100.0%; Score 59; DB 7; Length 723;
Best Local Similarity 100.0%; Pred. No. 1,1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 59
Db 15 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 73

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RESULT 3
US-10-375-356A-7
; Sequence 7, Application US/10375356A
; Publication No. US20040014707A1
; GENERAL INFORMATION:
; APPLICANT: Cirino, Nick M
; APPLICANT: Jackson, Paul J
; APPLICANT: Lehnert, Bruce B
; APPLICANT: Caastro, Alonso
; TITLE OF INVENTION: Method For The Detection Of Specific Nucleic Acid
; TITLE OF INVENTION: Sequences By Polymerase Nucleotide Incorporation
; FILE REFERENCE: S-97,788
; CURRENT APPLICATION NUMBER: US/10/375,356A
; CURRENT FILING DATE: 2003-02-27
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 867
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-375-356A-7

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```

Query Match          100.0%; Score 59; DB 7; Length 867;
Best Local Similarity 100.0%; Pred. No. 1,1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 59
Db 129 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTGATTCATTAGAAAGCACTPAAACCGG 187

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RESULT 4
US-10-402-466A-23
; Sequence 23, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gili, Iallan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152

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; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 34  
; SEQ ID NO 23  
; LENGTH: 1272  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION:  
; OTHER INFORMATION: DNA coding sequence from pBP113 for a PA deletion mutant PA47.  
US-10-402-466A-23

Query Match 100.0%; Score 59; DB 7; Length 1272;  
Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 564 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 622

## RESULT 5

US-10-332-282-10  
; Sequence 10, Application US/10332282  
; Publication No. US20030170263A1  
; GENERAL INFORMATION:  
; APPLICANT: The Secretary of State for Defence  
; APPLICANT: Williamson, Ethel D  
; APPLICANT: Miller, Julie  
; APPLICANT: Walker, Nicola J  
; APPLICANT: Baillie, Leslie WJ  
; APPLICANT: Holden, Paula T  
; APPLICANT: Flick-Smith, Helen C  
; APPLICANT: Bullifent, Helen L  
; APPLICANT: Tibball, Richard W  
; TITLE OF INVENTION: Expression System  
; FILE REFERENCE: CG/P/110/MOD  
; CURRENT APPLICATION NUMBER: US/10/332,282  
; CURRENT FILING DATE: 2003-01-07  
; PRIOR APPLICATION NUMBER: GB 0016702.3  
; PRIOR FILING DATE: 2000-07-08  
; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 10  
; LENGTH: 1278  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence  
; OTHER INFORMATION: used to encode SEQ ID NO: 9  
US-10-332-282-10

Query Match 100.0%; Score 59; DB 6; Length 1278;  
Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 993 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 1051

## RESULT 6

US-10-402-466A-15  
; Sequence 15, Application US/10402466A  
; Publication No. US20040028695A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Sukjoon  
; APPLICANT: Giti, Lailan  
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
; FILE REFERENCE: 18933-00005  
; CURRENT APPLICATION NUMBER: US/10/402,466A  
; CURRENT FILING DATE: 2003-03-20

; PRIOR APPLICATION NUMBER: 60/372,152  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 34  
; SEQ ID NO 15  
; LENGTH: 1515  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION:  
; OTHER INFORMATION: DNA coding sequence from pBP107 for an artificial LP-PA fusion  
US-10-402-466A-15

Query Match 100.0%; Score 59; DB 7; Length 1515;  
Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 807 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 865

## RESULT 7

US-10-442-502-4  
; Sequence 4, Application US/10442502  
; Publication No. US20040009945A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, JOHN SCOTT  
; APPLICANT: PUSHKO, PETER  
; APPLICANT: PARKER, MICHAEL D.  
; APPLICANT: SMITH, JONATHAN F.  
; APPLICANT: WELKOS, SUSAN L.  
; TITLE OF INVENTION: ANTHRAX VACCINES  
; FILE REFERENCE: ARMY135B  
; CURRENT APPLICATION NUMBER: US/10/442,502  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/350,729  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,416  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 1710  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
US-10-442-502-4

Query Match 100.0%; Score 59; DB 6; Length 1710;  
Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 59  
Db 1002 GGTGAAAGGCGGATAGCGGCGTTAATCTAGATCCATTAGAAAGACTAAACCGG 1060

## RESULT 8

US-10-402-466A-21  
; Sequence 21, Application US/10402466A  
; Publication No. US20040028695A1  
; GENERAL INFORMATION:  
; APPLICANT: Park, Sukjoon  
; APPLICANT: Giti, Lailan  
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING  
; FILE REFERENCE: 18933-00005  
; CURRENT APPLICATION NUMBER: US/10/402,466A  
; CURRENT FILING DATE: 2003-03-20  
; PRIOR APPLICATION NUMBER: 60/372,152  
; PRIOR FILING DATE: 2002-04-12  
; NUMBER OF SEQ ID NOS: 34



```
; SEQ ID NO 21
; LENGTH: 1722
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP11 for a PA deletion mutant PA64.
US-10-402-466A-21

Query Match          100.0%; Score 59; DB 7; Length 1722;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1014 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1072

RESULT 9
US-10-332-282-12
; Sequence 12, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Echel D
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibbail, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 12
; LENGTH: 1785
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
US-10-332-282-12

Query Match          100.0%; Score 59; DB 6; Length 1785;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1500 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1558

RESULT 10
US-10-402-466A-17
; Sequence 17, Application US/10402466A
; Publication No. US20040028655A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Gail, Lallan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
```

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; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 17
; LENGTH: 1974
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP108 for an artificial LP-PA fusion p
US-10-402-466A-17

Query Match          100.0%; Score 59; DB 7; Length 1974;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1266 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1324

RESULT 11
US-09-848-909-22
; Sequence 22, Application US/09848909
; Publication No. US20020039588A1
; GENERAL INFORMATION:
; APPLICANT: Sellman, Brett R.
; TITLE OF INVENTION: Compounds and Methods for the Treatment
; TITLE OF INVENTION: and Prevention of Bacterial Infection
; FILE REFERENCE: 00742/060002
; CURRENT APPLICATION NUMBER: US/09/848,909
; CURRENT FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: US 60/201,800
; PRIOR FILING DATE: 2000-04-04
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 22
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-09-848-909-22

Query Match          100.0%; Score 59; DB 3; Length 2208;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1500 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 1558

RESULT 12
US-10-332-282-14
; Sequence 14, Application US/10332282
; Publication No. US20030170263A1
; GENERAL INFORMATION:
; APPLICANT: The Secretary of State for Defence
; APPLICANT: Williamson, Echel D
; APPLICANT: Walker, Nicola J
; APPLICANT: Baillie, Leslie WJ
; APPLICANT: Holden, Paula T
; APPLICANT: Flick-Smith, Helen C
; APPLICANT: Bullifent, Helen L
; APPLICANT: Tibbail, Richard W
; TITLE OF INVENTION: Expression System
; FILE REFERENCE: CG/P/110/MOD
; CURRENT APPLICATION NUMBER: US/10/332,282
; CURRENT FILING DATE: 2003-01-07
; PRIOR APPLICATION NUMBER: GB 0016702.3
; PRIOR FILING DATE: 2000-07-08
; NUMBER OF SEQ ID NOS: 16
```



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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: DNA sequence
US-10-332-282-14

Query Match
Best Local Similarity 100.0%; Score 59; DB 6; Length 2208;
Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
Db
1500 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1558

RESULT 13
US-10-402-466A-8
; Sequence 8, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giti, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 8
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence for B. anthracis PA.
US-10-402-466A-8

Query Match
Best Local Similarity 100.0%; Score 59; DB 7; Length 2208;
Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
Db
1500 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1558

RESULT 14
US-10-402-466A-11
; Sequence 11, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giti, Lailan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 11
; LENGTH: 2208
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:

; NAME/KEY: CDS
; LOCATION:
; OTHER INFORMATION: DNA coding sequence from pBP105 for B. anthracis PA. The DNA
; OTHER INFORMATION: sequences for rPA (2208 bases) is identical to Sequence 8.
US-10-402-466A-11

Query Match
Best Local Similarity 100.0%; Score 59; DB 7; Length 2208;
Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
Db
1500 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1558

RESULT 15
US-10-442-502-2
; Sequence 2, Application US/10442502
; Publication No. US2004009945A1
; GENERAL INFORMATION:
; APPLICANT: LEE, JOHN SCOTT
; APPLICANT: PUSHKO, PETER
; APPLICANT: PARKER, MICHAEL D.
; APPLICANT: SMITH, JONATHAN F.
; APPLICANT: WELKOS, SUSAN L.
; TITLE OF INVENTION: ANTHRAX VACCINES
; FILE REFERENCE: ARMY135B
; CURRENT APPLICATION NUMBER: US/10/442,502
; CURRENT FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 09/350,729
; PRIOR FILING DATE: 1999-07-09
; PRIOR APPLICATION NUMBER: 60/092,416
; PRIOR FILING DATE: 1998-07-10
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2211
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; OTHER INFORMATION:
US-10-442-502-2

Query Match
Best Local Similarity 100.0%; Score 59; DB 6; Length 2211;
Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy
1 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 59
Db
1503 GGTAGAAAGCGCGGATAGCGCGGTTAATCCTAGATCCATTAGAAAGACTAAACCGG 1561

RESULT 16
US-10-638-006-3
; Sequence 3, Application US/10638006
; Publication No. US20040171121A1
; GENERAL INFORMATION:
; APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA as
; APPLICANT: represented by THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
; APPLICANT: HUMAN SERVICES
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Rosovoltz, Mary Jo
; APPLICANT: Hsu, S. Dana
; TITLE OF INVENTION: METHODS FOR PREPARING BACILLUS ANTHRACIS SPOULATION DEFICIENT
; TITLE OF INVENTION: MUTANTS AND FOR PRODUCING RECOMBINANT BACILLUS ANTHRACIS
; FILE REFERENCE: 4239-66891
; CURRENT FILING DATE: 2003-08-08
; PRIOR APPLICATION NUMBER: US/10/638,006
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 3
; LENGTH: 2235
```



```
/ TYPE: DNA
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Mature double mutant protective antigen
US-10-638-006-3

Query Match          100.0%; Score 59; DB 7; Length 2235;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
Db 1527 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 1585

RESULT 17
US-10-402-466A-19
/ Sequence 19, Application US/10402466A
/ Publication No. US20040028695A1
/ GENERAL INFORMATION:
/ APPLICANT: Park, Sukjoon
/ APPLICANT: Gil, Lailan
/ TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
/ TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
/ FILE REFERENCE: 18933-00005
/ CURRENT APPLICATION NUMBER: US/10/402,466A
/ PRIOR FILING DATE: 2003-03-20
/ PRIOR APPLICATION NUMBER: 60/372,152
/ PRIOR FILING DATE: 2002-04-12
/ NUMBER OF SEQ ID NOS: 34
/ SEQ ID NO 19
/ LENGTH: 2289
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION:
/ OTHER INFORMATION: DNA coding sequence from pBP109 for an artificial Lf-PA fusion pr
US-10-402-466A-19

Query Match          100.0%; Score 59; DB 7; Length 2289;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
Db 1581 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 1639

RESULT 18
US-10-442-502-3
/ Sequence 3, Application US/10442502
/ Publication No. US20040009945A1
/ GENERAL INFORMATION:
/ APPLICANT: LEE, JOHN SCOTT
/ APPLICANT: PARKER, MICHAEL D.
/ APPLICANT: SMITH, JONATHAN F.
/ APPLICANT: WELKOS, SUSAN L.
/ TITLE OF INVENTION: ANTHRAX VACCINES
/ FILE REFERENCE: ARMY135B
/ CURRENT APPLICATION NUMBER: US/10/442,502
/ CURRENT FILING DATE: 2003-05-21
/ PRIOR APPLICATION NUMBER: 09/350,729
/ PRIOR FILING DATE: 1999-07-09
/ PRIOR APPLICATION NUMBER: 60/092,416
/ PRIOR FILING DATE: 1998-07-10
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 2292
/ TYPE: DNA
```

```
/ ORGANISM: Bacillus anthracis
US-10-442-502-3

Query Match          100.0%; Score 59; DB 6; Length 2292;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
Db 1584 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 1642

RESULT 19
US-09-747-521-3
/ Sequence 3, Application US/09747521
/ Patent No. US20020051791A1
/ GENERAL INFORMATION:
/ APPLICANT: Galloway, Darrel
/ APPLICANT: Mateczun, Alfred
/ TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus An
/ FILE REFERENCE: 22727/04079
/ CURRENT APPLICATION NUMBER: US/09/747,521
/ CURRENT FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 3
/ LENGTH: 2295
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1) .. (2295)
US-09-747-521-3

Query Match          100.0%; Score 59; DB 3; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
Db 1587 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 1645

RESULT 20
US-10-106-014-3
/ Sequence 3, Application US/10106014
/ Publication No. US20020142002A1
/ GENERAL INFORMATION:
/ APPLICANT: Galloway, Darrel R.
/ APPLICANT: Mateczun, Alfred J.
/ TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus An
/ FILE REFERENCE: 22727/04114
/ CURRENT APPLICATION NUMBER: US/10/106,014
/ CURRENT FILING DATE: 2002-03-25
/ PRIOR APPLICATION NUMBER: US 09/747,521
/ PRIOR FILING DATE: 2000-12-21
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 3
/ LENGTH: 2295
/ TYPE: DNA
/ ORGANISM: Bacillus anthracis
/ FEATURE:
/ NAME/KEY: CDS
/ LOCATION: (1) .. (2295)
US-10-106-014-3

Query Match          100.0%; Score 59; DB 5; Length 2295;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAACGACTAAACCGG 59
```



Db 1587 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 21

US-10-105-695-3  
; Sequence 3, Application US/10105695  
; Publication No. US20020197272A1  
; GENERAL INFORMATION:  
; APPLICANT: Galloway, Darrel R.  
; APPLICANT: Mateczun, Alfred J.  
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis  
; FILE REFERENCE: 22727/04115  
; CURRENT APPLICATION NUMBER: US/10/105,695  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US 09/747,521  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2295  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2295)  
; OTHER INFORMATION:  
US-10-105-695-3

Query Match 100.0%; Score 59; DB 5; Length 2295;

Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
Db 1587 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 22

US-10-105-694-3  
; Sequence 3, Application US/10105694  
; Publication No. US20030003109A1  
; GENERAL INFORMATION:  
; APPLICANT: Galloway, Darrel R.  
; APPLICANT: Mateczun, Alfred J.  
; TITLE OF INVENTION: Methods for Protection Against Lethal Infection with Bacillus Anthracis  
; FILE REFERENCE: 22727/04116  
; CURRENT APPLICATION NUMBER: US/10/105,694  
; CURRENT FILING DATE: 2002-03-25  
; PRIOR APPLICATION NUMBER: US 09/747,521  
; PRIOR FILING DATE: 2000-12-21  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 3  
; LENGTH: 2295  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)..(2295)  
; OTHER INFORMATION:  
US-10-105-694-3

Query Match 100.0%; Score 59; DB 5; Length 2295;

Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
Db 1587 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 23

US-10-442-502-1  
; Sequence 1, Application US/10442502  
; Publication No. US20040009945A1  
; GENERAL INFORMATION:  
; APPLICANT: LEE, JOHN SCOTT  
; APPLICANT: PUSHKO, PETER  
; APPLICANT: PARKER, MICHAEL D.  
; APPLICANT: SMITH, JONATHAN F.  
; APPLICANT: WELKOS, SUSAN L.  
; TITLE OF INVENTION: ANTHRAX VACCINES  
; FILE REFERENCE: ARMY135B  
; CURRENT APPLICATION NUMBER: US/10/442,502  
; CURRENT FILING DATE: 2003-05-21  
; PRIOR APPLICATION NUMBER: 09/350,729  
; PRIOR FILING DATE: 1999-07-09  
; PRIOR APPLICATION NUMBER: 60/092,416  
; PRIOR FILING DATE: 1998-07-10  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 2295  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
US-10-442-502-1

Query Match 100.0%; Score 59; DB 6; Length 2295;

Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
Db 1587 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 1645

## RESULT 24

US-10-751-103-3  
; Sequence 3, Application US/10751103  
; Publication No. US20050148529A1  
; GENERAL INFORMATION:  
; APPLICANT: Schmaljohn, Connie S.  
; APPLICANT: Fuller, James T.  
; TITLE OF INVENTION: Nucleic Acid Immunization  
; FILE REFERENCE: 033267-021  
; CURRENT APPLICATION NUMBER: US/10/751,103  
; CURRENT FILING DATE: 2004-01-05  
; NUMBER OF SEQ ID NOS: 8  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 2605  
; TYPE: DNA  
; ORGANISM: Bacillus anthracis  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (174)...(2465)  
US-10-751-103-3

Query Match 100.0%; Score 59; DB 9; Length 2605;

Best Local Similarity 100.0%; Pred. No. 1.1e-24;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 59  
Db 1760 GGTAGAAAGCGGATAGCGGGCTTAATCTAGATCCATTAGAAACGACTAAACCGG 1818

## RESULT 25

US-10-410-647-29  
; Sequence 29, Application US/10410647  
; Publication No. US20030235818A1  
; GENERAL INFORMATION:  
; APPLICANT: PLEXUS VACCINE, INC.  
; APPLICANT: Katrielch, Veevold  
; APPLICANT: Bordner, Andrew



```

; APPLICANT: Deane, Robert
; TITLE OF INVENTION: IMMUNOGENIC PEPTIDES, AND METHOD OF IDENTIFYING SAME
; FILE REFERENCE: PLEX1110-1
; CURRENT APPLICATION NUMBER: US/10/410,647
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: US 60/373,668
; PRIOR FILING DATE: 2002-04-17
; PRIOR APPLICATION NUMBER: US 60/371,256
; PRIOR FILING DATE: 2002-04-08
; PRIOR APPLICATION NUMBER: US 60/371,250
; PRIOR FILING DATE: 2002-04-08
; NUMBER OF SEQ ID NOS: 46
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 29
; LENGTH: 4235
; TYPE: DNA
; ORGANISM: Bacillus anthracis
US-10-410-647-29
```

```

Query Match          100.0%; Score 59; DB 6; Length 4235;
Best Local Similarity 100.0%; Pred. No. 1.1e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
Db 3390 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 3448
```

```

RESULT 26
US-10-402-466A-7
; Sequence 7, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giri, Laljan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; CURRENT FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 7
; LENGTH: 8198
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Expression vector for B. anthracis Protective Antigen (PA). Ent1
; OTHER INFORMATION: sequence is shown since the vector sequence is different from the
; OTHER INFORMATION: of the pBR vectors. The PA coding sequence is from 3735 to 5942.
US-10-402-466A-7
```

```

Query Match          100.0%; Score 59; DB 7; Length 8198;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
Db 5234 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 5292
```

```

RESULT 27
US-10-402-466A-10
; Sequence 10, Application US/10402466A
; Publication No. US20040028695A1
; GENERAL INFORMATION:
; APPLICANT: Park, Sukjoon
; APPLICANT: Giri, Laljan
; TITLE OF INVENTION: RECOMBINANT IMMUNOGENIC COMPOSITIONS AND METHODS FOR PROTECTING
```

```

; TITLE OF INVENTION: AGAINST LETHAL INFECTIONS FROM BACILLUS ANTHRACIS
; FILE REFERENCE: 18933-00005
; CURRENT APPLICATION NUMBER: US/10/402,466A
; PRIOR FILING DATE: 2003-03-20
; PRIOR APPLICATION NUMBER: 60/372,152
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 10
; LENGTH: 9286
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; NAME/KEY:
; LOCATION:
; OTHER INFORMATION: Dual expression vector pBP105 for B. anthracis PA and LF30. Ent
; OTHER INFORMATION: sequence is shown since the vector sequence contains two coding
; OTHER INFORMATION: regions. The coding region for PA is from 3735 to 5942 and the
; OTHER INFORMATION: region for LF30 is from 6391 to 7161.
US-10-402-466A-10
```

```

Query Match          100.0%; Score 59; DB 7; Length 9286;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 1 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 59
Db 5234 GGTAGAAAGCGGATAGCGCGGTTAATCTAGTATCATTAGAAAGCACTAAACCGG 5292
```

```

RESULT 28
US-10-282-122A-20872
; Sequence 20872, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-06
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
```



```
; SEQ ID NO 20872
; LENGTH: 948
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-10-282-122A-20872

Query Match      30.5%; Score 18; DB 7; Length 948;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      34 TGATCCATTAGAAACGAC 51
Db      309 TGATCCATTAGAAACGAC 326

RESULT 29
US-09-815-242-6698
; Sequence 6698, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Karl L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6698
; LENGTH: 951
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(951)
US-09-815-242-6698

Query Match      30.5%; Score 18; DB 3; Length 951;
Best Local Similarity 100.0%; Pred. No. 2.4;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      34 TGATCCATTAGAAACGAC 51
Db      309 TGATCCATTAGAAACGAC 326

RESULT 30
US-09-070-927A-292
; Sequence 292, Application US/09070927A
; Patent No. US20020120116A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Kunesh

; Patrick J. Dillon
; Steven Barash
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides
; NUMBER OF SEQUENCES: 982
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/070,927A
; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8512
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 292:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20561 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 292:
US-09-070-927A-292

Query Match      30.5%; Score 18; DB 3; Length 20561;
Best Local Similarity 100.0%; Pred. No. 2.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      34 TGATCCATTAGAAACGAC 51
Db      5892 TGATCCATTAGAAACGAC 5909

RESULT 31
US-10-425-115-82080/C
; Sequence 82080, Application US/10425115
; Publication No. US20040214272A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 82080
; LENGTH: 236
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_174870C.1
```



US-10-425-115-82080

Query Match 28.8%; Score 17; DB 8; Length 236;  
Best Local Similarity 100.0%; Pred. No. 9.3;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TAGTGATCCATTAGAAA 47  
DB 60 TAGTGATCCATTAGAAA 44

RESULT 32

US-10-322-281-855/c  
; Sequence 855, Application US/10322281  
; Publication No. US20040126762A1  
; GENERAL INFORMATION:  
; APPLICANT: David W. Morris  
; APPLICANT: Marc S. Malandro  
; TITLE OF INVENTION: Novel Compositions and Methods in Cancer  
; FILE REFERENCE: 529452001000  
; CURRENT APPLICATION NUMBER: US/10/322,281  
; CURRENT FILING DATE: 2002-12-17  
; NUMBER OF SEQ ID NOS: 866  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 855  
; LENGTH: 125322  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)..(125322)  
; OTHER INFORMATION: n = A,T,C or G  
US-10-322-281-855

Query Match 28.8%; Score 17; DB 7; Length 125322;  
Best Local Similarity 100.0%; Pred. No. 9.9;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCCTAGTGCATTAG 44  
DB 45159 TCCTAGTGCATTAG 45143

RESULT 33  
US-10-229-834A-6/c  
; Sequence 6, Application US/10229834A  
; Publication No. US20030150003A1  
; GENERAL INFORMATION:  
; APPLICANT: Lawrence Berkeley National Laboratory  
; APPLICANT: Rubin, Edward  
; APPLICANT: Pennacchio, Len  
; TITLE OF INVENTION: A novel apolipoprotein gene involved in lipid metabolism  
; FILE REFERENCE: IB-1709  
; CURRENT APPLICATION NUMBER: US/10/229,834A  
; CURRENT FILING DATE: 2002-08-27  
; PRIOR APPLICATION NUMBER: US 60/318,219  
; PRIOR FILING DATE: 2001-08-27  
; NUMBER OF SEQ ID NOS: 48  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 6  
; LENGTH: 263744  
; TYPE: DNA  
; ORGANISM: Mus musculus  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (750)..(850)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1584)..(1683)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature

LOCATION: (2154)..(2154)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (2358)..(2457)  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (3208)..(3307)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4044)..(4143)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4809)..(4908)  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (4921)..(4921)  
; OTHER INFORMATION: gap of unknown length  
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; LOCATION: (5652)..(5751)  
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; LOCATION: (6465)..(6469)  
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; LOCATION: (6477)..(6477)  
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; LOCATION: (6482)..(6482)  
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; LOCATION: (6487)..(6487)  
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; LOCATION: (6489)..(6490)  
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; LOCATION: (6523)..(6622)  
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; NAME/KEY: misc\_feature  
; LOCATION: (6637)..(6637)  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (7410)..(7509)  
; OTHER INFORMATION: gap of unknown length  
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; NAME/KEY: misc\_feature  
; LOCATION: (8177)..(8177)  
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; LOCATION: (8248)..(8347)  
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; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (8358)..(8358)  
; OTHER INFORMATION: gap of unknown length  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (8967)..(8967)



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OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature
LOCATION: (9057)..(9057)
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NAME/KEY: misc_feature
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LOCATION: (10092)..(10092)
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LOCATION: (10827)..(10926)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
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OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (12565)..(12664)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (13327)..(13327)
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NAME/KEY: misc_feature
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OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (14133)..(14133)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (14213)..(14213)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (14293)..(14392)
OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature
LOCATION: (14559)..(14559)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (14900)..(14900)
OTHER INFORMATION: gap of unknown length

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FEATURE:
NAME/KEY: misc_feature
LOCATION: (15119)..(15218)
OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15231)..(15233)
OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15919)..(15919)
OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature
LOCATION: (15922)..(15922)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (15962)..(16061)
OTHER INFORMATION: gap of unknown length
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NAME/KEY: misc_feature
LOCATION: (16757)..(16757)
OTHER INFORMATION: gap of unknown length
FEATURE:
NAME/KEY: misc_feature

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Query Match 28.8%; Score 17; DB 6; Length 263744;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 28 TCCTAGTCATCCATTAG 44
DB 56092 TCCTAGTCATCCATTAG 56076

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RESULT 34
US-10-242-535A-58388
Sequence 58388, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR APPLICATION NUMBER: US 10/085,783
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 58388
LENGTH: 190
TYPE: DNA
ORGANISM: Human
US-10-242-535A-58388

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Query Match 27.1%; Score 16; DB 7; Length 190;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 33 GTGATCCATTAGAAAC 48
DB 93 GTGATCCATTAGAAAC 108

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RESULT 35

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US-10-085-783A-58388  
; Sequence 58388, Application US/10085783A  
; Publication No. US20040037841A1  
; GENERAL INFORMATION:  
; APPLICANT: ChondroGene Inc.  
; APPLICANT: Liew, C.C.  
; TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis  
; FILE REFERENCE: 4231/2002  
; CURRENT APPLICATION NUMBER: US/10/085,783A  
; CURRENT FILING DATE: 2002-02-28  
; PRIOR APPLICATION NUMBER: US 60/305,340  
; PRIOR FILING DATE: 2001-07-13  
; PRIOR APPLICATION NUMBER: US 60/275,017  
; PRIOR FILING DATE: 2001-03-12  
; PRIOR APPLICATION NUMBER: US 60/271,955  
; PRIOR FILING DATE: 2001-02-28  
; NUMBER OF SEQ ID NOS: 58994  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO: 58388  
; LENGTH: 190  
; TYPE: DNA  
; ORGANISM: Human  
US-10-085-783A-58388

Query Match 27.1%; Score 16; DB 7; Length 190;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 33 GTGATCCATTGAAC 48  
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Db 93 GTGATCCATTGAAC 108

RESULT 36  
US-09-864-761-23872  
; Sequence 23872, Application US/09864761  
; Patent No. US20020048763A1  
; GENERAL INFORMATION:  
; APPLICANT: Penn, Sharon G.  
; APPLICANT: Rank, David R.  
; APPLICANT: Hanzel, David K.  
; APPLICANT: Chen, Wenheng  
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR  
; FILE REFERENCE: Aecm1ca-X-1  
; CURRENT APPLICATION NUMBER: US/09/864,761  
; CURRENT FILING DATE: 2001-05-23  
; PRIOR APPLICATION NUMBER: US 60/180,312  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: US 60/207,456  
; PRIOR FILING DATE: 2000-05-26  
; PRIOR APPLICATION NUMBER: US 09/632,366  
; PRIOR FILING DATE: 2000-08-03  
; PRIOR APPLICATION NUMBER: GB 24263.6  
; PRIOR FILING DATE: 2000-10-04  
; PRIOR APPLICATION NUMBER: US 60/236,359  
; PRIOR FILING DATE: 2000-09-27  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00662  
; PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/00661  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 60/234,687  
; PRIOR FILING DATE: 2000-09-21  
; PRIOR APPLICATION NUMBER: US 09/608,408  
; PRIOR FILING DATE: 2000-06-30  
; PRIOR APPLICATION NUMBER: US 09/774,203  
; PRIOR FILING DATE: 2001-01-29  
; NUMBER OF SEQ ID NOS: 49117  
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1  
; SEQ ID NO: 23872  
; LENGTH: 403  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; OTHER INFORMATION: MAP TO AL161662.1  
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9  
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4  
; OTHER INFORMATION: EXPRESSED IN RETAL LIVER, SIGNAL = 1.8  
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7  
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.3  
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.4  
; OTHER INFORMATION: NT HIT: AL163246.2, EVALUE 3.00e-81  
; OTHER INFORMATION: EST HUMAN HIT: AW340174.1, EVALUE 2.00e-92  
; OTHER INFORMATION: SWISSPROT HIT: P33459, EVALUE 4.60e-01

US-09-864-761-23872

Query Match 27.1%; Score 16; DB 3; Length 403;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 29 CCTAGTATCCATTAG 44  
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Db 139 CCTAGTATCCATTAG 154

RESULT 37  
US-10-450-763-15671  
; Sequence 15671, Application US/10450763  
; Publication No. US20050196754A1  
; GENERAL INFORMATION:  
; APPLICANT: Hysed, Inc  
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES  
; FILE REFERENCE: 790CIP3/US  
; CURRENT APPLICATION NUMBER: US/10/450,763  
; CURRENT FILING DATE: 2003-06-11  
; PRIOR APPLICATION NUMBER: PCT/US01/08631  
; PRIOR FILING DATE: 2001-03-30  
; PRIOR APPLICATION NUMBER: 09/540,217  
; PRIOR FILING DATE: 2000-03-31  
; PRIOR APPLICATION NUMBER: 09/649,167  
; PRIOR FILING DATE: 2000-08-23  
; NUMBER OF SEQ ID NOS: 60736  
; SOFTWARE: Custom  
; SEQ ID NO: 15671  
; LENGTH: 469  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: SIMILAR  
; LOCATION: (1371)..(385)  
; OTHER INFORMATION: 75% homologous to Homo sapiens 03-JUL-1997 Human NF-kB-  
; OTHER INFORMATION: inducing kinase (NIK) polypeptide encoding cDNA, accession numbe  
; OTHER INFORMATION: V71603\_cdl, Smith-Waterman Score=1230.

US-10-450-763-15671

Query Match 27.1%; Score 16; DB 9; Length 469;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 29 CCTAGTATCCATTAG 44  
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Db 205 CCTAGTATCCATTAG 220

RESULT 38  
US-10-767-701-18748/c  
; Sequence 18748, Application US/10767701  
; Publication No. US20040172684A1  
; GENERAL INFORMATION:  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof For Plant Improvement  
; FILE REFERENCE: 38-21(5353)B  
; CURRENT FILING DATE: 2004-01-29  
; NUMBER OF SEQ ID NOS: 63128  
; SEQ ID NO 18748  
; LENGTH: 485  
; TYPE: DNA  
; ORGANISM: Sorghum bicolor  
; FEATURE:  
; OTHER INFORMATION: Clone ID: LIB3478-054-Q6-K1-C11  
US-10-767-701-18748

Query Match 27.1%; Score 16; DB 7; Length 485;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 TAGTATCCATTAGAA 46  
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Db 415 TAGTATCCATTAGAA 400

RESULT 39  
US-09-925-065A-462374  
; Sequence 462374, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR FILING DATE: 2001-05-09  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 462374  
; LENGTH: 511  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-462374

Query Match 27.1%; Score 16; DB 4; Length 511;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AGTATCCATTAGAAA 47  
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Db 253 AGTATCCATTAGAAA 268

RESULT 40  
US-10-027-632-233481  
; Sequence 233481, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129  
; CURRENT FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2002-04-30  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-07-12  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR FILING DATE: 2000-04-20  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR FILING DATE: 2000-03-29  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR FILING DATE: 2000-02-24  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR FILING DATE: 1999-11-23  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR FILING DATE: 1999-09-28  
; PRIOR FILING DATE: 1999-08-09  
; PRIOR FILING DATE: 1999-08-09  
; NUMBER OF SEQ ID NOS: 325720  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 233481  
; LENGTH: 529  
; TYPE: DNA  
; ORGANISM: Human  
US-10-027-632-233481

Query Match 27.1%; Score 16; DB 5; Length 529;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CCTAGTATCCATTAG 44  
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Db 49 CCTAGTATCCATTAG 64

Search completed: April 12, 2006, 06:04:51  
Job time : 182.815 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 05:20:02 : Search time 240.963 Seconds  
(without alignments)  
986.217 Million cell updates/sec

Title: US-10-712-654-24

Perfect score: 59

Sequence: 1 ggtagaagcgcgtagtcggy.....attagaacgactaacgcg 59

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 9281099 seqs, 2013915447 residues

Word size : 1

Total number of hits satisfying chosen parameters: 18561424

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database : Published Applications NA New:\*  
1: /SID55/ptcodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
2: /SID55/ptcodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /SID55/ptcodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /SID55/ptcodata/2/pubpna/ECT\_NEW\_PUB.seq:\*  
5: /SID55/ptcodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	2295	14	US-11-055-557-11
2	59	100.0	2295	14	US-11-055-557-15
3	59	100.0	2295	14	US-11-055-557-19
4	59	100.0	2304	14	US-11-055-557-1
5	59	100.0	2304	14	US-11-055-557-9
6	59	100.0	2304	14	US-11-055-557-13
7	59	100.0	2307	14	US-11-055-557-3
8	59	100.0	2307	14	US-11-055-557-5
9	59	100.0	2307	14	US-11-055-557-7
10	59	100.0	2307	14	US-11-055-557-17
11	59	50.8	30	8	US-09-925-065A-462374
12	16	27.1	511	6	US-10-301-480-519085
13	16	27.1	517	10	US-10-301-480-1132494
14	16	27.1	517	10	US-10-301-480-1132494
15	16	27.1	543	10	US-10-301-480-573320
16	16	27.1	543	10	US-10-301-480-1186729
17	16	27.1	577	6	US-09-925-065A-655740
18	16	27.1	577	6	US-09-925-065A-655741

C 19	16	27.1	594	6	US-09-925-065A-465382	Sequence 465382,
C 20	16	27.1	597	10	US-10-301-480-521401	Sequence 521401,
C 21	16	27.1	597	10	US-10-301-480-1134810	Sequence 1134810,
C 22	16	27.1	612	6	US-09-925-065A-225901	Sequence 225901,
C 23	16	27.1	615	10	US-10-301-480-310425	Sequence 310425,
C 24	16	27.1	615	10	US-10-301-480-923834	Sequence 923834,
C 25	16	27.1	989	8	US-10-750-185-40775	Sequence 40775, A
C 26	15	25.4	989	8	US-10-750-185-40775	Sequence 40775, A
C 27	15	25.4	19	12	US-11-101-244-431839	Sequence 431839,
C 28	15	25.4	19	13	US-11-083-784-431839	Sequence 431839,
C 29	15	25.4	201	14	US-11-124-368A-124112	Sequence 124112, A
C 30	15	25.4	455	6	US-09-925-065A-192307	Sequence 192307,
C 31	15	25.4	458	10	US-10-301-480-281859	Sequence 281859,
C 32	15	25.4	458	10	US-10-301-480-895268	Sequence 895268,
C 33	15	25.4	562	10	US-10-301-480-275388	Sequence 275388,
C 34	15	25.4	562	10	US-10-301-480-888797	Sequence 888797,
C 35	15	25.4	563	6	US-09-925-065A-488195	Sequence 488195,
C 36	15	25.4	616	6	US-09-925-065A-185140	Sequence 185140,
C 37	15	25.4	832	8	US-10-750-185-32769	Sequence 32769, A
C 38	15	25.4	832	8	US-10-750-185-32769	Sequence 32769, A
C 39	15	25.4	832	8	US-10-750-623-32769	Sequence 32769, A
C 40	15	25.4	983	6	US-09-925-065A-551799	Sequence 551799,
C 41	15	25.4	983	10	US-10-301-480-529749	Sequence 529749,
C 42	15	25.4	983	10	US-10-301-480-1143158	Sequence 1143158,
C 43	15	25.4	1825	6	US-09-925-065A-720779	Sequence 720779,
C 44	15	25.4	100000	14	US-11-124-368A-23906	Sequence 23906, Ap
C 45	15	25.4	148220	14	US-11-121-086-90	Sequence 96002, A
C 46	15	23.7	23	8	US-10-310-914A-96002	Sequence 131430,
C 47	14	23.7	25	9	US-10-932-182A-131430	Sequence 131430,
C 48	14	23.7	25	9	US-10-932-182A-131430	Sequence 131430,
C 49	14	23.7	25	9	US-10-934-048A-54459	Sequence 54459, A
C 50	14	23.7	25	14	US-11-121-849-10186	Sequence 10186, A
C 51	14	23.7	200	14	US-11-098-686-2823	Sequence 2823, Ap
C 52	14	23.7	459	6	US-09-925-065A-347369	Sequence 347369,
C 53	14	23.7	464	6	US-09-925-065A-565582	Sequence 565582,
C 54	14	23.7	473	10	US-10-301-480-419600	Sequence 419600,
C 55	14	23.7	473	10	US-10-301-480-1033009	Sequence 1033009,
C 56	14	23.7	492	9	US-10-932-182A-79688	Sequence 79688, A
C 57	14	23.7	537	10	US-10-932-182A-79688	Sequence 79688, A
C 58	14	23.7	537	10	US-10-301-480-452018	Sequence 452018,
C 59	14	23.7	537	10	US-10-301-480-1065427	Sequence 1065427,
C 60	14	23.7	542	6	US-09-925-065A-596635	Sequence 596635,
C 61	14	23.7	544	6	US-09-925-065A-781978	Sequence 781978,
C 62	14	23.7	544	6	US-09-925-065A-383097	Sequence 383097,
C 63	14	23.7	544	6	US-09-925-065A-794409	Sequence 794409,
C 64	14	23.7	550	10	US-10-301-480-358800	Sequence 358800,
C 65	14	23.7	550	10	US-10-301-480-972209	Sequence 972209,
C 66	14	23.7	552	6	US-09-925-065A-451991	Sequence 451991,
C 67	14	23.7	556	6	US-09-925-065A-281865	Sequence 281865,
C 68	14	23.7	561	9	US-10-301-480-30934	Sequence 30934, A
C 69	14	23.7	561	9	US-10-301-480-30935	Sequence 30935, A
C 70	14	23.7	561	9	US-10-301-480-30936	Sequence 30936, A
C 71	14	23.7	561	9	US-10-301-480-100937	Sequence 100937, A
C 72	14	23.7	561	10	US-10-301-480-644343	Sequence 644343,
C 73	14	23.7	561	10	US-10-301-480-644343	Sequence 644343,
C 74	14	23.7	561	10	US-10-301-480-644345	Sequence 644345,
C 75	14	23.7	561	10	US-10-301-480-644346	Sequence 644346,
C 76	14	23.7	563	6	US-09-925-065A-188302	Sequence 188302, A
C 77	14	23.7	563	6	US-09-925-065A-188332	Sequence 18832, A
C 78	14	23.7	563	9	US-10-301-480-120067	Sequence 120067,
C 79	14	23.7	563	9	US-10-301-480-120069	Sequence 120069,
C 80	14	23.7	563	10	US-10-301-480-733476	Sequence 733476,
C 81	14	23.7	563	10	US-10-301-480-733478	Sequence 733478,
C 82	14	23.7	564	9	US-10-301-480-630328	Sequence 63028, A
C 83	14	23.7	564	10	US-10-301-480-676437	Sequence 676437,
C 84	14	23.7	573	10	US-10-301-480-510961	Sequence 510961,
C 85	14	23.7	573	10	US-10-301-480-1124370	Sequence 1124370,
C 86	14	23.7	580	6	US-09-925-065A-944121	Sequence 944121,
C 87	14	23.7	580	6	US-09-925-065A-944122	Sequence 944122,
C 88	14	23.7	581	6	US-09-925-065A-454797	Sequence 454797,
C 89	14	23.7	583	14	US-11-112-908-111	Sequence 111, App
C 90	14	23.7	584	10	US-10-301-480-515232	Sequence 515232,
C 91	14	23.7	584	10	US-10-301-480-1126641	Sequence 1126641,



92	14	23.7	604	6	US-09-925-065A-836448	Sequence 836448,	165	13	22.0	19	14	US-11-127-877-373	Sequence 373, App
93	14	23.7	605	6	US-09-925-065A-902732	Sequence 902732,	166	13	22.0	19	14	US-11-127-877-398	Sequence 398, App
C 94	14	23.7	605	6	US-09-925-065A-908708	Sequence 908708,	167	13	22.0	19	14	US-11-127-877-414	Sequence 414, App
C 95	14	23.7	619	6	US-09-925-065A-163304	Sequence 163304,	168	13	22.0	21	14	US-11-127-877-280	Sequence 280, App
C 96	14	23.7	619	6	US-09-925-065A-163305	Sequence 163305,	169	13	22.0	21	14	US-11-127-877-323	Sequence 323, App
C 97	14	23.7	620	6	US-09-925-065A-643944	Sequence 643944,	170	13	22.0	21	14	US-11-127-877-329	Sequence 329, App
C 98	14	23.7	620	10	US-10-301-480-255773	Sequence 255773,	171	13	22.0	22	14	US-11-127-877-339	Sequence 339, App
C 99	14	23.7	620	10	US-10-301-480-255774	Sequence 255774,	172	13	22.0	22	8	US-10-310-914A-775430	Sequence 775430, App
C 100	14	23.7	620	10	US-10-301-480-255782	Sequence 869182,	173	13	22.0	25	9	US-10-932-182A-71949	Sequence 71949, A
C 101	14	23.7	620	10	US-10-301-480-869182	Sequence 869183,	174	13	22.0	25	9	US-10-932-182A-109058	Sequence 109058, A
C 102	14	23.7	627	6	US-09-925-065A-127951	Sequence 127951,	175	13	22.0	25	9	US-10-932-182A-71949	Sequence 71949, A
C 103	14	23.7	627	6	US-09-925-065A-127952	Sequence 127952,	176	13	22.0	25	9	US-10-932-182A-109058	Sequence 109058, A
C 104	14	23.7	629	6	US-09-925-065A-460587	Sequence 460587,	177	13	22.0	25	9	US-10-933-992-2990	Sequence 2990, App
C 105	14	23.7	632	6	US-09-925-065A-433869	Sequence 433869,	178	13	22.0	25	9	US-10-933-992-2995	Sequence 2995, App
C 106	14	23.7	632	10	US-10-301-480-224895	Sequence 224895,	179	13	22.0	25	9	US-10-933-992-1009	Sequence 3009, App
C 107	14	23.7	632	10	US-10-301-480-224896	Sequence 496114,	180	13	22.0	25	9	US-10-933-992-51684	Sequence 61684, A
C 108	14	23.7	632	10	US-10-301-480-966114	Sequence 517725,	181	13	22.0	25	9	US-10-933-992-51684	Sequence 51684, A
C 109	14	23.7	632	10	US-10-301-480-517725	Sequence 838304,	182	13	22.0	25	14	US-11-136-527-187401	Sequence 187401, A
C 110	14	23.7	632	10	US-10-301-480-838304	Sequence 838305,	183	13	22.0	25	14	US-11-136-527-187427	Sequence 187427, A
C 111	14	23.7	632	10	US-10-301-480-838305	Sequence 1109523,	184	13	22.0	25	14	US-11-136-527-187427	Sequence 187427, A
C 112	14	23.7	632	10	US-10-301-480-1109523	Sequence 1131134,	185	13	22.0	26	14	US-10-310-914A-775448	Sequence 775448, A
C 113	14	23.7	632	10	US-10-301-480-1131134	Sequence 516089,	186	13	22.0	27	8	US-10-310-914A-959776	Sequence 959776, A
C 114	14	23.7	649	6	US-09-925-065A-516089	Sequence 87375, A	187	13	22.0	135	6	US-09-925-065A-472213	Sequence 472213, A
C 115	14	23.7	766	6	US-09-925-065A-87375	Sequence 87376, A	188	13	22.0	50	14	US-11-175-859-20903	Sequence 20903, A
C 116	14	23.7	766	6	US-09-925-065A-87376	Sequence 87377, A	189	13	22.0	135	6	US-09-925-065A-472213	Sequence 472213, A
C 117	14	23.7	766	6	US-09-925-065A-87377	Sequence 188616,	190	13	22.0	153	8	US-10-467-657-1825	Sequence 1825, A
C 118	14	23.7	766	6	US-10-301-480-188616	Sequence 188617,	191	13	22.0	201	8	US-10-995-561-5825	Sequence 5825, A
C 119	14	23.7	766	9	US-10-301-480-188617	Sequence 188618,	192	13	22.0	201	8	US-10-995-561-5829	Sequence 5829, A
C 120	14	23.7	766	9	US-10-301-480-188618	Sequence 802025,	193	13	22.0	201	14	US-11-124-368A-14689	Sequence 14689, App
C 121	14	23.7	766	10	US-10-301-480-802025	Sequence 802026,	194	13	22.0	201	14	US-11-124-368A-14689	Sequence 14689, A
C 122	14	23.7	766	10	US-10-301-480-802026	Sequence 802027,	195	13	22.0	201	14	US-11-124-368A-15032	Sequence 15032, A
C 123	14	23.7	766	10	US-10-301-480-802027	Sequence 551962,	196	13	22.0	201	14	US-11-124-367A-17786	Sequence 17786, A
C 124	14	23.7	919	10	US-10-301-480-551962	Sequence 1165371,	197	13	22.0	231	11	US-11-079-63-2825	Sequence 2825, App
C 125	14	23.7	919	10	US-10-301-480-1165371	Sequence 600199,	198	13	22.0	232	6	US-09-925-065A-583055	Sequence 583055, A
C 126	14	23.7	930	10	US-10-301-480-600199	Sequence 1213608,	199	13	22.0	282	9	US-10-932-182A-166706	Sequence 166706, A
C 127	14	23.7	930	10	US-10-301-480-557798	Sequence 557799,	200	13	22.0	282	9	US-10-932-182A-166706	Sequence 166706, A
C 128	14	23.7	972	10	US-10-301-480-557798	Sequence 557799,	201	13	22.0	282	9	US-10-932-182A-166706	Sequence 166706, A
C 129	14	23.7	972	10	US-10-301-480-557799	Sequence 557799,	202	13	22.0	323	6	US-09-925-065A-592820	Sequence 592820, A
C 130	14	23.7	972	10	US-10-301-480-557799	Sequence 557799,	203	13	22.0	323	6	US-09-925-065A-584446	Sequence 584446, A
C 131	14	23.7	972	10	US-10-301-480-557799	Sequence 1171203,	204	13	22.0	405	6	US-09-925-065A-588430	Sequence 588430, A
C 132	14	23.7	972	10	US-10-301-480-1171203	Sequence 1171204,	205	13	22.0	418	6	US-09-925-065A-628645	Sequence 628645, A
C 133	14	23.7	977	11	US-11-096-568A-2882	Sequence 2882, App	206	13	22.0	425	10	US-10-301-480-67115	Sequence 67115, App
C 134	14	23.7	1681	8	US-10-750-185-41683	Sequence 41683, A	207	13	22.0	425	10	US-10-301-480-620124	Sequence 620124, A
C 135	14	23.7	1681	8	US-10-750-185-41683	Sequence 41683, A	208	13	22.0	501	9	US-09-925-065A-479701	Sequence 479701, A
C 136	14	23.7	1704	8	US-10-750-185-60968	Sequence 60968, A	209	13	22.0	501	9	US-10-932-182A-5934	Sequence 5934, App
C 137	14	23.7	1704	8	US-10-750-185-60968	Sequence 60968, A	210	13	22.0	501	9	US-10-932-182A-5934	Sequence 5934, App
C 138	14	23.7	1902	6	US-09-925-065A-862	Sequence 862, App	211	13	22.0	512	6	US-09-925-065A-402248	Sequence 402248, A
C 139	14	23.7	1902	6	US-09-925-065A-862	Sequence 102099,	212	13	22.0	520	6	US-09-925-065A-366776	Sequence 366776, A
C 140	14	23.7	1902	10	US-10-301-480-102099	Sequence 715508,	213	13	22.0	520	6	US-09-925-065A-366776	Sequence 366776, A
C 141	14	23.7	1968	10	US-10-301-480-715508	Sequence 9119, App	214	13	22.0	520	6	US-09-925-065A-366776	Sequence 366776, A
C 142	14	23.7	2253	11	US-11-096-568A-28480	Sequence 28480, A	215	13	22.0	520	6	US-09-925-065A-366776	Sequence 366776, A
C 143	14	23.7	2704	8	US-10-750-185-38967	Sequence 38967, A	216	13	22.0	523	6	US-09-925-065A-622864	Sequence 622864, A
C 144	14	23.7	2704	8	US-10-750-185-38967	Sequence 38967, A	217	13	22.0	523	6	US-09-925-065A-622864	Sequence 622864, A
C 145	14	23.7	3765	9	US-10-932-182A-77239	Sequence 77239, A	218	13	22.0	523	10	US-10-301-480-37162	Sequence 437162, A
C 146	14	23.7	3765	9	US-10-932-182A-77239	Sequence 77239, A	219	13	22.0	523	10	US-10-301-480-37162	Sequence 437162, A
C 147	14	23.7	121062	9	US-10-330-773-290	Sequence 290, App	220	13	22.0	523	10	US-10-301-480-37169	Sequence 437169, A
C 148	14	23.7	162289	14	US-11-121-086-20	Sequence 20, App	221	13	22.0	523	10	US-10-301-480-437170	Sequence 437170, A
C 149	14	23.7	172111	14	US-11-121-086-28	Sequence 28, App	222	13	22.0	523	10	US-10-301-480-1050571	Sequence 1050571, A
C 150	14	23.7	180862	14	US-11-112-908-40	Sequence 40, App	223	13	22.0	523	10	US-10-301-480-1050571	Sequence 1050571, A
C 151	14	23.7	210920	9	US-11-112-908-40	Sequence 99, App	224	13	22.0	523	10	US-10-301-480-1050571	Sequence 1050571, A
C 152	14	23.7	1457619	14	US-11-098-686-8739	Sequence 8639, App	225	13	22.0	523	10	US-10-301-480-1050579	Sequence 1050579, A
C 153	13	22.0		12	US-11-101-244-688621	Sequence 688621,	226	13	22.0	525	6	US-09-925-065A-510383	Sequence 510383, A
C 154	13	22.0		12	US-11-101-244-1034977	Sequence 1034977,	227	13	22.0	525	6	US-09-925-065A-510383	Sequence 510383, A
C 155	13	22.0		12	US-11-101-244-1035028	Sequence 1035028,	228	13	22.0	525	6	US-09-925-065A-510383	Sequence 510383, A
C 156	13	22.0		12	US-11-101-244-1144711	Sequence 1144711,	229	13	22.0	526	6	US-09-925-065A-565711	Sequence 565711, A
C 157	13	22.0		12	US-11-101-244-1177353	Sequence 1177353,	230	13	22.0	526	6	US-09-925-065A-565711	Sequence 565711, A
C 158	13	22.0		12	US-11-083-784-688621	Sequence 688621,	231	13	22.0	527	10	US-10-301-480-469317	Sequence 469317, A
C 159	13	22.0		12	US-11-083-784-1034977	Sequence 1034977,	232	13	22.0	527	10	US-10-301-480-1082726	Sequence 1082726, A
C 160	13	22.0		12	US-11-083-784-1035028	Sequence 1035028,	233	13	22.0	534	6	US-09-925-065A-59976	Sequence 59976, A
C 161	13	22.0		12	US-11-083-784-1144711	Sequence 1144711,	234	13	22.0	540	10	US-10-301-480-669057	Sequence 669057, A
C 162	13	22.0		12	US-11-083-784-1177353	Sequence 1177353,	235	13	22.0	540	10	US-10-301-480-882466	Sequence 882466, A
C 163	13	22.0		12	US-11-127-877-128	Sequence 127, App	236	13	22.0	542	6	US-09-925-065A-366772	Sequence 366772, A
C 164	13	22.0		12	US-11-127-877-128	Sequence 128, App	237	13	22.0	542	6	US-09-925-065A-366774	Sequence 366774, A



C 238	13	22.0	542	6	US-09-925-065A-366777	Sequence 366777,	311	13	22.0	584	10	US-10-301-480-815720	Sequence 815720,
239	13	22.0	543	6	US-09-925-065A-178013	Sequence 178013,	312	13	22.0	585	10	US-10-301-480-379351	Sequence 379351,
240	13	22.0	545	6	US-09-925-065A-762388	Sequence 762388,	313	13	22.0	585	10	US-10-301-480-3791760	Sequence 991760,
C 241	13	22.0	547	6	US-09-925-065A-386710	Sequence 386710,	C 314	13	22.0	587	6	US-09-925-065A-564344	Sequence 564344,
C 242	13	22.0	547	9	US-10-301-480-47110	Sequence 47110, A	315	13	22.0	588	10	US-10-301-480-379749	Sequence 379749,
244	13	22.0	550	10	US-10-301-480-660519	Sequence 660519,	316	13	22.0	588	10	US-10-301-480-993158	Sequence 993158,
245	13	22.0	550	10	US-10-301-480-119788	Sequence 419788	317	13	22.0	589	6	US-09-925-065A-649367	Sequence 649367,
C 246	13	22.0	551	10	US-10-301-480-1031197	Sequence 1031197,	318	13	22.0	589	10	US-10-301-480-437160	Sequence 437160,
C 247	13	22.0	551	10	US-10-301-480-363096	Sequence 363096,	319	13	22.0	589	10	US-10-301-480-437165	Sequence 437165,
248	13	22.0	552	6	US-10-301-480-976505	Sequence 976505,	320	13	22.0	589	10	US-10-301-480-437167	Sequence 437167,
249	13	22.0	553	6	US-09-925-065A-480886	Sequence 480886	321	13	22.0	589	10	US-10-301-480-1050569	Sequence 1050569,
250	13	22.0	553	6	US-09-925-065A-150618	Sequence 150618,	322	13	22.0	589	10	US-10-301-480-1050574	Sequence 1050574,
C 251	13	22.0	553	6	US-09-925-065A-150619	Sequence 150619,	323	13	22.0	589	10	US-10-301-480-1050576	Sequence 1050576,
252	13	22.0	553	10	US-10-301-480-244565	Sequence 244565,	324	13	22.0	591	6	US-09-925-065A-306513	Sequence 306513,
C 253	13	22.0	553	10	US-10-301-480-517837	Sequence 517837,	325	13	22.0	591	6	US-09-925-065A-928648	Sequence 928648,
254	13	22.0	553	10	US-10-301-480-857974	Sequence 857974,	C 327	13	22.0	591	6	US-09-925-065A-950322	Sequence 950322,
255	13	22.0	553	10	US-10-301-480-857975	Sequence 857975,	C 328	13	22.0	592	6	US-09-925-065A-579617	Sequence 579617,
C 256	13	22.0	553	10	US-10-301-480-1131246	Sequence 1131246,	C 329	13	22.0	592	6	US-09-925-065A-579618	Sequence 579618,
257	13	22.0	555	6	US-09-925-065A-365916	Sequence 365916,	C 330	13	22.0	592	6	US-09-925-065A-579619	Sequence 579619,
258	13	22.0	557	6	US-09-925-065A-304499	Sequence 304499,	C 331	13	22.0	592	6	US-09-925-065A-659663	Sequence 659663,
C 259	13	22.0	557	6	US-09-925-065A-304500	Sequence 304500,	C 332	13	22.0	593	10	US-10-301-480-653664	Sequence 653664,
260	13	22.0	558	6	US-09-925-065A-460715	Sequence 460715,	C 333	13	22.0	593	10	US-10-301-480-225387	Sequence 225387,
C 261	13	22.0	559	6	US-09-925-065A-403360	Sequence 403360,	C 334	13	22.0	593	10	US-10-301-480-225388	Sequence 225388,
262	13	22.0	559	10	US-10-301-480-380576	Sequence 380576,	C 335	13	22.0	593	10	US-10-301-480-838796	Sequence 838796,
263	13	22.0	559	10	US-10-301-480-993985	Sequence 993985,	C 336	13	22.0	595	6	US-09-925-065A-951804	Sequence 951804,
264	13	22.0	561	10	US-10-301-480-436608	Sequence 436608,	337	13	22.0	595	9	US-10-301-480-197913	Sequence 197913,
265	13	22.0	561	10	US-10-301-480-1049817	Sequence 1049817,	338	13	22.0	595	10	US-10-301-480-811332	Sequence 811332,
C 266	13	22.0	563	6	US-09-925-065A-366761	Sequence 366761,	339	13	22.0	596	6	US-09-925-065A-276950	Sequence 276950, A
C 267	13	22.0	563	6	US-09-925-065A-366762	Sequence 366762,	340	13	22.0	596	6	US-09-925-065A-276956	Sequence 276956,
C 268	13	22.0	563	6	US-09-925-065A-366763	Sequence 366763,	341	13	22.0	599	6	US-09-925-065A-130694	Sequence 130694,
C 269	13	22.0	563	10	US-10-301-480-455270	Sequence 455270,	C 342	13	22.0	599	6	US-09-925-065A-353539	Sequence 353539,
C 270	13	22.0	563	10	US-10-301-480-106679	Sequence 106679,	C 343	13	22.0	599	6	US-09-925-065A-353540	Sequence 353540,
271	13	22.0	565	6	US-09-925-065A-751963	Sequence 751963,	C 344	13	22.0	599	10	US-10-301-480-276578	Sequence 276578,
C 273	13	22.0	565	6	US-09-925-065A-902292	Sequence 902292,	345	13	22.0	599	10	US-10-301-480-276587	Sequence 889987,
C 274	13	22.0	568	6	US-09-925-065A-366764	Sequence 366764,	C 346	13	22.0	600	6	US-09-925-065A-128588	Sequence 128588,
C 275	13	22.0	568	6	US-09-925-065A-366769	Sequence 366769,	C 347	13	22.0	600	6	US-09-925-065A-128589	Sequence 128589,
C 276	13	22.0	568	10	US-09-925-065A-366771	Sequence 366771,	348	13	22.0	600	6	US-09-925-065A-186443	Sequence 186443,
C 277	13	22.0	568	10	US-10-301-480-470372	Sequence 470372,	C 349	13	22.0	600	6	US-09-925-065A-473898	Sequence 473898,
C 278	13	22.0	568	10	US-10-301-480-1083781	Sequence 1083781,	C 350	13	22.0	600	8	US-09-925-065A-473898	Sequence 473898,
C 279	13	22.0	569	9	US-10-301-480-68165	Sequence 68165, A	351	13	22.0	600	8	US-10-750-185-21195	Sequence 21195, A
C 280	13	22.0	569	9	US-10-301-480-68166	Sequence 68166, A	C 352	13	22.0	600	8	US-10-750-185-21195	Sequence 21195, A
C 281	13	22.0	569	10	US-10-301-480-681574	Sequence 681574,	353	13	22.0	600	8	US-10-750-623-21195	Sequence 21195, A
282	13	22.0	571	6	US-09-925-065A-367924	Sequence 367924,	C 354	13	22.0	600	14	US-11-136-527-77737	Sequence 77737, Ap
283	13	22.0	571	6	US-09-925-065A-367925	Sequence 367925,	C 355	13	22.0	601	9	US-10-301-480-29727	Sequence 29727, A
284	13	22.0	572	6	US-09-925-065A-302078	Sequence 302078,	C 356	13	22.0	601	9	US-10-301-480-29728	Sequence 29728, A
C 285	13	22.0	572	6	US-09-925-065A-366765	Sequence 366765,	C 357	13	22.0	601	9	US-10-301-480-29729	Sequence 29729, A
C 286	13	22.0	572	6	US-09-925-065A-366767	Sequence 366767,	358	13	22.0	601	10	US-10-301-480-355950	Sequence 355950,
C 287	13	22.0	572	6	US-09-925-065A-366768	Sequence 366768,	C 360	13	22.0	601	10	US-10-301-480-441293	Sequence 441293,
C 288	13	22.0	572	6	US-09-925-065A-366773	Sequence 366773,	C 361	13	22.0	601	10	US-10-301-480-643136	Sequence 643136,
C 289	13	22.0	573	6	US-09-925-065A-528316	Sequence 528316,	C 362	13	22.0	601	10	US-10-301-480-643137	Sequence 643137,
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C 292	13	22.0	575	6	US-09-925-065A-238897	Sequence 238897,	365	13	22.0	602	6	US-10-301-480-1054702	Sequence 1054702,
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296	13	22.0	575	10	US-10-301-480-437164	Sequence 437164,	C 369	13	22.0	603	10	US-10-301-480-407280	Sequence 407280,
297	13	22.0	575	10	US-10-301-480-437168	Sequence 437168,	C 370	13	22.0	603	10	US-10-301-480-407280	Sequence 407280,
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299	13	22.0	575	10	US-10-301-480-1050572	Sequence 1050572,	C 372	13	22.0	603	10	US-10-301-480-101619	Sequence 101619,
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305	13	22.0	580	10	US-10-301-480-537055	Sequence 537055,	C 378	13	22.0	606	10	US-10-301-480-1114298	Sequence 1114298,
306	13	22.0	580	10	US-10-301-480-645449	Sequence 645449,	C 379	13	22.0	608	6	US-09-925-065A-328848	Sequence 328848,
307	13	22.0	580	10	US-10-301-480-1150464	Sequence 1150464,	C 380	13	22.0	608	10	US-10-301-480-425192	Sequence 425192,
308	13	22.0	582	10	US-10-301-480-381050	Sequence 381050,	C 381	13	22.0	608	10	US-10-301-480-1038601	Sequence 1038601,
309	13	22.0	582	10	US-10-301-480-994459	Sequence 994459,	C 382	13	22.0	608	10	US-10-301-480-1038602	Sequence 1038602,
310	13	22.0	584	9	US-10-301-480-202311	Sequence 202311,	C 383	13	22.0	610	6	US-09-925-065A-767734	Sequence 767734,



C 384	13	22.0	610	6	US-09-925-065A-767735	Sequence 767735,	457	13	22.0	801	9	US-10-932-182A-76513	Sequence 76513, A
C 385	13	22.0	614	6	US-09-925-065A-798952	Sequence 798952,	C 458	13	22.0	839	8	US-10-750-185-62911	Sequence 62911, A
C 386	13	22.0	616	6	US-09-925-065A-515811	Sequence 515811,	C 459	13	22.0	839	8	US-10-750-623-12911	Sequence 62311, A
C 387	13	22.0	617	6	US-09-925-065A-767932	Sequence 767932,	C 460	13	22.0	843	9	US-10-932-182A-79842	Sequence 79842, A
C 388	13	22.0	620	6	US-09-925-065A-862622	Sequence 862622,	C 461	13	22.0	843	9	US-10-932-182A-79842	Sequence 79842, A
C 389	13	22.0	622	6	US-10-301-480-61130	Sequence 61130, A	C 462	13	22.0	858	9	US-10-932-182A-4226	Sequence 4226, Ap
C 390	13	22.0	625	10	US-10-301-480-674539	Sequence 674539,	C 463	13	22.0	858	9	US-10-932-182A-4226	Sequence 4226, Ap
C 391	13	22.0	622	10	US-10-301-480-334057	Sequence 334057,	C 464	13	22.0	897	10	US-10-301-480-564559	Sequence 564559, Ap
C 392	13	22.0	625	10	US-10-301-480-947466	Sequence 947466,	C 465	13	22.0	897	10	US-10-301-480-1173868	Sequence 1173868,
C 393	13	22.0	626	6	US-09-925-065A-524549	Sequence 524549,	C 466	13	22.0	903	8	US-10-750-185-53220	Sequence 53220, A
C 394	13	22.0	627	6	US-09-925-065A-463831	Sequence 463831,	C 467	13	22.0	903	8	US-10-750-623-32294	Sequence 22994, A
C 395	13	22.0	631	6	US-09-925-065A-255225	Sequence 255225,	C 468	13	22.0	914	10	US-10-301-480-632403	Sequence 632403,
C 396	13	22.0	633	6	US-09-925-065A-111737	Sequence 111737,	C 469	13	22.0	914	10	US-10-301-480-594320	Sequence 594320,
C 397	13	22.0	633	6	US-09-925-065A-111738	Sequence 111738,	C 470	13	22.0	927	10	US-10-301-480-594315	Sequence 594315,
C 398	13	22.0	634	9	US-10-301-480-26911	Sequence 26911, A	C 471	13	22.0	927	10	US-10-301-480-594317	Sequence 594317,
C 399	13	22.0	634	9	US-10-301-480-26912	Sequence 26912, A	C 472	13	22.0	927	10	US-10-301-480-594318	Sequence 594318,
C 400	13	22.0	634	10	US-10-301-480-640320	Sequence 640320,	C 473	13	22.0	927	10	US-10-301-480-594319	Sequence 594319,
C 401	13	22.0	634	10	US-10-301-480-640321	Sequence 640321,	C 474	13	22.0	927	10	US-10-301-480-594320	Sequence 594320,
C 402	13	22.0	635	6	US-09-925-065A-632536	Sequence 632536,	C 475	13	22.0	927	10	US-10-301-480-594321	Sequence 594321,
C 403	13	22.0	635	6	US-09-925-065A-632537	Sequence 632537,	C 476	13	22.0	927	10	US-10-301-480-594322	Sequence 594322,
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C 405	13	22.0	641	9	US-10-301-480-211097	Sequence 211097,	C 478	13	22.0	927	10	US-10-301-480-1207725	Sequence 1207725,
C 406	13	22.0	641	10	US-10-301-480-824505	Sequence 824505,	C 479	13	22.0	927	10	US-10-301-480-1207726	Sequence 1207726,
C 407	13	22.0	641	10	US-10-301-480-824506	Sequence 824506,	C 480	13	22.0	927	10	US-10-301-480-1207727	Sequence 1207727,
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C 409	13	22.0	643	6	US-09-925-065A-537291	Sequence 537291,	C 482	13	22.0	927	10	US-10-301-480-1207729	Sequence 1207729,
C 410	13	22.0	643	6	US-09-925-065A-591456	Sequence 591456,	C 483	13	22.0	927	10	US-10-301-480-1207730	Sequence 1207730,
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C 413	13	22.0	648	10	US-10-301-480-982202	Sequence 982202,	C 486	13	22.0	928	10	US-10-301-480-1207732	Sequence 1207732,
C 414	13	22.0	648	10	US-10-301-480-982202	Sequence 982202,	C 487	13	22.0	928	10	US-10-301-480-1207732	Sequence 1207732,
C 415	13	22.0	656	6	US-09-925-065A-291917	Sequence 291917,	C 488	13	22.0	930	10	US-10-301-480-533566	Sequence 533566,
C 416	13	22.0	657	6	US-09-925-065A-254022	Sequence 254022,	C 489	13	22.0	930	10	US-10-301-480-1146975	Sequence 1146975,
C 417	13	22.0	657	6	US-09-925-065A-902953	Sequence 902953,	C 490	13	22.0	931	10	US-10-301-480-591760	Sequence 591760,
C 418	13	22.0	658	9	US-09-925-065A-1499	Sequence 1499, Ap	C 491	13	22.0	931	10	US-10-301-480-1205169	Sequence 1205169,
C 419	13	22.0	658	9	US-10-301-480-102736	Sequence 102736,	C 492	13	22.0	945	9	US-10-932-182A-1347	Sequence 1347, Ap
C 420	13	22.0	660	10	US-10-301-480-116145	Sequence 716145,	C 493	13	22.0	945	9	US-10-932-182A-1347	Sequence 1347, Ap
C 421	13	22.0	660	10	US-09-925-065A-534796	Sequence 534796,	C 494	13	22.0	960	6	US-09-925-065A-117063	Sequence 117063,
C 422	13	22.0	660	10	US-10-301-480-333069	Sequence 333069,	C 495	13	22.0	960	6	US-09-925-065A-117063	Sequence 117063,
C 423	13	22.0	662	10	US-10-301-480-846478	Sequence 846478,	C 496	13	22.0	960	6	US-09-925-065A-117065	Sequence 117065,
C 424	13	22.0	662	10	US-10-301-480-318205	Sequence 318205,	C 497	13	22.0	960	6	US-09-925-065A-117065	Sequence 117065,
C 425	13	22.0	662	10	US-10-301-480-318206	Sequence 318206,	C 498	13	22.0	960	6	US-09-925-065A-117067	Sequence 117067,
C 426	13	22.0	662	10	US-10-301-480-931614	Sequence 931614,	C 499	13	22.0	960	6	US-09-925-065A-717068	Sequence 717068,
C 427	13	22.0	663	10	US-10-301-480-931615	Sequence 931615,	C 500	13	22.0	984	11	US-11-096-568A-97168	Sequence 97168, Ap
C 428	13	22.0	663	10	US-10-301-480-90718	Sequence 90718, A	C 501	13	22.0	985	14	US-11-124-68A-60	Sequence 9786, Ap
C 429	13	22.0	663	10	US-10-301-480-704127	Sequence 704127,	C 502	13	22.0	991	10	US-10-301-480-575734	Sequence 575734, Ap
C 430	13	22.0	671	6	US-09-925-065A-777714	Sequence 777714,	C 503	13	22.0	991	10	US-10-301-480-575937	Sequence 575937,
C 431	13	22.0	672	6	US-09-925-065A-791040	Sequence 791040,	C 504	13	22.0	991	10	US-10-301-480-597113	Sequence 597113,
C 432	13	22.0	673	9	US-09-925-065A-41992	Sequence 41992, A	C 505	13	22.0	991	10	US-10-301-480-1189143	Sequence 1189143,
C 433	13	22.0	673	9	US-10-301-480-143230	Sequence 143230,	C 506	13	22.0	991	10	US-10-301-480-1189346	Sequence 1189346,
C 434	13	22.0	673	10	US-10-301-480-756639	Sequence 756639,	C 507	13	22.0	991	10	US-10-301-480-1210522	Sequence 1210522,
C 435	13	22.0	674	6	US-09-925-065A-235399	Sequence 235399,	C 508	13	22.0	993	10	US-10-301-480-594974	Sequence 594974,
C 436	13	22.0	674	6	US-09-925-065A-235400	Sequence 235400,	C 509	13	22.0	993	10	US-10-301-480-594974	Sequence 594974,
C 437	13	22.0	682	6	US-09-925-065A-748100	Sequence 748100,	C 510	13	22.0	999	10	US-10-301-480-542405	Sequence 542405,
C 438	13	22.0	683	6	US-09-925-065A-833475	Sequence 833475,	C 511	13	22.0	999	10	US-10-301-480-542405	Sequence 542405,
C 439	13	22.0	691	6	US-09-925-065A-928659	Sequence 928659,	C 512	13	22.0	1023	9	US-10-932-182A-819	Sequence 115814,
C 440	13	22.0	693	9	US-10-932-182A-77694	Sequence 77694, A	C 513	13	22.0	1023	9	US-10-932-182A-819	Sequence 819, App
C 441	13	22.0	698	10	US-10-301-480-556586	Sequence 556586,	C 514	13	22.0	1024	6	US-09-925-065A-8512	Sequence 8512, A
C 442	13	22.0	698	10	US-10-301-480-1169935	Sequence 1169935,	C 515	13	22.0	1024	9	US-09-925-065A-149750	Sequence 149750,
C 443	13	22.0	702	14	US-11-136-527-3641	Sequence 3641, Ap	C 516	13	22.0	1024	9	US-10-301-480-163159	Sequence 163159,
C 444	13	22.0	720	6	US-09-925-065A-933205	Sequence 933205,	C 517	13	22.0	1047	8	US-10-520-820-20	Sequence 20, Appl
C 445	13	22.0	731	10	US-10-301-480-40004	Sequence 40004, A	C 518	13	22.0	1077	9	US-10-932-182A-82679	Sequence 82679, A
C 446	13	22.0	731	10	US-10-301-480-653413	Sequence 653413,	C 519	13	22.0	1077	9	US-10-932-182A-82679	Sequence 82679, A
C 447	13	22.0	739	6	US-09-925-065A-949864	Sequence 949864,	C 520	13	22.0	1093	6	US-09-925-065A-711588	Sequence 711588,
C 448	13	22.0	748	8	US-10-750-185-3168	Sequence 3168, A	C 521	13	22.0	1093	6	US-09-925-065A-711589	Sequence 711589,
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C 451	13	22.0	769	6	US-09-925-065A-917991	Sequence 917991,	C 524	13	22.0	1132	8	US-10-750-185-44331	Sequence 44331, A
C 452	13	22.0	769	6	US-09-925-065A-917992	Sequence 917992,	C 525	13	22.0	1132	8	US-10-750-623-44331	Sequence 44331, A
C 453	13	22.0	769	6	US-09-925-065A-917993	Sequence 917993,	C 526	13	22.0	1136	8	US-10-750-185-34870	Sequence 34870, A
C 454	13	22.0	772	8	US-09-925-065A-917993	Sequence 917993,	C 527	13	22.0	1136	8	US-10-750-623-34870	Sequence 34870, A
C 455	13	22.0	772	8	US-10-750-185-31157	Sequence 31157, A	C 528	13	22.0	1137	8	US-10-750-185-46521	Sequence 46521, A
C 456	13	22.0	801	9	US-10-932-182A-76513	Sequence 76513, A	C 529	13	22.0	1137	8	US-10-750-623-46521	Sequence 46521, A



C 530	13	22.0	1141	6	US-09-925-065A-286120	Sequence 286120,	C 603	13	22.0	2214	11	US-11-096-568A-25918	Sequence 25918, A
C 531	13	22.0	1162	9	US-10-301-480-37428	Sequence 37428, A	C 604	13	22.0	2223	11	US-11-079-925-3205	Sequence 3205, Ap
C 532	13	22.0	1162	9	US-10-301-480-650837	Sequence 650837, A	C 605	13	22.0	2250	6	US-09-925-065A-86027	Sequence 86027, A
C 533	13	22.0	1165	14	US-11-024-959-49	Sequence 49, Appl	C 606	13	22.0	2250	6	US-09-925-065A-86028	Sequence 86028, A
C 534	13	22.0	1208	9	US-10-301-480-94810	Sequence 94810, A	C 607	13	22.0	2250	9	US-10-301-480-88814	Sequence 88814, A
C 535	13	22.0	1208	10	US-10-301-480-708219	Sequence 708219, A	C 608	13	22.0	2250	9	US-10-301-480-88815	Sequence 88815, A
C 536	13	22.0	1212	8	US-10-750-185-55460	Sequence 55460, A	C 609	13	22.0	2250	9	US-10-301-480-187267	Sequence 187267, A
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C 538	13	22.0	1221	11	US-11-079-463-2840	Sequence 2840, Ap	C 611	13	22.0	2250	10	US-10-301-480-702223	Sequence 702223, A
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C 540	13	22.0	1222	10	US-10-301-480-651825	Sequence 651825, A	C 613	13	22.0	2250	10	US-10-301-480-800676	Sequence 800676, A
C 541	13	22.0	1284	8	US-10-750-185-62902	Sequence 62902, A	C 614	13	22.0	2250	10	US-10-301-480-800677	Sequence 800677, A
C 542	13	22.0	1284	8	US-10-750-623-62902	Sequence 62902, A	C 615	13	22.0	2290	14	US-11-127-877-13	Sequence 13, Appl
C 543	13	22.0	1326	11	US-11-079-463-1180	Sequence 3180, Ap	C 616	13	22.0	2422	7	US-10-960-414-266	Sequence 266, App
C 544	13	22.0	1335	9	US-10-301-480-28250	Sequence 28250, A	C 617	13	22.0	2426	8	US-10-750-185-32812	Sequence 32812, A
C 545	13	22.0	1335	10	US-10-301-480-642859	Sequence 642859, A	C 618	13	22.0	2426	8	US-10-750-623-32812	Sequence 32812, A
C 546	13	22.0	1356	6	US-09-925-065A-91994	Sequence 91994, A	C 619	13	22.0	2436	6	US-10-793-626-3398	Sequence 4398, Ap
C 547	13	22.0	1356	6	US-10-301-480-193235	Sequence 193235, A	C 620	13	22.0	2473	8	US-09-925-065A-685772	Sequence 685772, A
C 548	13	22.0	1356	10	US-10-301-480-806644	Sequence 806644, A	C 621	13	22.0	2504	14	US-11-136-527-3803	Sequence 3803, Ap
C 549	13	22.0	1359	9	US-10-301-480-89777	Sequence 89777, A	C 622	13	22.0	2565	9	US-10-932-182A-80399	Sequence 80399, A
C 550	13	22.0	1359	10	US-10-301-480-703186	Sequence 703186, A	C 623	13	22.0	2565	9	US-10-932-182A-80399	Sequence 80399, A
C 551	13	22.0	1363	14	US-11-124-368A-61	Sequence 61, Appl	C 624	13	22.0	2781	11	US-11-232-405A-33	Sequence 33, Appl
C 552	13	22.0	1383	9	US-10-932-182A-78730	Sequence 78730, A	C 625	13	22.0	3099	11	US-11-079-463-2589	Sequence 2589, Ap
C 553	13	22.0	1383	9	US-10-932-182A-78730	Sequence 78730, A	C 626	13	22.0	3161	8	US-10-750-185-26534	Sequence 26534, A
C 554	13	22.0	1407	11	US-11-079-463-3733	Sequence 3733, Ap	C 627	13	22.0	3161	8	US-10-750-623-26534	Sequence 26534, A
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C 556	13	22.0	1500	9	US-10-932-182A-1568	Sequence 1568, Ap	C 629	13	22.0	3217	8	US-10-793-626-4051	Sequence 4051, Ap
C 557	13	22.0	1525	8	US-10-750-185-51610	Sequence 51610, A	C 630	13	22.0	3379	8	US-10-750-185-53288	Sequence 53288, A
C 558	13	22.0	1525	8	US-10-750-623-51610	Sequence 51610, A	C 631	13	22.0	3379	8	US-10-750-623-53288	Sequence 53288, A
C 559	13	22.0	1553	6	US-09-925-065A-709605	Sequence 709605, A	C 632	13	22.0	3581	8	US-10-750-185-59945	Sequence 59945, A
C 560	13	22.0	1553	6	US-09-925-065A-709606	Sequence 709606, A	C 633	13	22.0	3581	8	US-10-750-623-59945	Sequence 59945, A
C 561	13	22.0	1581	9	US-10-932-182A-5933	Sequence 5933, Ap	C 634	13	22.0	3824	14	US-11-136-527-2977	Sequence 2977, Ap
C 562	13	22.0	1581	9	US-10-932-182A-5933	Sequence 5933, Ap	C 635	13	22.0	3929	8	US-10-793-626-3938	Sequence 3938, Ap
C 563	13	22.0	1617	8	US-10-467-657-3869	Sequence 3869, Ap	C 636	13	22.0	4416	9	US-10-932-182A-47	Sequence 47, Appl
C 564	13	22.0	1617	11	US-11-096-568A-26142	Sequence 26142, A	C 637	13	22.0	4416	9	US-10-932-182A-47	Sequence 47, Appl
C 565	13	22.0	1626	11	US-11-096-568A-27458	Sequence 27458, A	C 638	13	22.0	4605	14	US-11-102-476-3	Sequence 3, Appl
C 566	13	22.0	1639	9	US-10-301-480-86414	Sequence 86414, A	C 639	13	22.0	4729	7	US-10-204-639-100	Sequence 100, App
C 567	13	22.0	1639	9	US-10-301-480-86415	Sequence 86415, A	C 640	13	22.0	5269	9	US-10-932-182A-191082	Sequence 191082, A
C 568	13	22.0	1639	10	US-10-301-480-699823	Sequence 699823, A	C 641	13	22.0	5269	9	US-10-932-182A-191082	Sequence 191082, A
C 569	13	22.0	1639	10	US-10-301-480-699824	Sequence 699824, A	C 642	13	22.0	6274	14	US-11-000-488-66	Sequence 66, Appl
C 570	13	22.0	1656	14	US-11-017-814-15	Sequence 15, Appl	C 643	13	22.0	6425	14	US-11-131-479-37	Sequence 37, Appl
C 571	13	22.0	1661	14	US-11-017-814-8	Sequence 8, Appl	C 644	13	22.0	8040	11	US-11-004-399-378	Sequence 378, Appl
C 572	13	22.0	1681	6	US-09-925-065A-68113	Sequence 68113, A	C 645	13	22.0	8082	11	US-11-004-399-378	Sequence 378, Appl
C 573	13	22.0	1681	6	US-10-301-480-169352	Sequence 169352, A	C 646	13	22.0	8082	11	US-11-004-399-483	Sequence 483, App
C 574	13	22.0	1681	10	US-10-301-480-782761	Sequence 782761, A	C 647	13	22.0	8082	11	US-11-004-399-605	Sequence 605, App
C 575	13	22.0	1699	8	US-10-750-185-34175	Sequence 34175, A	C 648	13	22.0	9348	11	US-11-004-399-605	Sequence 605, App
C 576	13	22.0	1699	8	US-10-750-623-34175	Sequence 34175, A	C 649	13	22.0	9348	11	US-11-004-399-605	Sequence 605, App
C 577	13	22.0	1704	8	US-10-750-185-37321	Sequence 37321, A	C 650	13	22.0	9348	11	US-11-004-399-605	Sequence 605, App
C 578	13	22.0	1704	8	US-10-750-623-37321	Sequence 37321, A	C 651	13	22.0	9348	11	US-11-004-399-605	Sequence 605, App
C 579	13	22.0	1726	8	US-10-750-185-41207	Sequence 41207, A	C 652	13	22.0	10591	11	US-11-004-399-3533	Sequence 3533, App
C 580	13	22.0	1726	8	US-10-750-623-41207	Sequence 41207, A	C 653	13	22.0	10591	11	US-11-004-399-3533	Sequence 3533, App
C 581	13	22.0	1740	14	US-11-124-368A-62	Sequence 62, Appl	C 654	13	22.0	10591	11	US-11-004-399-3738	Sequence 3738, Ap
C 582	13	22.0	1926	9	US-10-932-182A-5383	Sequence 5383, Ap	C 655	13	22.0	14670	8	US-10-995-561-3321	Sequence 3321, A
C 583	13	22.0	1926	9	US-10-932-182A-5383	Sequence 5383, Ap	C 656	13	22.0	30140	14	US-11-052-544-29	Sequence 29, Appl
C 584	13	22.0	1976	11	US-11-072-512-1680	Sequence 1680, Ap	C 657	13	22.0	33126	8	US-10-330-773-823	Sequence 523, App
C 585	13	22.0	1992	9	US-10-301-480-93785	Sequence 93785, A	C 658	13	22.0	38703	14	US-11-052-544-28	Sequence 28, Appl
C 586	13	22.0	1992	10	US-10-301-480-707165	Sequence 707165, A	C 659	13	22.0	43985	8	US-10-995-561-3337	Sequence 1337, A
C 587	13	22.0	2005	6	US-09-925-065A-714227	Sequence 714227, A	C 660	13	22.0	85682	14	US-11-117-187-205	Sequence 205, App
C 588	13	22.0	2005	6	US-09-925-065A-714227	Sequence 714227, A	C 661	13	22.0	95058	9	US-10-330-773-701	Sequence 701, App
C 589	13	22.0	2005	8	US-10-750-185-61441	Sequence 61441, A	C 662	13	22.0	95050	8	US-10-330-773-701	Sequence 701, App
C 590	13	22.0	2005	8	US-10-750-623-61441	Sequence 61441, A	C 663	13	22.0	100000	14	US-11-124-368A-2883	Sequence 2883, Ap
C 591	13	22.0	2034	6	US-09-925-065A-710770	Sequence 710770, A	C 664	13	22.0	101001	8	US-10-995-561-13255	Sequence 13255, A
C 592	13	22.0	2064	9	US-10-932-182A-77996	Sequence 77996, A	C 665	13	22.0	109661	9	US-10-330-773-795	Sequence 795, App
C 593	13	22.0	2064	9	US-10-932-182A-77996	Sequence 77996, A	C 666	13	22.0	116297	9	US-10-330-773-795	Sequence 795, App
C 594	13	22.0	2073	8	US-10-750-185-53658	Sequence 53658, A	C 667	13	22.0	124972	14	US-11-121-086-100	Sequence 100, App
C 595	13	22.0	2073	8	US-10-750-623-53658	Sequence 53658, A	C 668	13	22.0	134174	14	US-11-121-086-99	Sequence 99, Appl
C 596	13	22.0	2089	14	US-11-127-877-14	Sequence 14, Appl	C 669	13	22.0	156250	14	US-11-121-086-86	Sequence 86, Appl
C 597	13	22.0	2128	14	US-11-078-189-7	Sequence 7, Appl	C 670	13	22.0	164527	14	US-11-121-086-71	Sequence 71, Appl
C 598	13	22.0	2188	6	US-09-925-065A-77775	Sequence 77775, A	C 671	13	22.0	168753	14	US-11-181-234-1	Sequence 1, Appl
C 599	13	22.0	2188	6	US-10-301-480-179014	Sequence 179014, A	C 672	13	22.0	180654	14	US-11-121-086-58	Sequence 58, Appl
C 600	13	22.0	2188	10	US-10-301-480-792423	Sequence 792423, A	C 673	13	22.0	186854	11	US-11-238-025-34	Sequence 34, Appl
C 601	13	22.0	2196	9	US-10-932-182A-77504	Sequence 77504, A	C 674	13	22.0	187745	14	US-11-121-086-83	Sequence 83, Appl
C 602	13	22.0	2196	9	US-10-932-182A-77504	Sequence 77504, A	C 675	13	22.0	207600	14	US-11-112-908-31	Sequence 31, Appl



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C 677	13	22.0	220895	8	US-10-775-169-88	Sequence 88, Appl	C 750	12	20.3	25	9	US-10-933-982-19151	Sequence 49151, A
C 678	13	22.0	228835	9	US-10-338-773-398	Sequence 398, App	C 751	12	20.3	25	9	US-10-933-982-116545	Sequence 116545, A
C 679	13	22.0	235033	14	US-11-157-389-1	Sequence 1, Appl1	C 752	12	20.3	25	9	US-10-933-982-147173	Sequence 147173, A
C 680	13	22.0	237326	14	US-11-157-389-2	Sequence 2, Appl1	C 753	12	20.3	25	9	US-10-933-982-158947	Sequence 158947, A
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C 682	13	22.0	393323	9	US-10-330-773-23	Sequence 23, Appl	C 755	12	20.3	25	9	US-10-933-982-217379	Sequence 217379, A
C 683	13	22.0	611587	14	US-11-117-187-209	Sequence 209, App	C 756	12	20.3	25	9	US-10-933-982-221981	Sequence 221981, A
C 684	13	22.0	1634968	7	US-10-506-454-1690	Sequence 1690, App	C 757	12	20.3	25	9	US-10-934-048A-152482	Sequence 221982, A
C 685	13	22.0		19	US-11-101-244-46246	Sequence 46246, A	C 758	12	20.3	25	9	US-10-934-048A-152482	Sequence 156241, A
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C 687	12	20.3		19	US-11-101-244-547881	Sequence 547881, A	C 760	12	20.3	25	9	US-10-934-048A-95401	Sequence 95401, A
C 688	12	20.3		19	US-11-101-244-547894	Sequence 547894, A	C 761	12	20.3	25	9	US-10-934-048A-113141	Sequence 113141, A
C 689	12	20.3		19	US-11-101-244-788515	Sequence 788515, A	C 762	12	20.3	25	9	US-11-121-849-98986	Sequence 117329, A
C 690	12	20.3		19	US-11-101-244-922808	Sequence 922808, A	C 763	12	20.3	25	14	US-11-121-849-98986	Sequence 98986, A
C 691	12	20.3		19	US-11-101-244-922823	Sequence 922823, A	C 764	12	20.3	25	14	US-11-121-849-98986	Sequence 279326, A
C 692	12	20.3		19	US-11-101-244-1007041	Sequence 1007041, A	C 765	12	20.3	25	14	US-11-121-849-283362	Sequence 283362, A
C 693	12	20.3		19	US-11-101-244-1007065	Sequence 1007065, A	C 766	12	20.3	25	14	US-11-121-849-283363	Sequence 283363, A
C 694	12	20.3		19	US-11-101-244-1034946	Sequence 1034946, A	C 767	12	20.3	25	14	US-11-121-849-283364	Sequence 283364, A
C 695	12	20.3		19	US-11-101-244-1177337	Sequence 1177337, A	C 768	12	20.3	25	14	US-11-121-849-314061	Sequence 314061, A
C 696	12	20.3		19	US-11-101-244-1391864	Sequence 1391864, A	C 769	12	20.3	25	14	US-11-121-849-327814	Sequence 316266, A
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C 699	12	20.3		19	US-11-101-244-1446765	Sequence 1446765, A	C 772	12	20.3	25	14	US-11-121-849-633273	Sequence 633273, A
C 700	12	20.3		19	US-11-083-784-46246	Sequence 46246, A	C 773	12	20.3	25	14	US-11-121-849-633273	Sequence 633274, A
C 701	12	20.3		19	US-11-083-784-502874	Sequence 502874, A	C 774	12	20.3	25	14	US-11-121-849-633274	Sequence 633275, A
C 702	12	20.3		19	US-11-083-784-547881	Sequence 547881, A	C 775	12	20.3	25	14	US-11-121-849-663329	Sequence 663329, A
C 703	12	20.3		19	US-11-083-784-547894	Sequence 547894, A	C 776	12	20.3	25	14	US-11-121-849-663330	Sequence 663330, A
C 704	12	20.3		19	US-11-083-784-788515	Sequence 788515, A	C 777	12	20.3	25	14	US-11-136-527-64483	Sequence 64483, A
C 705	12	20.3		19	US-11-083-784-922808	Sequence 922808, A	C 778	12	20.3	25	14	US-11-136-527-64493	Sequence 64493, A
C 706	12	20.3		19	US-11-083-784-922823	Sequence 922823, A	C 779	12	20.3	25	14	US-11-136-527-64493	Sequence 64495, A
C 707	12	20.3		19	US-11-083-784-1007041	Sequence 1007041, A	C 780	12	20.3	25	14	US-11-136-527-64495	Sequence 64495, A
C 708	12	20.3		19	US-11-083-784-1034946	Sequence 1034946, A	C 781	12	20.3	25	14	US-11-136-527-64498	Sequence 64498, A
C 709	12	20.3		19	US-11-083-784-1177337	Sequence 1177337, A	C 782	12	20.3	25	14	US-11-136-527-64503	Sequence 64503, A
C 710	12	20.3		19	US-11-083-784-1391864	Sequence 1391864, A	C 783	12	20.3	25	14	US-11-136-527-64508	Sequence 64508, A
C 711	12	20.3		19	US-11-083-784-1446729	Sequence 1446729, A	C 784	12	20.3	25	14	US-11-136-527-187439	Sequence 187439, A
C 712	12	20.3		19	US-11-083-784-1446757	Sequence 1446757, A	C 785	12	20.3	25	14	US-10-310-914A-1124911	Sequence 1124911, A
C 713	12	20.3		19	US-11-083-784-1446765	Sequence 1446765, A	C 786	12	20.3	26	14	US-11-146-523-2	Sequence 2, Appl1
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C 715	12	20.3		20	US-10-310-914A-598432	Sequence 598432, A	C 788	12	20.3	30	14	US-11-175-859-70527	Sequence 70527, A
C 716	12	20.3		20	US-10-310-914A-1190857	Sequence 1190857, A	C 789	12	20.3	50	14	US-11-175-859-94428	Sequence 94428, A
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C 718	12	20.3		21	US-10-770-726-37597	Sequence 37597, A	C 791	12	20.3	114	8	US-10-467-657-94301	Sequence 4301, App
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C 720	12	20.3		21	US-10-310-914A-335352	Sequence 335352, A	C 793	12	20.3	171	9	US-10-933-182A-173373	Sequence 173373, A
C 721	12	20.3		21	US-10-310-914A-563749	Sequence 563749, A	C 794	12	20.3	171	9	US-11-098-686-631	Sequence 631, App
C 722	12	20.3		22	US-10-310-914A-298913	Sequence 298913, A	C 795	12	20.3	200	14	US-11-098-686-1190	Sequence 1190, App
C 723	12	20.3		22	US-10-310-914A-598452	Sequence 598452, A	C 796	12	20.3	200	14	US-11-098-686-1457	Sequence 1457, App
C 724	12	20.3		22	US-10-310-914A-614234	Sequence 614234, A	C 797	12	20.3	200	14	US-11-098-686-1671	Sequence 1671, App
C 725	12	20.3		22	US-10-310-914A-563705	Sequence 563705, A	C 798	12	20.3	200	14	US-11-098-686-1155	Sequence 3155, App
C 726	12	20.3		23	US-10-310-914A-563722	Sequence 563722, A	C 799	12	20.3	200	14	US-11-098-686-3473	Sequence 3473, App
C 727	12	20.3		23	US-10-310-914A-563755	Sequence 563755, A	C 800	12	20.3	200	14	US-11-098-686-6675	Sequence 6675, App
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C 730	12	20.3		24	US-10-310-914A-598443	Sequence 598443, A	C 803	12	20.3	201	8	US-10-995-561-48195	Sequence 48195, A
C 731	12	20.3		24	US-10-310-914A-598453	Sequence 598453, A	C 804	12	20.3	201	8	US-10-995-561-48205	Sequence 48205, A
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C 733	12	20.3		24	US-10-310-914A-1278508	Sequence 1278508, A	C 806	12	20.3	201	8	US-10-995-561-53065	Sequence 53065, A
C 734	12	20.3		24	US-10-310-914A-1278508	Sequence 1278508, A	C 807	12	20.3	201	8	US-10-995-561-53065	Sequence 53065, A
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## ALIGNMENTS

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; Sequence 11, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugee, Thomas H.
; APPLICANT: as represented by The Government of the United States of America
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 2295
; TYPE: DNA
; ORGANISM: Bacillus anthracis
; FEATURE:
; OTHER INFORMATION: wild-type homo-oligomeric anthrax toxin protective
; OTHER INFORMATION: antigen (PrAg)
US-11-055-557-11
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; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugee, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
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; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
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US-11-055-557-15
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; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugee, Thomas H.
; APPLICANT: as represented by The Government of the United States of America
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
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; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
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; SOFTWARE: PatentIn Ver. 2.1  
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; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
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US-11-055-557-1

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; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 9  
; LENGTH: 2304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified

; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (Prag) Prag-U2-K197A (Pa-U-K197A)  
US-11-055-557-9

Query Match 100.0%; Score 59; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 2.5e-26;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCCATTAGAAAGACTAAACCGG 59  
Db 1596 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCCATTAGAAAGACTAAACCGG 1654

## RESULT 6

US-11-055-557-13  
; Sequence 13, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 2304  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:modified  
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen  
; OTHER INFORMATION: (Prag) Prag-U2  
US-11-055-557-13

Query Match 100.0%; Score 59; DB 14; Length 2304;  
Best Local Similarity 100.0%; Pred. No. 2.5e-26;  
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Query 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCCATTAGAAAGACTAAACCGG 59  
Db 1596 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCCATTAGAAAGACTAAACCGG 1654

## RESULT 7

US-11-055-557-3  
; Sequence 3, Application US/11055557  
; Publication No. US20050255083A1  
; GENERAL INFORMATION:  
; APPLICANT: Leppla, Stephen H.  
; APPLICANT: Liu, Shi-Hui  
; APPLICANT: Bugge, Thomas H.  
; APPLICANT: The Government of the United States of America  
; APPLICANT: as represented by The Secretary of the  
; APPLICANT: Department of Health and Human Services  
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having  
; TITLE OF INVENTION: Multiple Identifying Characteristics  
; FILE REFERENCE: 015280-501100US  
; CURRENT APPLICATION NUMBER: US/11/055,557  
; PRIOR FILING DATE: 2005-02-09  
; PRIOR APPLICATION NUMBER: US 60/543,417  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3



```

; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-1210A (PA-M-1210A)
US-11-055-557-3

Query Match          100.0%; Score 59; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1599 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1657

RESULT 8
US-11-055-557-5
; Sequence 5, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 5
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-K214A (PA-M-K214A)
US-11-055-557-5

Query Match          100.0%; Score 59; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1599 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1657

RESULT 9
US-11-055-557-7
; Sequence 7, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
```

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; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 7
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1-R178A (PA-M-R178A)
US-11-055-557-7

Query Match          100.0%; Score 59; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1599 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1657

RESULT 10
US-11-055-557-17
; Sequence 17, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by The Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; CURRENT FILING DATE: 2005-02-09
; PRIOR FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 17
; LENGTH: 2307
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:modified
; OTHER INFORMATION: homo-oligomeric anthrax toxin protective antigen
; OTHER INFORMATION: (PrAg) PrAg-L1
US-11-055-557-17

Query Match          100.0%; Score 59; DB 14; Length 2307;
Best Local Similarity 100.0%; Pred. No. 2.5e-26;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 59
DB 1599 GGTAGAAAGCGGATAGCGCGGTTAATCCTAGTATCATTAGAAAGCACTAAACCGG 1657

RESULT 11
US-10-889-197-42/C
; Sequence 42, Application US/10889197
; Publication No. US20050271689A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, CHUN-MING
; APPLICANT: ZHANG, JIANFENG
; APPLICANT: TANG, DE-CHU
; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
; TITLE OF INVENTION: THERAPY AGAINST ANTHRAX
```



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; FILE REFERENCE: 858610-2006.1
; CURRENT APPLICATION NUMBER: US/10/889,197
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,369
; PRIOR FILING DATE: 2003-07-11
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 42
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-889-197-42

Query Match          50.8%; Score 30; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 1,7e-08;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      9  GCGGATAGCGCGGTAACTCTAGTGATC 38
Db      30  GCGGATAGCGCGGTAACTCTAGTGATC 1

RESULT 12
US-09-925-065A-462374
; Sequence 462374, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 462374
; LENGTH: 511
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-462374

Query Match          27.1%; Score 16; DB 6; Length 511;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32  AGTGATCCATTAGAAA 47
Db      253  AGTGATCCATTAGAAA 268

RESULT 13
US-10-301-480-519085
; Sequence 519085, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 519085
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-519085

Query Match          27.1%; Score 16; DB 10; Length 517;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32  AGTGATCCATTAGAAA 47
Db      253  AGTGATCCATTAGAAA 268

RESULT 14
US-10-301-480-1132494
; Sequence 1132494, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1132494
; LENGTH: 517
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1132494

Query Match          27.1%; Score 16; DB 10; Length 517;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      32  AGTGATCCATTAGAAA 47
Db      253  AGTGATCCATTAGAAA 268

RESULT 15
US-10-301-480-573320
; Sequence 573320, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 573320
; LENGTH: 543
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```

; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-573320

```

Query Match	27.1%;	Score 16;	DB 10;	Length 543;
Best Local Similarity	100.0%;	Pred. No. 8.8;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	29	CCTAGTGATCCATTAG	44
Db	63	CCTAGTGATCCATTAG	78

RESULT 16  
US-10-301-480-1186729  
; Sequence 1186729, Application US/10301480  
; Publication No. US20060057564A1

```

1 // APPLICANT: WANG, David G.
2 // TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
3 // TITLE OF INVENTION: in the Human Genome
4 // FILE REFERENCE: 108827.137
5 // CURRENT APPLICATION NUMBER: US/10/301,480
6 // CURRENT FILING DATE: 2002-11-21
7 // PRIOR APPLICATION NUMBER: US 10/215,598
8 // PRIOR FILING DATE: 2002-08-09
9 // PRIOR APPLICATION NUMBER: US 60/311,695
10 // PRIOR FILING DATE: 2001-08-10
11 // NUMBER OF SEQ. ID NOS: 122618
12 // SOFTWARE: FASTSEQ for Windows Version 4.0
13 // SEQ. ID NO 1186729
14 // LENGTH: 543

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Query Match	27.1%;	Score 16;	DB 10;	Length 543;
Best Local Similarity	100.0%;	Pred. No. 8.8;		
Matches 16; Conservative	0;	Mismatches	0;	Indels 0;
				Gaps 0;

QY	29	CCTAGTGATCCATTAG	44
Db	63	CCTAGTGATCCATTAG	78

RESULT 17  
US-09-925-065A-655740

; Sequence 655740, Application US/09925065A  
; Publication No. US20040181048A1

```

1  APPLICATION: SINGLE-CELL GENOMICS
2  TITLE OF INVENTION: Identification and Mapping of Single
3  TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
4  FILE REFERENCE: 108827.135
5  CURRENT APPLICATION NUMBER: US/09/925, 065A
6  PRIOR FILING DATE: 2001-08-08
7  PRIOR APPLICATION NUMBER: US 60/243, 096
8  PRIOR FILING DATE: 2000-10-24
9  PRIOR APPLICATION NUMBER: US 60/252,147
10 PRIOR FILING DATE: 2000-11-20
11 PRIOR APPLICATION NUMBER: US 60/250, 092
12 PRIOR FILING DATE: 2000-11-30
13 PRIOR APPLICATION NUMBER: US 60/261, 766
14 PRIOR FILING DATE: 2001-01-16
15 PRIOR APPLICATION NUMBER: US 60/289, 846
16 PRIOR FILING DATE: 2001-05-09
17 NUMBER OF SEQ ID NOS: 957086
18 SOFTWARE: FastSeq for Windows Version 4.0
19 SEQ ID NO 655740

```

Query Match	27.1%	Score 16;	DB 6;	Length 577;
Best Local Similarity	100.0%	Pred. No. 8.8;		
Matches	16;	Conservative	0;	Mismatches
			0;	Indels
				Gaps
				0;

QY	29	CCTAGTGATCCATTAG	44
D6	264	CCTAGTGATCCATTAG	279

RESULT 18  
US-09-925-065A-655741  
; Sequence 655741, Application US/09925065A  
; Publication No. US20040181048A1

```

APPLICANT: Wang, David G.
TITLE OR INVENTION: Identification and Mapping of Single
TITLE OR INVENTION: Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 108827.13
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243, 096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289, 846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: Fast-Seq for Windows Version 4.0
SEQ ID NO 655741
LENGTH: 577
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-655741

```

Query Match	27.1%	Score 16;	DB 6;	Length 577;
Best local Similarity	100.0%	Pred. No. 8/8;	0;	Indels 0;
Matches 16; Conservative	0;	Mismatches	0;	Gaps 0;

QY		29	CCTAGTGATCCATTAG	44
Db		264	CCTAGTGATCCATTAG	279

RESULT 19  
US-09-925-065A-465382/c

```

? AFFILIATION: Wang, David S.
? TITLE OF INVENTION: Identification and Mapping of Single
? TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
? FILE REFERENCE: 108827.135
? CURRENT APPLICATION NUMBER: US/09/925,065A
? PRIORITY FILING DATE: 2001-08-08
? PRIOR APPLICATION NUMBER: US 60/243,096
? PRIOR FILING DATE: 2000-10-24
? PRIOR APPLICATION NUMBER: US 60/252,147
? PRIOR FILING DATE: 2000-11-20
? PRIOR APPLICATION NUMBER: US 60/250,092
? PRIOR FILING DATE: 2000-11-30
? PRIOR APPLICATION NUMBER: US 60/261,766
? PRIOR FILING DATE: 2001-01-16
? PRIOR APPLICATION NUMBER: US 60/289,846
? PRIOR FILING DATE: 2001-05-09
? NUMBER OF SEQ ID NOS: 957086
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 465382
? LENGTH: 594

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TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-465382

Query Match 27.1%; Score 16; DB 6; Length 594;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTGATCCATTAG 44  
DB 552 CCTAGTGATCCATTAG 537

RESULT 20  
US-10-301-480-521401/c  
Sequence 521401, Application US/10301480  
Publication No. US20060057564A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
FILE REFERENCE: 108827.137  
CURRENT APPLICATION NUMBER: US/10/301,480  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 10/215,598  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,695  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 1226818  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 521401  
LENGTH: 597  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-301-480-521401

Query Match 27.1%; Score 16; DB 10; Length 597;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTGATCCATTAG 44  
DB 552 CCTAGTGATCCATTAG 537

RESULT 21  
US-10-301-480-1134810/c  
Sequence 1134810, Application US/10301480  
Publication No. US20060057564A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
FILE REFERENCE: 108827.137  
CURRENT APPLICATION NUMBER: US/10/301,480  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 10/215,598  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,695  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 1226818  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 1134810  
LENGTH: 597  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-301-480-1134810

Query Match 27.1%; Score 16; DB 10; Length 597;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTGATCCATTAG 44

DB 552 CCTAGTGATCCATTAG 537

RESULT 22  
US-09-925-065A-225901  
Sequence 225901, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 225901  
LENGTH: 612  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-225901

Query Match 27.1%; Score 16; DB 6; Length 612;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTGATCCATTAG 44  
DB 21 CCTAGTGATCCATTAG 36

RESULT 23  
US-10-301-480-310425  
Sequence 310425, Application US/10301480  
Publication No. US20060057564A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
FILE REFERENCE: 108827.137  
CURRENT APPLICATION NUMBER: US/10/301,480  
CURRENT FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 10/215,598  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,695  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 1226818  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 310425  
LENGTH: 615  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-301-480-310425

Query Match 27.1%; Score 16; DB 10; Length 615;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTGATCCATTAG 44  
DB 24 CCTAGTGATCCATTAG 39



```
RESULT 24
US-10-301-480-923834
; Sequence 923834, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT FILING DATE: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923834
; LENGTH: 615
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-923834

Query Match      27.1%; Score 16; DB 10; Length 615;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      29 CCTAGTGCATTG 44
DB      24 CCTAGTGCATTG 39

RESULT 25
US-10-750-185-40775
; Sequence 40775, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40775
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Bovine 19866881356188
US-10-750-185-40775

Query Match      27.1%; Score 16; DB 8; Length 989;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 GTGATCCATTAGAAC 48
DB      780 GTGATCCATTAGAAC 795

RESULT 26
US-10-750-623-40775
; Sequence 40775, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
```

```
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40775
; LENGTH: 989
; TYPE: DNA
; ORGANISM: Bovine 19866881356188
US-10-750-623-40775

Query Match      27.1%; Score 16; DB 8; Length 989;
Best Local Similarity 100.0%; Pred. No. 9.1;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      33 GTGATCCATTAGAAC 48
DB      780 GTGATCCATTAGAAC 795

RESULT 27
US-11-101-244-431839
; Sequence 431839, Application US/11101244
; Publication No. US20050246794A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13499US
; CURRENT APPLICATION NUMBER: US/11/101,244
; CURRENT FILING DATE: 2005-04-07
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 431839
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-101-244-431839

Query Match      25.4%; Score 15; DB 12; Length 19;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

QY      23 GTTAATCTAGTAT 37
DB      4 GUUAUCCUAGUGAU 18

RESULT 28
US-11-083-784-431839
; Sequence 431839, Application US/11083784
; Publication No. US20050245475A1
; GENERAL INFORMATION:
; APPLICANT: Dharmacon, Inc.
; APPLICANT: Khvorova, Anastasia
```



```

; APPLICANT: Reynolds, Angela
; APPLICANT: Leake, Devin
; APPLICANT: Marshall, William
; APPLICANT: Scaringe, Stephen
; TITLE OF INVENTION: Functional and Hyperfunctional siRNA
; FILE REFERENCE: 13493US
; CURRENT APPLICATION NUMBER: US/11/083,784
; CURRENT FILING DATE: 2005-03-18
; PRIOR APPLICATION NUMBER: US/10/714,333
; PRIOR FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: 60/502,050
; PRIOR FILING DATE: 2003-09-10
; PRIOR APPLICATION NUMBER: 60/426,137
; PRIOR FILING DATE: 2002-11-14
; NUMBER OF SEQ ID NOS: 1591911
; SOFTWARE: Proprietary
; SEQ ID NO 431839
; LENGTH: 19
; TYPE: RNA
; ORGANISM: Homo sapiens
US-11-083-784-431839

Query Match          25.4%; Score 15; DB 13; Length 19;
Best Local Similarity 60.0%; Pred. No. 31;
Matches 9; Conservative 6; Mismatches 0; Indels 0; Gaps 0;

Oy      23 GTTATCCTAGTGAT 37
Db      4 GUDAAUCCUAGUGAU 18

RESULT 29
US-11-124-368A-12412
; Sequence 12412, Application US/11124368A
; Publication No. US20050287559A1
; GENERAL INFORMATION:
; APPLICANT: Michele Cargill
; APPLICANT: James J. Devlin
; APPLICANT: May Luke
; TITLE OF INVENTION: Genetic Polymorphisms Associated with
; TITLE OF INVENTION: Vascular Diseases, Methods of Detection and Uses Thereof
; FILE REFERENCE: CL001524
; CURRENT APPLICATION NUMBER: US/11/124,368A
; CURRENT FILING DATE: 2005-05-09
; PRIOR APPLICATION NUMBER: US 60/568,845
; PRIOR FILING DATE: 2004-05-07
; PRIOR APPLICATION NUMBER: US 60/625,936
; PRIOR FILING DATE: 2004-11-09
; NUMBER OF SEQ ID NOS: 21112
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12412
; LENGTH: 201
; TYPE: DNA
; ORGANISM: Homo sapiens
US-11-124-368A-12412

Query Match          25.4%; Score 15; DB 14; Length 201;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      24 TTAATCCTAGTGATC 38
Db      118 TTAATCCTAGTGATC 132

RESULT 30
US-09-925-065A-192307
; Sequence 192307, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```

; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 192307
; LENGTH: 455
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-192307

Query Match          25.4%; Score 15; DB 6; Length 455;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      29 CCTAGTATCCATTA 43
Db      408 CCTAGTATCCATTA 422

RESULT 31
US-10-301-480-281859
; Sequence 281859, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 281859
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-281859

Query Match          25.4%; Score 15; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      29 CCTAGTATCCATTA 43
Db      411 CCTAGTATCCATTA 425

RESULT 32
US-10-301-480-895268
; Sequence 895268, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
```



```

; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 895268
; LENGTH: 458
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-895268
```

```

Query Match      25.4%; Score 15; DB 10; Length 458;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      29 CCTAGTGATCCATT 43
Db      411 CCTAGTGATCCATT 425
```

```

RESULT 33
US-10-301-480-275388
; Sequence 275388, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275388
; LENGTH: 562
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-275388
```

```

Query Match      25.4%; Score 15; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      29 CCTAGTGATCCATT 43
Db      91 CCTAGTGATCCATT 105
```

```

RESULT 34
US-10-301-480-888797
; Sequence 888797, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 888797
; LENGTH: 562
; TYPE: DNA
```

```

; ORGANISM: Homo sapien
US-10-301-480-888797
```

```

Query Match      25.4%; Score 15; DB 10; Length 562;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      29 CCTAGTGATCCATT 43
Db      91 CCTAGTGATCCATT 105
```

```

RESULT 35
US-09-925-065A-488195/c
; Sequence 488195, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 488195
; LENGTH: 563
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-488195
```

```

Query Match      25.4%; Score 15; DB 6; Length 563;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      37 TCCATTAGAAACGAC 51
Db      542 TCCATTAGAAACGAC 528
```

```

RESULT 36
US-09-925-065A-185140/c
; Sequence 185140, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
```



SEQ ID NO 185140  
LENGTH: 564  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-185140

Query Match 25.4%; Score 15; DB 6; Length 564;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 29 CTTAGTATCCATT 43  
|||||  
Db 473 CTTAGTATCCATT 459

RESULT 37  
US-09-925-065A-471480  
Sequence 471480, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 471480  
LENGTH: 616  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-471480

Query Match 25.4%; Score 15; DB 6; Length 616;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 TTATCTAGTATC 38  
|||||  
Db 445 TTATCTAGTATC 459

RESULT 38  
US-10-750-185-32769/c  
Sequence 32769, Application US/10750185  
Publication No. US20050260603A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFIELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-2  
CURRENT APPLICATION NUMBER: US/10/750,185  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1

SEQ ID NO 32769  
LENGTH: 832  
TYPE: DNA  
ORGANISM: Bovine  
US-10-750-185-32769

Query Match 25.4%; Score 15; DB 8; Length 832;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TGATCCATTAGAAAC 48  
|||||  
Db 278 TGATCCATTAGAAAC 264

RESULT 39  
US-10-750-623-32769/c  
Sequence 32769, Application US/10750623  
Publication No. US20050267531A1  
GENERAL INFORMATION:  
APPLICANT: MMI GENOMICS, INC.  
APPLICANT: DENISE, Sue K.  
APPLICANT: KERR, Richard  
APPLICANT: ROSENFIELD, David  
APPLICANT: HOLM, Tom  
APPLICANT: BATES, Stephen  
APPLICANT: FANTIN, Dennis  
TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
FILE REFERENCE: MM1100-1  
CURRENT APPLICATION NUMBER: US/10/750,623  
CURRENT FILING DATE: 2003-12-31  
PRIOR APPLICATION NUMBER: US 60/437,482  
PRIOR FILING DATE: 2002-12-31  
NUMBER OF SEQ ID NOS: 64922  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 32769  
LENGTH: 832  
TYPE: DNA  
ORGANISM: Bovine  
US-10-750-623-32769

Query Match 25.4%; Score 15; DB 8; Length 832;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 34 TGATCCATTAGAAAC 48  
|||||  
Db 278 TGATCCATTAGAAAC 264

RESULT 40  
US-09-925-065A-551799  
Sequence 551799, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
CURRENT FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0



; SEQ ID NO 551799  
; LENGTH: 983  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-551799

Query Match 25.4%; Score 15; DB 6; Length 983;  
Best Local Similarity 100.0%; Pred. No. 38;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 TCCTAGTGATCCATT 42  
Db 315 TCCTAGTGATCCATT 329

Search completed: April 12, 2006, 07:07:45  
Job time : 249.963 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 812.351 Seconds  
(without alignments)  
3398.084 Million cell updates/sec

Title: US-10-712-654-24

Perfect score: 59

Sequence: 1 ggtagaagcgcgatagcg.....attagaacgactaacgg 59

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 2339354128 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_hic:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_est7:\*  
9: gb\_gse1:\*  
10: gb\_gse2:\*  
11: gb\_gse3:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32.2	221	10	CE516034	CE516034 t1gr-g88-
2	32.2	430	11	CR067686	CR067686 Reverse 8
3	32.2	518	9	BH042558	BH042558 RPT-24-3
4	32.2	664	9	AO974432	AO974432 RPT-23-3
5	32.2	660	8	CA432289	CA432289 JGI_XZ62
6	30.5	730	9	AZ400559	AZ400559 IM0166123
7	30.5	773	9	BZ267479	BZ267479 CH230-315
8	30.5	773	8	DR813392	DR813392 ZM_BFB004
9	30.5	853	9	CC679999	CC679999 OGKAV887C
10	30.5	891	9	BZ728527	BZ728527 OGBRJ487C
11	28.8	265	10	CE296452	CE296452 t1gr-g88-
12	28.8	342	10	CE776306	CE776306 t1gr-g88-
13	28.8	388	10	CE454063	CE454063 t1gr-g88-
14	28.8	390	10	CE561277	CE561277 t1gr-g88-
15	28.8	443	2	BF294016	BF294016 WHE2162 H
16	28.8	446	9	AO490035	AO490035 RPT-11-2
17	28.8	471	9	AZ653505	AZ653505 1M0527008
18	28.8	516	9	AO439149	AO439149 HS_5051_A
19	28.8	534	11	CNS07HW8	AL611594 Atopheles
20	28.8	602	10	CE327120	CE327120 t1gr-g88-
21	28.8	624	10	CE655765	CE655765 t1gr-g88-
22	28.8	648	1	AV374156	AV374156 AV374156

23	17	28.8	652	10	CW975216	CW975216 A1AA-aaa8
24	17	28.8	654	9	AZ51768	AZ51768 1M0090A04
25	17	28.8	694	9	CE047792	CE047792 t1gr-g88-
26	17	28.8	730	9	CE068977	CE068977 t1gr-g88-
27	17	28.8	741	10	CE427878	CE427878 t1gr-g88-
28	17	28.8	743	10	CG293819	CG293819 OGBH59TH
29	17	28.8	748	9	AO894668	AO894668 HS_3148_A
30	17	28.8	749	9	AZ883925	AZ883925 RPT-23-2
31	17	28.8	792	9	AZ992510	AZ992510 2M0277N08
32	17	28.8	801	6	CF451309	CF451309 EST687654
33	17	28.8	816	11	CR221675	CR221675 Reverse 8
34	17	28.8	846	9	BZ702421	BZ702421 PUCDD13TD
35	17	28.8	848	10	CG262429	CG262429 OGBM53TV
36	17	28.8	918	10	CG305394	CG305394 OGB3C16TH
37	17	28.8	1042	10	CG431663	CG431663 Bg156-T3
38	17	28.8	1346	10	AG052577	AG052577 Pan t1og1
39	17	28.8	1366	4	AK035963	AK035963 Mus muscu
40	17	28.8	255	4	CNS080DT	CE196377 t1gr-g88-
41	16	27.1	282	9	CE196377	CE196377 t1gr-g88-
42	16	27.1	285	10	CG837672	CG837672 ZMMBR-C021
43	16	27.1	303	9	AZ449803	AZ449803 1M0248P11
44	16	27.1	307	11	AO355879	AO355879 CITR1-E1-
45	16	27.1	312	10	CE701386	CE701386 t1gr-g88-
46	16	27.1	335	10	CE417492	CE417492 t1gr-g88-
47	16	27.1	336	10	CE681667	CE681667 t1gr-g88-
48	16	27.1	343	8	NA5792	NA5792 T1467 MVAR4
49	16	27.1	355	9	BH065349	BH065349 RPT-24-3
50	16	27.1	357	10	CE300624	CE300624 t1gr-g88-
51	16	27.1	367	5	BX276702	BX276702 BX276702
52	16	27.1	374	10	CE538167	CE538167 t1gr-g88-
53	16	27.1	379	10	CM451304	CM451304 f6bd001f1
54	16	27.1	394	10	CE703069	CE703069 t1gr-g88-
55	16	27.1	398	3	BW736574	BW736574 952038C07
56	16	27.1	405	1	AV811589	AV811589 AV811589
57	16	27.1	409	3	BM660669	BM660669 952040F08
58	16	27.1	422	10	CE484138	CE484138 t1gr-g88-
59	16	27.1	423	10	CE112615	CE112615 t1gr-g88-
60	16	27.1	423	10	CL876601	CL876601 abf14903.
61	16	27.1	424	10	CE384201	CE384201 t1gr-g88-
62	16	27.1	429	10	CE736028	CE736028 t1gr-g88-
63	16	27.1	430	6	CD744529	CD744529 IRB18_B12
64	16	27.1	430	10	CE557200	CE557200 t1gr-g88-
65	16	27.1	434	10	CM021312	CM021312 104_160_1
66	16	27.1	446	5	BX567400	BX567400 BX567400
67	16	27.1	459	3	BM587366	BM587366 170006873
68	16	27.1	461	10	CE828358	CE828358 t1gr-g88-
69	16	27.1	462	1	AW399461	AW399461 EST30961
70	16	27.1	476	10	CE535167	CE535167 t1gr-g88-
71	16	27.1	479	10	CG033341	CG033341 PURU108TB
72	16	27.1	495	10	CE466242	CE466242 t1gr-g88-
73	16	27.1	496	9	CE228545	CE228545 t1gr-g88-
74	16	27.1	499	10	CE334502	CE334502 t1gr-g88-
75	16	27.1	505	9	AO826776	AO826776 HS_5495_B
76	16	27.1	506	10	CM248559	CM248559 104_710_1
77	16	27.1	507	9	CE251308	CE251308 t1gr-g88-
78	16	27.1	509	3	BM606627	BM606627 170006870
79	16	27.1	509	9	CE126365	CE126365 t1gr-g88-
80	16	27.1	513	9	CE244383	CE244383 t1gr-g88-
81	16	27.1	513	6	CD744528	CD744528 IRB203_F1
82	16	27.1	514	1	AW641163	AW641163 cm04a11.w
83	16	27.1	514	10	BX194833	BX194833 Danilo rer
84	16	27.1	517	10	CE589670	CE589670 t1gr-g88-
85	16	27.1	522	7	CE268379	CE268379 t1gr-g88-
86	16	27.1	526	7	CR755318	CR755318 CR755318
87	16	27.1	527	7	CR755318	CR755318 CR755318
88	16	27.1	527	9	AZ282746	AZ282746 RPT-23-1
89	16	27.1	529	10	CG230824	CG230824 OGVV85TH
90	16	27.1	546	8	CY183934	CY183934 A04_45-53
91	16	27.1	560	7	CO617030	CO617030 DG9-17095
92	16	27.1	567	3	BQ047881	BQ047881 952045E03
93	16	27.1	569	6	CD744527	CD744527 IRB5_G11
94	16	27.1	573	9	AO607175	AO607175 HS_5326_B
95	16	27.1	581	9	AO285673	AO285673 RPT111-69



c 96	16	27.1	586	9	CE168317	CE168317 t1gr-g88-	169	16	27.1	789	10	CG131764	CG131764 PUEBNT6TB
c 97	16	27.1	590	10	CG802327	CG802327 g118029D	c 170	16	27.1	791	10	CG272203	CG272203 OGXCIN15T
c 98	16	27.1	597	9	BH745243	BH745243 gu77h05_b	c 171	16	27.1	795	2	BE033977	BE033977 MG0H04_M
c 99	16	27.1	597	9	CE000502	CE000502 t1gr-g88-	c 172	16	27.1	797	9	CC703544	CC703544 OGJG35TH
c 100	16	27.1	599	10	AG953994	AG953994 Di080p11	c 173	16	27.1	799	5	BX081512	BX081512 BX081512
c 101	16	27.1	600	10	CG781340	CG781340 1123044F0	c 174	16	27.1	809	10	CL930143	CL930143 OA_Aba003
c 102	16	27.1	601	9	CE096168	CE096168 t1gr-g88-	c 175	16	27.1	814	6	AG895216	AG895216 EST648008
c 103	16	27.1	604	10	CE775306	CE775306 t1gr-g88-	c 176	16	27.1	835	10	CB827367	CB827367 Suf_acroF
c 104	16	27.1	605	8	CX259990	CX259990 1313368_N	c 177	16	27.1	836	7	CV120423	CV120423 AGENCOURT
c 105	16	27.1	609	9	CE016048	CE016048 t1gr-g88-	c 178	16	27.1	836	9	B2967175	B2967175 PUGG189TB
c 106	16	27.1	610	10	CE515481	CE515481 t1gr-g88-	c 179	16	27.1	841	9	CC847156	CC847156 NDJ_11F9
c 107	16	27.1	613	9	CE073185	CE073185 t1gr-g88-	c 180	16	27.1	856	9	B2141560	B2141560 CH230-245
c 108	16	27.1	614	9	CC384991	CC384991 PUES21TB	c 181	16	27.1	857	7	CC0799605	CC0799605 AGENCOURT
c 109	16	27.1	614	10	CE630535	CE630535 t1gr-g88-	c 182	16	27.1	862	9	CC705375	CC705375 OGUF859TV
c 110	16	27.1	614	10	CE751231	CE751231 t1gr-g88-	c 183	16	27.1	865	10	C2235634	C2235634 A1MA_aag1
c 111	16	27.1	616	10	CE838050	CE838050 t1gr-g88-	c 184	16	27.1	867	9	BH280696	BH280696 CH230-49E
c 112	16	27.1	621	10	CE853242	CE853242 t1gr-g88-	c 185	16	27.1	873	10	CG272197	CG272197 OGXCIN15TH
c 113	16	27.1	622	1	AM645479	AM645479 cm53d06_w	c 186	16	27.1	879	10	CG768705	CG768705 TCB49_3_G
c 114	16	27.1	624	3	BM577495	BM577495 170006871	c 187	16	27.1	887	2	BE036002	BE036002 MO17H09_M
c 115	16	27.1	625	3	BI931634	BI931634 EST551523	c 188	16	27.1	887	6	CA512123	CA512123 UI-R-FU0-
c 116	16	27.1	625	6	CB545428	CB545428 AMGNNUC-C	c 189	16	27.1	892	6	CD327616	CD327616 AGENCOURT
c 117	16	27.1	625	10	CE773725	CE773725 t1gr-g88-	c 190	16	27.1	894	10	AG828969	AG828969 Suf_acroF
c 118	16	27.1	629	10	CE737946	CE737946 104_523_1	c 191	16	27.1	906	9	CC014619	CC014619 PUDT90TD
c 119	16	27.1	629	10	CE471317	CE471317 t1gr-g88-	c 192	16	27.1	907	10	CNS00CRH	AL055646 Di080p11
c 120	16	27.1	632	5	BX081511	BX081511 BX081511	c 193	16	27.1	917	10	CL472713	CL472713 SA1L_184
c 121	16	27.1	633	9	CE059539	CE059539 t1gr-g88-	c 194	16	27.1	919	9	CC703551	CC703551 OGUG36TV
c 122	16	27.1	634	9	CE247634	CE247634 t1gr-g88-	c 195	16	27.1	921	7	CK268586	CK268586 EST714664
c 123	16	27.1	636	9	CE000647	CE000647 t1gr-g88-	c 196	16	27.1	939	2	BR378843	BR378843 601237370
c 124	16	27.1	639	10	CE708421	CE708421 t1gr-g88-	c 197	16	27.1	940	10	CG770101	CG770101 TCB50_4_E
c 125	16	27.1	641	9	CE077802	CE077802 t1gr-g88-	c 198	16	27.1	940	10	CM954546	CM954546 TCB49_4_H
c 126	16	27.1	645	10	CE751088	CE751088 t1gr-g88-	c 199	16	27.1	950	10	CG455036	CG455036 PUKY74TB
c 127	16	27.1	646	10	CE577058	CE577058 t1gr-g88-	c 200	16	27.1	950	2	BG251889	BG251889 602364511
c 128	16	27.1	653	9	CC572936	CC572936 CH240_449	c 201	16	27.1	972	10	CL490354	CL490354 SA1L_536
c 129	16	27.1	660	9	CE203405	CE203405 t1gr-g88-	c 202	16	27.1	979	9	B2557158	B2557158 Single_re
c 130	16	27.1	664	11	CR822335	CR822335 GR04AA52A	c 203	16	27.1	979	9	B2557158	B2557158 pac81-60
c 131	16	27.1	669	9	CE133610	CE133610 t1gr-g88-	c 204	16	27.1	988	6	CD253481	CD253481 AGENCOURT
c 132	16	27.1	670	10	AG033623	AG033623 Pan_txcg1	c 205	16	27.1	1016	11	CNS073XN	AL428097 clone BAO
c 133	16	27.1	671	10	CG913248	CG913248 ZMMBB037	c 206	16	27.1	1024	4	CNS08BYA	BX036014 Single_re
c 134	16	27.1	672	7	CF893304	CF893304 A012E12-	c 207	16	27.1	1056	5	B0876690	B0876690 AGENCOURT
c 135	16	27.1	673	7	CR999296	CR999296 CR999296	c 208	16	27.1	1061	6	CD455767	CD455767 TMMpMfc10
c 136	16	27.1	673	10	CG320188	CG320188 OG5AH60TC	c 209	16	27.1	1101	10	CNS00G7M	AL071748 Di080p11
c 137	16	27.1	676	9	CE172172	CE172172 t1gr-g88-	c 210	16	27.1	1120	10	CL237086	CL237086 ZMMBB058
c 138	16	27.1	676	10	CM136947	CM136947 104_523_1	c 211	16	27.1	1175	3	BI334983	BI334983 602998876
c 139	16	27.1	679	10	CE457335	CE457335 t1gr-g88-	c 212	16	27.1	1324	2	BG643982	BG643982 102400400
c 140	16	27.1	681	9	CE246486	CE246486 t1gr-g88-	c 213	16	27.1	1681	2	BE777756	BE777756 601348229
c 141	16	27.1	687	10	CE675830	CE675830 t1gr-g88-	c 214	15	25.4	128	9	BH799253	BH799253 1008107C0
c 142	16	27.1	687	10	CE800149	CE800149 t1gr-g88-	c 215	15	25.4	213	10	CB586883	CB586883 t1gr-g88-
c 143	16	27.1	695	9	CE167628	CE167628 t1gr-g88-	c 216	15	25.4	220	10	CM364760	CM364760 f8bD001F0
c 144	16	27.1	696	2	BE161696	BE161696 MR3-HT044	c 217	15	25.4	245	1	AM659437	AM659437 96606 MAR
c 145	16	27.1	696	6	CA356833	CA356833 629096_NC	c 218	15	25.4	267	9	CE081876	CE081876 t1gr-g88-
c 146	16	27.1	698	6	CA245321	CA245321 SCBGF1507	c 219	15	25.4	282	1	BB052229	BB052229 BB052229
c 147	16	27.1	707	3	BJ078522	BJ078522 BJ078522	c 220	15	25.4	289	7	CM630909	CM630909 taF53b03.
c 148	16	27.1	707	9	CE079833	CE079833 t1gr-g88-	c 221	15	25.4	290	1	AM831875	AM831875 bm36906_Y
c 149	16	27.1	709	9	AO933709	AO933709 RPCI-23-2	c 222	15	25.4	309	1	BB163687	BB163687 BB163687
c 150	16	27.1	709	10	CE401850	CE401850 t1gr-g88-	c 223	15	25.4	310	1	AM010795	AM010795 AM010795
c 151	16	27.1	710	9	BH940247	BH940247 odF76C05.	c 224	15	25.4	310	2	BE325394	BE325394 NF087E06S
c 152	16	27.1	710	9	BZ053579	BZ053579 jnq98b10.	c 225	15	25.4	314	10	CB373996	CB373996 t1gr-g88-
c 153	16	27.1	711	9	CE092267	CE092267 t1gr-g88-	c 226	15	25.4	316	9	AZ715885	AZ715885 PPCI-24-H
c 154	16	27.1	713	10	CL774603	CL774603 OR_BB4008	c 227	15	25.4	321	6	CB145278	CB145278 K-BEST0200
c 155	16	27.1	715	10	CL852753	CL852753 OR_CBA008	c 228	15	25.4	326	1	AJ801273	AJ801273 AJ801273
c 156	16	27.1	720	10	CE296643	CE296643 t1gr-g88-	c 229	15	25.4	333	1	AM674084	AM674084 ba58f02_Y
c 157	16	27.1	721	2	BG647658	BG647658 BST509277	c 230	15	25.4	341	1	AA306309	AA306309 EST177273
c 158	16	27.1	733	10	CE804693	CE804693 t1gr-g88-	c 231	15	25.4	346	1	AU293293	AU293293 AU293293
c 159	16	27.1	744	10	CE839189	CE839189 t1gr-g88-	c 232	15	25.4	353	9	AZ616324	AZ616324 1M0446004
c 160	16	27.1	745	9	BZ787999	BZ787999 PUFBC31TB	c 233	15	25.4	355	9	AZ806540	AZ806540 2M0068111
c 161	16	27.1	746	4	CNS09GHW	BX057456 Single_re	c 234	15	25.4	360	1	AJ484797	AJ484797 AJ484797
c 162	16	27.1	753	9	BH718895	BH718895 BOMPL42TR	c 235	15	25.4	366	7	CM631244	CM631244 taF53b03.
c 163	16	27.1	756	11	CR822410	CR822410 GR0AA52A	c 236	15	25.4	368	10	CG777126	CG777126 1123052C0
c 164	16	27.1	758	9	CC790105	CC790105 ZMMBB015	c 237	15	25.4	372	7	CE246792	CE246792 t1gr-g88-
c 165	16	27.1	759	10	AG557141	AG557141 Mus_muscu	c 238	15	25.4	375	9	CK767993	CK767993 nad03_1c8
c 166	16	27.1	765	10	AG493316	AG493316 Mus_muscu	c 239	15	25.4	375	9	BH917469	BH917469 3526_1_56
c 167	16	27.1	765	10	CG133269	CG133269 PUEBKT77TB	c 240	15	25.4	381	9	CC597747	CC597747 ZMMBB040
c 168	16	27.1	776	10	CNS01GWM	AL143329 Anopheles	c 241	15	25.4	382	7	CN771991	CN771991 tad94a06.



242	15	25.4	391	7	CN414549	170005321	315	15	25.4	568	10	CT723288	CL723288 OR_BBa005
243	15	25.4	395	3	BP824914	BP824914	316	15	25.4	569	6	CA767438	CA767438 AP53-Rpf
244	15	25.4	395	3	A0849579	LMARFV1_1	317	15	25.4	572	9	CE244904	CE224904 t1gr-g8s-
245	15	25.4	397	1	AT043992	UT-R-C1-j	318	15	25.4	574	1	AT806323	AT806323 AT806323
246	15	25.4	404	10	CG781342	1123044F0	319	15	25.4	574	6	CD659785	CD659785 EctSteF37
247	15	25.4	407	1	AV806897	AV806897	320	15	25.4	574	10	CB492344	CB492344 t1gr-g8s-
248	15	25.4	409	6	CD700511	CD700511	321	15	25.4	575	3	BM521814	BM521814 sak76d10.
249	15	25.4	416	9	BH800978	BH800978	322	15	25.4	575	4	AY808994	AY808994 SchiSto80
250	15	25.4	418	10	CE653797	CE653797	323	15	25.4	575	5	BK732580	BK732580 BX732580
251	15	25.4	419	1	AA136680	AA136680	324	15	25.4	581	3	BP200412	BP200412 BP200412
252	15	25.4	419	1	AA136680	AA136680	325	15	25.4	581	3	BP338383	BP338383
253	15	25.4	423	1	BH807998	BH807998	326	15	25.4	581	7	CO259336	CO259336 4130772 B
254	15	25.4	423	1	AV421409	AV421409	327	15	25.4	582	3	BP205188	BP205188 BP205188
255	15	25.4	425	10	CM054302	CM054302	328	15	25.4	582	3	BP248066	BP248066 BP248066
256	15	25.4	426	11	CR153709	CR153709	329	15	25.4	582	3	BP257904	BP257904 BP257904
257	15	25.4	428	9	A0858344	A0858344	330	15	25.4	584	1	AM965815	AM965815
258	15	25.4	431	2	BF545336	BF545336	331	15	25.4	587	1	AV995618	AV995618 AV995618
259	15	25.4	434	10	C2912760	C2912760	332	15	25.4	587	6	CD342494	CD342494 EctSteF52
260	15	25.4	438	7	CO541253	CO541253	333	15	25.4	589	3	BI504924	BI504924
261	15	25.4	438	9	BH800998	BH800998	334	15	25.4	589	9	BH917467	BH917467
262	15	25.4	440	1	AZ923525	AZ923525	335	15	25.4	590	10	CZ631334	CZ631334 OM_Ba017
263	15	25.4	441	1	AA404617	AA404617	336	15	25.4	591	9	BH892356	BH892356 3526_1_20
264	15	25.4	452	5	BU649222	BU649222	337	15	25.4	591	10	CZ039308	CZ039308 OM_Ba002
265	15	25.4	453	7	CN771740	CN771740	338	15	25.4	592	3	BP237823	BP237823 BP237823
266	15	25.4	456	10	BX974036	BX974036	339	15	25.4	593	10	CG782211	CG782211 1123049C0
267	15	25.4	461	1	AA816716	AA816716	340	15	25.4	594	5	BQ470183	BQ470183 HX02A11r
268	15	25.4	468	10	CW757905	CW757905	341	15	25.4	594	6	CB64983	CB64983 OSUNET15A
269	15	25.4	477	10	CE516517	CE516517	342	15	25.4	598	6	CA269049	CA269049 SCRUR1306
270	15	25.4	479	9	BH339302	BH339302	343	15	25.4	598	10	CM402799	CM402799 fdbb001f0
271	15	25.4	480	9	AZ233378	AZ233378	344	15	25.4	600	7	CF843205	CF843205 p8HB001f0
272	15	25.4	487	2	BI196125	BI196125	345	15	25.4	600	9	BH876435	BH876435 h121b01_9
273	15	25.4	489	7	CZ606384	CZ606384	346	15	25.4	600	10	CM258118	CM258118 104_723_1
274	15	25.4	489	7	CN035177	CN035177	347	15	25.4	603	6	CF481659	CF481659 POL1_73_F
275	15	25.4	496	1	AA056283	AA056283	348	15	25.4	604	2	BG503323	BG503323 602550734
276	15	25.4	500	1	AJ805629	AJ805629	349	15	25.4	605	10	CM4559139	CM4559139 fdbb001f2
277	15	25.4	503	3	BM305520	BM305520	350	15	25.4	605	10	AG257031	AG257031 Lotus cor
278	15	25.4	503	10	BX233064	BX233064	351	15	25.4	606	10	CM221580	CM221580 104_656_1
279	15	25.4	506	1	AI708680	AI708680	352	15	25.4	609	9	AO713620	AO713620 HS_2093_B
280	15	25.4	506	1	AM675027	AM675027	353	15	25.4	611	3	BO402124	BO402124 BU042124
281	15	25.4	507	10	CZ654913	CZ654913	354	15	25.4	611	6	CA269053	CA269053 SCRUR1306
282	15	25.4	512	6	CA629499	CA629499	355	15	25.4	615	10	CZ648623	CZ648623 t1gr-g8s-
283	15	25.4	516	10	CN101843	CN101843	356	15	25.4	615	10	CE321251	CE321251 t1gr-g8s-
284	15	25.4	516	10	BX188133	BX188133	357	15	25.4	616	2	BG502134	BG502134 602554881
285	15	25.4	517	9	BZ160725	BZ160725	358	15	25.4	616	9	BM876434	BM876434 h121b01_b
286	15	25.4	518	6	CA662157	CA662157	359	15	25.4	619	7	CN101842	CN101842 EC2CA19D
287	15	25.4	527	9	AZ394857	AZ394857	360	15	25.4	620	7	CN414546	CN414546 170005999
288	15	25.4	527	10	CM447069	CM447069	361	15	25.4	621	8	CX525923	CX525923 b13DNF32D
289	15	25.4	532	10	CF875457	CF875457	362	15	25.4	622	10	CZ623582	CZ623582 OM_Ba016
290	15	25.4	535	6	CF806542	CF806542	363	15	25.4	624	5	BU675201	BU675201 UI-GF-D01
291	15	25.4	538	7	CF850584	CF850584	364	15	25.4	624	8	DR002583	DR002583 TC107306
292	15	25.4	539	6	CF483812	CF483812	365	15	25.4	625	7	CF839861	CF839861 p8HB004xC
293	15	25.4	541	9	CC880780	CC880780	366	15	25.4	626	9	AO258333	AO258333 nbx0020M
294	15	25.4	541	10	CG777220	CG777220	367	15	25.4	628	10	CM252882	CM252882 104_716_1
295	15	25.4	545	3	BP512353	BP512353	368	15	25.4	631	8	DR701471	DR701471 A8T_00946
296	15	25.4	545	10	AG241644	AG241644	369	15	25.4	632	9	BZ315256	BZ315256 1A6fT05.D
297	15	25.4	548	1	AA944049	AA944049	370	15	25.4	632	9	BM833877	BM833877 K-EST0108
298	15	25.4	549	10	CG775479	CG775479	371	15	25.4	638	3	CD692747	CD692747 EST9270 h
299	15	25.4	551	7	CF844120	CF844120	372	15	25.4	638	9	BZ756315	BZ756315 PUDCT45TD
300	15	25.4	551	9	BZ266823	BZ266823	373	15	25.4	639	3	BI507346	BI507346
301	15	25.4	552	10	CZ608380	CZ608380	374	15	25.4	639	8	DN968993	DN968993 ISPL-P9-A
302	15	25.4	554	10	CG777082	CG777082	375	15	25.4	639	9	BZ756312	BZ756312 PUDCT45TB
303	15	25.4	554	1	AA944049	AA944049	376	15	25.4	640	9	CC966140	CC966140 B0IDY93TR
304	15	25.4	554	7	AJ798367	AJ798367	377	15	25.4	641	11	DE069198	DE069198 Oryzias_1
305	15	25.4	558	1	CF954016	CF954016	378	15	25.4	644	1	AL596753	AL596753 CIT-HSP-205
306	15	25.4	559	3	BM092933	BM092933	379	15	25.4	647	9	BG584188	BG584188 DKPZ045ID
307	15	25.4	561	7	CN444358	CN444358	380	15	25.4	647	1	BM584188	BM584188 S014111-0
308	15	25.4	562	10	CM833615	CM833615	381	15	25.4	650	5	AZ521971	AZ521971 200PB507
309	15	25.4	563	1	AM142403	AM142403	382	15	25.4	654	2	BG502023	BG502023 602548355
310	15	25.4	563	2	BP281524	BP281524	383	15	25.4	654	3	BJ019848	BJ019848
311	15	25.4	563	3	BP240116	BP240116	384	15	25.4	654	10	CZ634932	CZ634932 OM_Ba017
312	15	25.4	563	10	CG775433	CG775433	385	15	25.4	657	3	BJ749229	BJ749229
313	15	25.4	568	1	AI755869	AI755869	386	15	25.4	657	10	CW579141	CW579141 OA_ABa010
314	15	25.4	568	10	CW754791	CW754791	387	15	25.4	657	10		



C 388	15	25.4	659	7	CS587707	CR587707		461	15	25.4	754	3	BUI47455	BUI47455	
C 389	15	25.4	661	8	DR706639	Asn_07166		462	15	25.4	761	1	AJB14780	AJB14780	
C 390	15	25.4	661	10	CZ657477	OM_Ba00		463	15	25.4	761	2	BG501708	BG501708	
C 391	15	25.4	662	8	DN968888	ISPL-P8-G		464	15	25.4	761	2	BG502396	BG502396	
C 392	15	25.4	665	10	CL928494	OA_ABa003		465	15	25.4	761	2	BG504829	BG504829	
C 393	15	25.4	666	5	CA014590	HTIMLOr		466	15	25.4	761	2	BG744175	BG744175	
C 394	15	25.4	666	9	BZ174814	CH230-268		467	15	25.4	762	10	CL598170	CL598170	
C 395	15	25.4	668	10	CG672951	CRB0683_t		468	15	25.4	762	11	CR129098	CR129098	
C 396	15	25.4	669	9	BH005764	BMBAC10B1		469	15	25.4	762	11	CR145229	CR145229	
C 397	15	25.4	669	10	CZ912822	4012012M0		470	15	25.4	764	2	BG504861	BG504861	
C 398	15	25.4	670	10	CG672953	rR80685_t		471	15	25.4	764	2	BG613217	BG613217	
C 399	15	25.4	670	10	CG672954	rR80686_t		472	15	25.4	764	7	CJ409686	CJ409686	
C 400	15	25.4	671	8	DRE31927	E8T102205		473	15	25.4	764	10	DU077171	DU077171	
C 401	15	25.4	672	8	DN382316	L1B38534-		474	15	25.4	764	10	CL183364	CL183364	
C 402	15	25.4	672	9	AQ471634	CITIBI-E1-		475	15	25.4	766	10	AG432156	AG432156	
C 403	15	25.4	673	9	AO051486	nbbd0002b		476	15	25.4	767	9	CB872010	CB872010	
C 404	15	25.4	673	10	CM221579	104_656_1		477	15	25.4	768	3	B1758657	B1758657	
C 405	15	25.4	674	3	BUT373432	BUT373432_		478	15	25.4	769	10	CM881881	CM881881	
C 406	15	25.4	676	2	BE533141	601235430		479	15	25.4	770	8	CX114191	CX114191	
C 407	15	25.4	677	10	CL723285	OR_BBA005		480	15	25.4	772	8	CXA32007	CXA32007	
C 408	15	25.4	680	9	BH565280	BOHIT78TR		481	15	25.4	773	1	CU787628	CU787628	
C 409	15	25.4	681	7	CM414556	170006001		482	15	25.4	774	7	CM414548	CM414548	
C 410	15	25.4	683	7	CO900832	Mdfrc3061		483	15	25.4	774	9	CC778375	CC778375	
C 411	15	25.4	684	1	AV730172	AV730172		484	15	25.4	776	9	AO862199	AO862199	
C 412	15	25.4	684	7	CF890717	UI-CF-DU1		485	15	25.4	778	3	BM014911	BM014911	
C 413	15	25.4	684	8	CV925175	PV030D12		486	15	25.4	778	10	CM005143	CM005143	
C 414	15	25.4	684	10	CZ912761	4012011G0		487	15	25.4	780	1	AJ786971	AJ786971	
C 415	15	25.4	687	1	AME58322	EST306017		488	15	25.4	781	5	BUI95203	BUI95203	
C 416	15	25.4	687	9	BZ949122	CH240_370		489	15	25.4	782	1	AUI31048	AUI31048	
C 417	15	25.4	687	10	CM505636	OP_Ba000		490	15	25.4	783	3	BP380971	BP380971	
C 418	15	25.4	687	10	BX176848	DAnTo_ref		491	15	25.4	784	2	BG504842	BG504842	
C 419	15	25.4	689	10	CM255363	CJ415599		492	15	25.4	790	3	B1522746	B1522746	
C 420	15	25.4	690	6	CD204254	HS1_4_B06		493	15	25.4	791	5	BX910206	BX910206	
C 421	15	25.4	691	6	BH952538	cdh02501_		494	15	25.4	791	10	CX206604	CX206604	
C 422	15	25.4	695	9	CA500705	BH952538		495	15	25.4	791	10	CX206691	CX206691	
C 423	15	25.4	698	6	CA500705	CA500705		496	15	25.4	792	7	CJ428290	CJ428290	
C 424	15	25.4	698	6	CD866230	AZ02_1020		497	15	25.4	796	10	CD2030296	CD2030296	
C 425	15	25.4	698	9	BH012491	TDGAK10TH		498	15	25.4	798	5	BUI911303	BUI911303	
C 426	15	25.4	699	10	CZ029433	OM_Ba000		499	15	25.4	798	8	DR674406	DR674406	
C 427	15	25.4	701	9	BH990795	oeFB6f11_		500	15	25.4	800	2	B1253515	B1253515	
C 428	15	25.4	701	7	CP886849	UI-CF-DU1		501	15	25.4	800	9	AO861643	AO861643	
C 429	15	25.4	703	10	CZ324743	ZMMBP0028		502	15	25.4	800	10	CL759250	CL759250	
C 430	15	25.4	704	8	DN992974	TC109722		503	15	25.4	801	2	BG717111	BG717111	
C 431	15	25.4	706	8	BG719528	602690076		504	15	25.4	801	10	CG253763	CG253763	
C 432	15	25.4	709	1	AJ792196	AJ792196		505	15	25.4	802	2	BG504760	BG504760	
C 433	15	25.4	709	1	BZ020113	oeo40905_		506	15	25.4	802	6	CF518824	CF518824	
C 434	15	25.4	712	9	BH973652	cd1424h11_		507	15	25.4	806	10	CZ283367	CZ283367	
C 435	15	25.4	713	9	BH973652	cd1424h11_		508	15	25.4	806	10	CZ283367	CZ283367	
C 436	15	25.4	713	1	AUI29756	AUI29756		509	15	25.4	810	11	CR032771	CR032771	
C 437	15	25.4	721	1	AJ935204	AJ935204		510	15	25.4	811	2	BG504282	BG504282	
C 438	15	25.4	721	2	BI223327	602941386		511	15	25.4	811	9	BZ989981	BZ989981	
C 439	15	25.4	722	8	CV813845	AGENCOURT		512	15	25.4	814	5	BUI55229	BUI55229	
C 440	15	25.4	723	7	CM415457	170004241		513	15	25.4	815	8	DR621020	DR621020	
C 441	15	25.4	723	9	CM415457	170004241		514	15	25.4	817	7	CJ419026	CJ419026	
C 442	15	25.4	735	3	BI858352	603383937		515	15	25.4	817	10	CZ284302	CZ284302	
C 443	15	25.4	738	10	CM168524	104_578_1		516	15	25.4	817	10	AG184827	AG184827	
C 444	15	25.4	740	10	CG446249	OGTREG25TV		517	15	25.4	819	5	BQ436009	BQ436009	
C 445	15	25.4	742	6	BG503398	BG503398		518	15	25.4	820	1	AUI133069	AUI133069	
C 446	15	25.4	742	6	CF489484	POL1_57_G		519	15	25.4	820	2	BE538876	BE538876	
C 447	15	25.4	743	8	DR155725	HESC2_57_G		520	15	25.4	820	7	CM821938	CM821938	
C 448	15	25.4	743	9	BH430964	BOGOF92TF		521	15	25.4	821	8	CX878945	CX878945	
C 449	15	25.4	743	9	CC825485	ZMMBBb017		522	15	25.4	823	8	DR580813	DR580813	
C 450	15	25.4	746	1	AJ802378	AJ802378		523	15	25.4	827	9	BH554382	BH554382	
C 451	15	25.4	746	7	CK124441	BES182410		524	15	25.4	827	10	CZ208757	CZ208757	
C 452	15	25.4	747	2	BG505113	602551570		525	15	25.4	828	8	CX436959	CX436959	
C 453	15	25.4	748	8	BZ424096	1d56h09_9		526	15	25.4	828	8	DN535523	DN535523	
C 454	15	25.4	749	2	BG503863	602549951		527	15	25.4	832	10	DU072520	DU072520	
C 455	15	25.4	750	10	CM454470	fbd000f11		528	15	25.4	832	8	CX861418	CX861418	
C 456	15	25.4	750	2	BG505582	602551805		529	15	25.4	832	10	BX966179	BX966179	
C 457	15	25.4	752	10	CZ794941	OC_Ba016		530	15	25.4	836	10	DU072520	DU072520	
C 458	15	25.4	752	2	BG505237	602551714		531	15	25.4	836	11	CR019422	CR019422	
C 459	15	25.4	752	9	CX112937	Et079C13		532	15	25.4	840	10	CM946543	CM946543	
C 460	15	25.4	752	9	CC948237	BOICGB1TF		533	15	25.4	843	1	AUI29637	AUI29637	



C 534	15	25.4	843	8	DR618639	ESR100896	C 607	15	25.4	1049	11	CNS050WB	AL349793 Tetraddon
C 535	15	25.4	845	8	CX772725	UI-RH-HG0	C 608	15	25.4	1050	10	CL248773	CL248773 ZMMBBD059
C 536	15	25.4	846	2	BG109255	602281285	C 609	15	25.4	1078	5	BX386129	BX386129
C 537	15	25.4	851	10	CM939895	TGB20.3_F	C 610	15	25.4	1095	3	BM455343	BM455343 AGENCOURT
C 538	15	25.4	857	11	CR215167	Reverse 8	C 611	15	25.4	1104	4	CC250941	CC250941 CH261-129
C 539	15	25.4	858	10	CM522251	OP Ba002	C 612	15	25.4	1115	4	CNS0G14F	CR97475 Tetraddon
C 540	15	25.4	861	8	CV815744	AGENCOURT	C 613	15	25.4	1128	5	BO950054	BO950054 AGENCOURT
C 541	15	25.4	866	2	BG501687	BG501687 602548737	C 614	15	25.4	1138	5	BX465139	BX465139
C 542	15	25.4	867	10	CC928865	246148 TO	C 615	15	25.4	1155	10	CL061252	CL061252 CH216--95D
C 543	15	25.4	867	10	CG387287	CG387287 ZMMBBD056	C 616	15	25.4	1160	2	BG505623	BG505623 602551866
C 544	15	25.4	868	1	AL542778	AL542778	C 617	15	25.4	1161	2	BG257052	BG257052 602370601
C 545	15	25.4	872	9	CC976938	ZUAH053TV	C 618	15	25.4	1200	5	BX426080	BX426080 BX426080
C 546	15	25.4	875	10	DU011564	DU011564 228045 TO	C 619	15	25.4	1212	9	CC270544	CC270544 CH261-16A
C 547	15	25.4	876	2	BR969104	BR969104 601650083	C 620	15	25.4	1221	2	BG177396	BG177396 602314022
C 548	15	25.4	878	10	DU054797	DU054797 92530 Tom	C 621	15	25.4	1244	10	AG507488	AG507488 Mus muscu
C 549	15	25.4	882	2	BI091341	BI091341 602855995	C 622	15	25.4	1246	8	DR134879	DR134879 49079665
C 550	15	25.4	883	10	DU002851	DU002851 285281 TO	C 623	15	25.4	1262	10	AG094503	AG094503 Pan trogl
C 551	15	25.4	884	10	CL506333	SATL 765	C 624	15	25.4	1312	5	BQ676089	BQ676089 AGENCOURT
C 552	15	25.4	885	2	BG501821	BG501821 602548919	C 625	15	25.4	1330	9	CC263281	CC263281 CH261-1P1
C 553	15	25.4	885	6	CF518911	CF518911 CAP0007_I	C 626	15	25.4	1384	9	CC255759	CC255759 CH261-184
C 554	15	25.4	886	9	CC086738	CSU-K33F_	C 627	15	25.4	1402	10	AG357407	AG357407 Mus muscu
C 555	15	25.4	886	5	BQ439678	BQ439678 AGENCOURT	C 628	15	25.4	1493	3	BM467445	BM467445 AGENCOURT
C 556	15	25.4	889	5	BF312758	BF312758 601898289	C 629	15	25.4	1556	3	BM478603	BM478603 AGENCOURT
C 557	15	25.4	890	2	BG504685	BG504685 602552983	C 630	15	25.4	1598	10	CL958139	CL958139 OaIFCC000
C 558	15	25.4	891	5	BU181580	BU181580 AGENCOURT	C 631	15	25.4	1947	10	CL483801	CL483801 SATL 386
C 559	15	25.4	892	8	CV805967	CV805967 AGENCOURT	C 632	15	25.4	2339	4	AK078021	AK078021 Mus muscu
C 560	15	25.4	894	2	BG502391	BG502391 602550284	C 633	15	25.4	2350	4	CR598980	CR598980 Full-1eng
C 561	15	25.4	896	5	BX451467	BX451467	C 634	15	25.4	2579	4	AK086336	AK086336 Mus muscu
C 562	15	25.4	896	2	CC383790	CC383790 PUH123TJD	C 635	15	25.4	3164	4	AK029270	AK029270 Mus muscu
C 563	15	25.4	902	10	CM943618	CM943618	C 636	15	25.4	3810	4	AK082130	AK082130 Mus muscu
C 564	15	25.4	903	7	BM011098	BM011098 603634795	C 637	14	23.7	106	1	AA755563	AA755563 v828a06_r
C 565	15	25.4	911	3	BH429288	BH429288 BONEA03TR	C 638	14	23.7	112	9	AO967797	AO967797 LERV108TR
C 566	15	25.4	915	2	BE559857	BE559857 601345756	C 639	14	23.7	131	5	BY659446	BY659446 BY659446
C 567	15	25.4	916	10	DU057772	DU057772 97599 Tom	C 640	14	23.7	133	7	CO352382	CO352382 DR AOV SU
C 568	15	25.4	918	2	DU057772	DU057772 97599 Tom	C 641	14	23.7	133	1	AU268106	AU268106 AU268106
C 569	15	25.4	921	10	CG250278	CG250278 GWM2-19L1	C 642	14	23.7	146	2	BE126152	BE126152 DGL 66 DO
C 570	15	25.4	923	2	BG389475	BG389475 602414177	C 643	14	23.7	147	3	BO075014	BO075014 f22Ea06_Y
C 571	15	25.4	925	10	DU044065	DU044065 158491 TO	C 644	14	23.7	149	7	CV521876	CV521876 0089P0066
C 572	15	25.4	926	2	BE888362	BE888362 601514092	C 645	14	23.7	152	10	CE594979	CE594979 t1gr-g88-
C 573	15	25.4	926	5	BQ439634	BQ439634 AGENCOURT	C 646	14	23.7	153	11	CR400008	CR400008 t1gr-g88-
C 574	15	25.4	926	10	CG156133	PURC209TJD	C 647	14	23.7	154	6	CA532626	CA532626 C0336G07-
C 575	15	25.4	928	10	CL247775	CL247775 ZMMBBD059	C 648	14	23.7	156	10	CE364201	CE364201 t1gr-g88-
C 576	15	25.4	930	5	BU195324	BU195324 AGENCOURT	C 649	14	23.7	159	10	CE340641	CE340641 t1gr-g88-
C 577	15	25.4	934	2	BF794744	BF794744 602256563	C 650	14	23.7	164	9	CE148569	CE148569 t1gr-g88-
C 578	15	25.4	934	7	CO731866	CO731866 JBM027H03	C 651	14	23.7	164	10	CE435157	CE435157 t1gr-g88-
C 579	15	25.4	936	9	CC131901	CC131901 ND1.40116	C 652	14	23.7	167	2	BI008151	BI008151 MR4-RT002
C 580	15	25.4	936	10	DU054044	DU054044 140644 TO	C 653	14	23.7	167	10	CE606034	CE606034 t1gr-g88-
C 581	15	25.4	938	10	CZ987492	CZ987492 202018 TO	C 654	14	23.7	168	1	AI018946	AI018946 SMSST0586
C 582	15	25.4	940	2	BG106685	BG106685 602290528	C 655	14	23.7	171	9	CR059366	CR059366 t1gr-g88-
C 583	15	25.4	944	2	BG287568	BG287568 602384595	C 656	14	23.7	172	10	CE853367	CE853367 t1gr-g88-
C 584	15	25.4	947	2	BE562017	BE562017 601345648	C 657	14	23.7	175	10	CE737611	CE737611 t1gr-g88-
C 585	15	25.4	947	6	CA469776	CA469776 AGENCOURT	C 658	14	23.7	178	9	CE104889	CE104889 t1gr-g88-
C 586	15	25.4	953	10	CM002705	CM002705 ZMMBBD1000	C 659	14	23.7	178	10	CE372654	CE372654 t1gr-g88-
C 587	15	25.4	954	9	CC421701	CC421701 PUHBN89TB	C 660	14	23.7	179	9	CE239410	CE239410 t1gr-g88-
C 588	15	25.4	955	2	BE782045	BE782045 601467815	C 661	14	23.7	180	10	CL962263	CL962263 OaIFCC007
C 589	15	25.4	956	2	BE779910	BE779910 601467834	C 662	14	23.7	182	9	CE088622	CE088622 t1gr-g88-
C 590	15	25.4	961	2	BG284608	BG284608 602408775	C 663	14	23.7	183	9	CE032213	CE032213 t1gr-g88-
C 591	15	25.4	970	5	BU186666	BU186666 AGENCOURT	C 664	14	23.7	184	10	CE570617	CE570617 t1gr-g88-
C 592	15	25.4	974	10	CG390703	CG390703 ZMMBBD057	C 665	14	23.7	185	10	CE713121	CE713121 t1gr-g88-
C 593	15	25.4	977	10	CG004736	CG004736 ZUAHX81TV	C 666	14	23.7	186	6	CB973509	CB973509 CAB30003
C 594	15	25.4	979	3	BM084724	BM084724 PPAF 10 F	C 667	14	23.7	186	6	CB973523	CB973523 CAB30003
C 595	15	25.4	981	5	BU858017	BU858017 AGENCOURT	C 668	14	23.7	188	10	CE563131	CE563131 t1gr-g88-
C 596	15	25.4	986	10	CZ941145	CZ941145 323165 TO	C 669	14	23.7	190	2	BE001488	BE001488 PM2-BN008
C 597	15	25.4	992	3	BM559499	BM559499 AGENCOURT	C 670	14	23.7	190	9	CE037129	CE037129 t1gr-g88-
C 598	15	25.4	993	2	BG243254	BG243254 60235675	C 671	14	23.7	191	5	BU825015	BU825015 UK102E11
C 599	15	25.4	994	2	BF790822	BF790822 602250601	C 672	14	23.7	191	10	AG260028	AG260028 Lotus cot
C 600	15	25.4	995	7	CM648238	CM648238 ILLUMIGEN	C 673	14	23.7	191	10	CE265003	CE265003 t1gr-g88-
C 601	15	25.4	1002	6	CA786595	CA786595 AGENCOURT	C 674	14	23.7	191	10	CE320442	CE320442 t1gr-g88-
C 602	15	25.4	1003	2	BG284536	BG284536 602408683	C 675	14	23.7	192	2	BI266311	BI266311 NF091A021
C 603	15	25.4	1009	10	CL496180	SATL_620	C 676	14	23.7	194	10	CE403290	CE403290 t1gr-g88-
C 604	15	25.4	1030	10	CL125759	ISB1-87K2	C 677	14	23.7	195	9	CE227989	CE227989 t1gr-g88-
C 605	15	25.4	1033	10	AG046899	Pan trogl	C 678	14	23.7	195	10	CE272164	CE272164 t1gr-g88-
C 606	15	25.4	1042	5	BX462126	BX462126	C 679	14	23.7	195	10	CE533637	CE533637 t1gr-g88-



C 680	14	23.7	197	9	CE082277	CE082277	t1gr-g88-	753	14	23.7	244	10	CE643360	CE643360	t1gr-g88-
C 681	14	23.7	197	9	CE088709	CE088709	t1gr-g88-	754	14	23.7	245	10	CE745048	CE745048	t1gr-g88-
C 682	14	23.7	197	10	CE413732	CE413732	t1gr-g88-	755	14	23.7	245	3	B1299369	B1299369	UI-R-CV2-
C 683	14	23.7	199	10	CE704764	CE704764	t1gr-g88-	756	14	23.7	246	9	CE256578	CE256578	t1gr-g88-
C 684	14	23.7	199	10	CE836550	CE836550	t1gr-g88-	757	14	23.7	246	10	CE847163	CE847163	t1gr-g88-
C 685	14	23.7	200	10	CE848383	CE848383	t1gr-g88-	758	14	23.7	247	1	BB076658	BB076658	BB076658
C 686	14	23.7	201	9	CE253495	CE253495	t1gr-g88-	759	14	23.7	248	9	CE038566	CE038566	t1gr-g88-
C 687	14	23.7	201	10	CE253495	CE253495	t1gr-g88-	760	14	23.7	248	9	CE176962	CE176962	t1gr-g88-
C 688	14	23.7	202	9	CE200351	CE200351	t1gr-g88-	761	14	23.7	248	10	CE556473	CE556473	t1gr-g88-
C 689	14	23.7	202	10	CE415390	CE415390	t1gr-g88-	762	14	23.7	249	10	CE342747	CE342747	t1gr-g88-
C 690	14	23.7	202	10	CE710847	CE710847	t1gr-g88-	763	14	23.7	249	11	CR818045	CR818045	GR0AA43D
C 691	14	23.7	203	10	CE315100	CE315100	t1gr-g88-	764	14	23.7	250	8	CV994281	CV994281	IPCGF3_3
C 692	14	23.7	204	10	CE696772	CE696772	t1gr-g88-	765	14	23.7	250	10	CE329417	CE329417	CV994281
C 693	14	23.7	205	9	BZ552022	BZ552022	hm79f12.g	766	14	23.7	250	10	CE333584	CE333584	CV994281
C 694	14	23.7	205	9	CE046390	CE046390	t1gr-g88-	767	14	23.7	251	10	CE388793	CE388793	CV994281
C 695	14	23.7	205	9	CE287375	CE287375	t1gr-g88-	768	14	23.7	253	10	CE554416	CE554416	t1gr-g88-
C 696	14	23.7	206	10	CE393059	CE393059	t1gr-g88-	769	14	23.7	253	10	CE597195	CE597195	t1gr-g88-
C 697	14	23.7	206	10	CE579374	CE579374	t1gr-g88-	770	14	23.7	253	10	CE618453	CE618453	t1gr-g88-
C 698	14	23.7	207	1	AU269275	AU269275	AU269275	771	14	23.7	253	10	CE711995	CE711995	t1gr-g88-
C 699	14	23.7	209	9	CE027432	CE027432	t1gr-g88-	772	14	23.7	253	10	CE733669	CE733669	t1gr-g88-
C 700	14	23.7	209	10	CE634443	CE634443	t1gr-g88-	773	14	23.7	254	10	CE739211	CE739211	t1gr-g88-
C 701	14	23.7	210	9	CE198724	CE198724	t1gr-g88-	774	14	23.7	255	1	A1434777	A1434777	t1gr-g88-
C 702	14	23.7	212	10	CE465071	CE465071	t1gr-g88-	775	14	23.7	255	2	BB606425	BB606425	BB606425
C 703	14	23.7	212	10	CE547944	CE547944	t1gr-g88-	776	14	23.7	255	8	CV827003	CV827003	EST001301
C 704	14	23.7	213	5	B0828911	B0828911	K031P09P	777	14	23.7	255	10	CE283366	CE283366	CV827003
C 705	14	23.7	213	10	CE516591	CE516591	t1gr-g88-	778	14	23.7	255	10	CE390129	CE390129	t1gr-g88-
C 706	14	23.7	213	10	CE707973	CE707973	t1gr-g88-	779	14	23.7	256	1	BB050652	BB050652	BB050652
C 707	14	23.7	216	4	AK195045	AK195045	M08_mubu	780	14	23.7	256	10	CE447178	CE447178	t1gr-g88-
C 708	14	23.7	217	10	CE315018	CE315018	t1gr-g88-	781	14	23.7	256	10	CE582298	CE582298	t1gr-g88-
C 709	14	23.7	218	9	AZ431672	AZ431672	1M0216B14	782	14	23.7	256	10	CE605808	CE605808	t1gr-g88-
C 710	14	23.7	218	10	CE485013	CE485013	t1gr-g88-	783	14	23.7	257	1	AV270245	AV270245	AV270245
C 711	14	23.7	219	9	CE030211	CE030211	t1gr-g88-	784	14	23.7	257	10	CE442195	CE442195	t1gr-g88-
C 712	14	23.7	220	9	CE116948	CE116948	t1gr-g88-	785	14	23.7	257	10	CE515367	CE515367	t1gr-g88-
C 713	14	23.7	220	10	CE203421	CE203421	t1gr-g88-	786	14	23.7	258	10	CE402352	CE402352	t1gr-g88-
C 714	14	23.7	220	10	BX653443	BX653443	ArabiIdop8	787	14	23.7	260	2	BB570897	BB570897	BB570897
C 715	14	23.7	224	6	CE767474	CE767474	t1gr-g88-	788	14	23.7	261	10	CE524104	CE524104	t1gr-g88-
C 716	14	23.7	226	6	CA541128	CA541128	C0601B10-	789	14	23.7	261	10	CE754714	CE754714	t1gr-g88-
C 717	14	23.7	226	9	CE029449	CE029449	t1gr-g88-	790	14	23.7	262	10	CE030239	CE030239	t1gr-g88-
C 718	14	23.7	226	9	CE117313	CE117313	t1gr-g88-	791	14	23.7	263	9	CE341108	CE341108	t1gr-g88-
C 719	14	23.7	227	10	CE308165	CE308165	t1gr-g88-	792	14	23.7	263	10	CE366320	CE366320	t1gr-g88-
C 720	14	23.7	228	9	CE084469	CE084469	t1gr-g88-	793	14	23.7	264	7	CO318167	CO318167	t1gr-g88-
C 721	14	23.7	229	9	CE044231	CE044231	t1gr-g88-	794	14	23.7	264	10	CE671073	CE671073	t1gr-g88-
C 722	14	23.7	231	10	CE663308	CE663308	t1gr-g88-	795	14	23.7	264	10	CE789072	CE789072	t1gr-g88-
C 723	14	23.7	231	10	CE737731	CE737731	t1gr-g88-	796	14	23.7	265	10	CE282363	CE282363	t1gr-g88-
C 724	14	23.7	232	1	A1018876	A1018876	SME570515	797	14	23.7	265	10	CE341108	CE341108	t1gr-g88-
C 725	14	23.7	232	9	CE209812	CE209812	t1gr-g88-	798	14	23.7	265	10	CE614715	CE614715	t1gr-g88-
C 726	14	23.7	232	10	CE542349	CE542349	t1gr-g88-	799	14	23.7	266	7	CO292516	CO292516	BK200349
C 727	14	23.7	232	10	CE747949	CE747949	t1gr-g88-	800	14	23.7	266	10	CE626862	CE626862	t1gr-g88-
C 728	14	23.7	233	10	CE320406	CE320406	t1gr-g88-	801	14	23.7	266	10	CE669983	CE669983	t1gr-g88-
C 729	14	23.7	234	10	CE282954	CE282954	t1gr-g88-	802	14	23.7	268	10	CE541588	CE541588	t1gr-g88-
C 730	14	23.7	234	10	CE544713	CE544713	t1gr-g88-	803	14	23.7	268	10	CE695518	CE695518	t1gr-g88-
C 731	14	23.7	235	10	CE753818	CE753818	t1gr-g88-	804	14	23.7	269	5	BM074858	BM074858	BM074858
C 732	14	23.7	235	10	CE774645	CE774645	t1gr-g88-	805	14	23.7	270	10	CE551160	CE551160	t1gr-g88-
C 733	14	23.7	237	10	CE174629	CE174629	ZMMBC034	806	14	23.7	272	10	CE372321	CE372321	t1gr-g88-
C 734	14	23.7	238	10	CE288576	CE288576	t1gr-g88-	807	14	23.7	273	9	CE227914	CE227914	t1gr-g88-
C 735	14	23.7	239	5	C91227	C91227	C91227	808	14	23.7	273	10	CE276613	CE276613	t1gr-g88-
C 736	14	23.7	239	6	CF609226	CF609226	INP1001_0	809	14	23.7	273	10	CE562162	CE562162	t1gr-g88-
C 737	14	23.7	239	10	CE323516	CE323516	t1gr-g88-	810	14	23.7	273	10	CE566631	CE566631	t1gr-g88-
C 738	14	23.7	239	10	CE359651	CE359651	t1gr-g88-	811	14	23.7	274	9	CE003746	CE003746	t1gr-g88-
C 739	14	23.7	239	10	CE827334	CE827334	t1gr-g88-	812	14	23.7	275	10	CE466007	CE466007	t1gr-g88-
C 740	14	23.7	240	1	AU074204	AU074204	AU074204	813	14	23.7	275	10	CE518515	CE518515	t1gr-g88-
C 741	14	23.7	240	10	CE449479	CE449479	t1gr-g88-	814	14	23.7	276	10	CE347570	CE347570	t1gr-g88-
C 742	14	23.7	241	10	CE038194	CE038194	t1gr-g88-	815	14	23.7	276	10	CE400255	CE400255	t1gr-g88-
C 743	14	23.7	241	10	CE681871	CE681871	t1gr-g88-	816	14	23.7	276	10	CE412397	CE412397	t1gr-g88-
C 744	14	23.7	241	10	CE705042	CE705042	t1gr-g88-	817	14	23.7	276	10	CE509544	CE509544	t1gr-g88-
C 745	14	23.7	242	2	BF764190	BF764190	IL2-CS005	818	14	23.7	277	9	CE213573	CE213573	t1gr-g88-
C 746	14	23.7	242	8	CE362493	CE362493	GBN002K03	819	14	23.7	277	10	CE288755	CE288755	t1gr-g88-
C 747	14	23.7	242	9	CE135797	CE135797	t1gr-g88-	820	14	23.7	277	10	CE404035	CE404035	t1gr-g88-
C 748	14	23.7	242	10	CE814878	CE814878	t1gr-g88-	821	14	23.7	277	10	CE531219	CE531219	t1gr-g88-
C 749	14	23.7	242	10	CE821911	CE821911	t1gr-g88-	822	14	23.7	278	5	BM210387	BM210387	t1gr-g88-
C 750	14	23.7	243	9	CE091235	CE091235	t1gr-g88-	823	14	23.7	278	10	CE491763	CE491763	t1gr-g88-
C 751	14	23.7	243	10	CE408285	CE408285	t1gr-g88-	824	14	23.7	279	9	CE108446	CE108446	t1gr-g88-
C 752	14	23.7	244	10	CE502415	CE502415	t1gr-g88-	825	14	23.7	279	10	CE482337	CE482337	t1gr-g88-



826	14	23.7	279	10	CE801799	CE801799	l1gr-g88-	899	14	23.7	302	10	CE509041	CE509041	l1gr-g88-
827	14	23.7	280	2	BP34078	BP34078	l1gr-g88-	900	14	23.7	302	10	CE539323	CE539323	l1gr-g88-
828	14	23.7	281	9	CE229071	CE229071	l1gr-g88-	901	14	23.7	302	10	CE537744	CE537744	l1gr-g88-
829	14	23.7	281	10	CE612788	CE612788	l1gr-g88-	902	14	23.7	302	10	CE763143	CE763143	l1gr-g88-
830	14	23.7	281	10	CE647332	CE647332	l1gr-g88-	903	14	23.7	303	6	CA534330	CA534330	l1gr-g88-
831	14	23.7	281	10	CE651834	CE651834	l1gr-g88-	904	14	23.7	303	10	CE472858	CE472858	l1gr-g88-
832	14	23.7	281	10	CE790901	CE790901	l1gr-g88-	905	14	23.7	303	10	CE472858	CE472858	l1gr-g88-
833	14	23.7	281	10	CE794663	CE794663	l1gr-g88-	906	14	23.7	303	10	CE632662	CE632662	l1gr-g88-
834	14	23.7	281	10	CE844392	CE844392	l1gr-g88-	907	14	23.7	303	10	CE648003	CE648003	l1gr-g88-
835	14	23.7	282	2	BB287392	BB287392	l1gr-g88-	908	14	23.7	303	10	CE715809	CE715809	l1gr-g88-
836	14	23.7	282	9	CE239611	CE239611	l1gr-g88-	909	14	23.7	304	8	RO8640	RO8640	l1gr-g88-
837	14	23.7	283	10	CE441212	CE441212	l1gr-g88-	910	14	23.7	304	9	W13592	W13592	l1gr-g88-
838	14	23.7	283	10	CE482836	CE482836	l1gr-g88-	911	14	23.7	304	9	CE257789	CE257789	l1gr-g88-
839	14	23.7	283	10	CE560259	CE560259	l1gr-g88-	912	14	23.7	304	10	CE285808	CE285808	l1gr-g88-
840	14	23.7	283	10	CE806860	CE806860	l1gr-g88-	913	14	23.7	305	9	CE162361	CE162361	l1gr-g88-
841	14	23.7	284	6	CD092887	CD092887	l1gr-g88-	914	14	23.7	305	9	CE253984	CE253984	l1gr-g88-
842	14	23.7	284	7	CO217258	CO217258	l1gr-g88-	915	14	23.7	305	10	CE309109	CE309109	l1gr-g88-
843	14	23.7	284	10	CE319612	CE319612	l1gr-g88-	916	14	23.7	305	10	CE336143	CE336143	l1gr-g88-
844	14	23.7	284	10	CE540248	CE540248	l1gr-g88-	917	14	23.7	305	10	CE492414	CE492414	l1gr-g88-
845	14	23.7	286	10	CE313748	CE313748	l1gr-g88-	918	14	23.7	305	10	CE496634	CE496634	l1gr-g88-
846	14	23.7	286	10	CE619069	CE619069	l1gr-g88-	919	14	23.7	305	10	CE513744	CE513744	l1gr-g88-
847	14	23.7	288	10	CE484015	CE484015	l1gr-g88-	920	14	23.7	305	10	CE539504	CE539504	l1gr-g88-
848	14	23.7	289	9	AO948772	AO948772	Sheared D	921	14	23.7	305	10	CG652130	CG652130	OST414599
849	14	23.7	289	9	CE156853	CE156853	l1gr-g88-	922	14	23.7	306	10	CE332697	CE332697	l1gr-g88-
850	14	23.7	289	10	CE2074142	CE2074142	OM_BA006	923	14	23.7	306	10	CE394727	CE394727	l1gr-g88-
851	14	23.7	290	10	CE264848	CE264848	l1gr-g88-	924	14	23.7	306	10	CE581897	CE581897	l1gr-g88-
852	14	23.7	290	10	CE517004	CE517004	l1gr-g88-	925	14	23.7	306	10	CE724015	CE724015	l1gr-g88-
853	14	23.7	292	9	BH122441	BH122441	NPCT-24-2	926	14	23.7	307	9	CE261711	CE261711	l1gr-g88-
854	14	23.7	292	10	CE470905	CE470905	l1gr-g88-	927	14	23.7	307	10	CE273551	CE273551	l1gr-g88-
855	14	23.7	292	10	CE522960	CE522960	l1gr-g88-	928	14	23.7	307	10	CE475653	CE475653	l1gr-g88-
856	14	23.7	293	6	CB702310	CB702310	AMGNNUC:C	929	14	23.7	307	10	CE489360	CE489360	l1gr-g88-
857	14	23.7	293	9	CE193529	CE193529	l1gr-g88-	930	14	23.7	307	10	CE700060	CE700060	l1gr-g88-
858	14	23.7	293	10	CE352287	CE352287	l1gr-g88-	931	14	23.7	308	10	CE288112	CE288112	l1gr-g88-
859	14	23.7	293	10	CE565139	CE565139	l1gr-g88-	932	14	23.7	308	10	CE707838	CE707838	l1gr-g88-
860	14	23.7	293	10	CE599952	CE599952	l1gr-g88-	933	14	23.7	309	10	CE518128	CE518128	l1gr-g88-
861	14	23.7	294	9	CE8050171	CE8050171	l1gr-g88-	934	14	23.7	309	10	CE614721	CE614721	l1gr-g88-
862	14	23.7	294	10	CE207713	CE207713	l1gr-g88-	935	14	23.7	309	10	CE646843	CE646843	l1gr-g88-
863	14	23.7	294	10	CE307218	CE307218	l1gr-g88-	936	14	23.7	310	5	CE24108	CE24108	l1gr-g88-
864	14	23.7	294	10	CE612898	CE612898	l1gr-g88-	937	14	23.7	310	9	CE064828	CE064828	l1gr-g88-
865	14	23.7	295	10	CE652269	CE652269	l1gr-g88-	938	14	23.7	310	9	CE103837	CE103837	l1gr-g88-
866	14	23.7	295	10	CE695167	CE695167	l1gr-g88-	939	14	23.7	310	9	CE145971	CE145971	l1gr-g88-
867	14	23.7	295	10	CE709006	CE709006	l1gr-g88-	940	14	23.7	311	3	BM138758	BM138758	l1gr-g88-
868	14	23.7	296	3	BP094522	BP094522	l1gr-g88-	941	14	23.7	311	9	CE203360	CE203360	l1gr-g88-
869	14	23.7	296	9	CE175150	CE175150	l1gr-g88-	942	14	23.7	311	10	CE308433	CE308433	l1gr-g88-
870	14	23.7	296	9	CE223557	CE223557	l1gr-g88-	943	14	23.7	311	10	CE488820	CE488820	l1gr-g88-
871	14	23.7	296	10	CE481918	CE481918	l1gr-g88-	944	14	23.7	311	10	CE672943	CE672943	l1gr-g88-
872	14	23.7	296	10	CE799780	CE799780	l1gr-g88-	945	14	23.7	311	10	CE764821	CE764821	l1gr-g88-
873	14	23.7	297	9	CE099585	CE099585	l1gr-g88-	946	14	23.7	311	10	CE801953	CE801953	l1gr-g88-
874	14	23.7	297	9	CE105499	CE105499	l1gr-g88-	947	14	23.7	311	10	CE853756	CE853756	l1gr-g88-
875	14	23.7	297	9	CE117855	CE117855	l1gr-g88-	948	14	23.7	312	1	AL796644	AL796644	l1gr-g88-
876	14	23.7	297	9	CE144843	CE144843	l1gr-g88-	949	14	23.7	312	2	BF936268	BF936268	l1gr-g88-
877	14	23.7	297	10	CE292392	CE292392	l1gr-g88-	950	14	23.7	312	10	CE775573	CE775573	l1gr-g88-
878	14	23.7	297	10	CE479624	CE479624	l1gr-g88-	951	14	23.7	312	9	BH855727	BH855727	l1gr-g88-
879	14	23.7	297	10	CE482777	CE482777	l1gr-g88-	952	14	23.7	312	9	CE040137	CE040137	l1gr-g88-
880	14	23.7	297	10	CE617265	CE617265	l1gr-g88-	953	14	23.7	312	9	CE040761	CE040761	l1gr-g88-
881	14	23.7	298	10	CE299251	CE299251	l1gr-g88-	954	14	23.7	312	10	CE566053	CE566053	l1gr-g88-
882	14	23.7	298	10	CE686997	CE686997	l1gr-g88-	955	14	23.7	312	10	CE777557	CE777557	l1gr-g88-
883	14	23.7	298	10	CE711319	CE711319	l1gr-g88-	956	14	23.7	313	10	CE857382	CE857382	l1gr-g88-
884	14	23.7	298	10	CE849344	CE849344	l1gr-g88-	957	14	23.7	313	10	CE837028	CE837028	l1gr-g88-
885	14	23.7	299	9	CE234754	CE234754	l1gr-g88-	958	14	23.7	314	1	AL013003	AL013003	l1gr-g88-
886	14	23.7	299	10	CE523116	CE523116	l1gr-g88-	959	14	23.7	314	10	CE354846	CE354846	l1gr-g88-
887	14	23.7	299	10	CE686068	CE686068	l1gr-g88-	960	14	23.7	314	10	CE593328	CE593328	l1gr-g88-
888	14	23.7	300	10	CE2585263	CE2585263	OA_BBA017	961	14	23.7	314	10	CE819355	CE819355	l1gr-g88-
889	14	23.7	300	10	CE355752	CE355752	l1gr-g88-	962	14	23.7	314	10	CE850606	CE850606	l1gr-g88-
890	14	23.7	300	10	CE434918	CE434918	l1gr-g88-	963	14	23.7	315	5	BU019050	BU019050	QHR20C06
891	14	23.7	300	10	CE852443	CE852443	l1gr-g88-	964	14	23.7	315	9	CE100540	CE100540	l1gr-g88-
892	14	23.7	301	2	BE067660	BE067660	MR4_BT035	965	14	23.7	315	9	CE166286	CE166286	l1gr-g88-
893	14	23.7	301	9	CE142969	CE142969	l1gr-g88-	966	14	23.7	315	10	CE301679	CE301679	l1gr-g88-
894	14	23.7	301	9	CE148734	CE148734	l1gr-g88-	967	14	23.7	315	10	CE704908	CE704908	l1gr-g88-
895	14	23.7	301	10	CE407025	CE407025	l1gr-g88-	968	14	23.7	315	10	CE762974	CE762974	l1gr-g88-
896	14	23.7	302	8	T95005	T95005	Y638C04_81	969	14	23.7	316	2	BE15197	BE15197	PMO-HT033
897	14	23.7	302	9	CE066467	CE066467	l1gr-g88-	970	14	23.7	316	9	CE033694	CE033694	l1gr-g88-
898	14	23.7	302	10	CE433656	CE433656	l1gr-g88-	971	14	23.7	316	10	CE284705	CE284705	l1gr-g88-



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972 14 23.7 316 10 CES61044      CES61044 tigr-gss-
973 14 23.7 316 10 CB693437      CB693437 tigr-gss-
974 14 23.7 316 10 CB806561      CB806561 tigr-gss-
975 14 23.7 317 7  CN580937      CN580937 Mdlw2031a
976 14 23.7 317 9  CB021582      CB021582 tigr-gss-
977 14 23.7 317 9  CB240717      CB240717 tigr-gss-
978 14 23.7 317 10 CB292503      CB292503 tigr-gss-
979 14 23.7 317 10 CB387241      CB387241 tigr-gss-
980 14 23.7 317 10 CB836129      CB836129 tigr-gss-
981 14 23.7 318 3  BU647748      BU647748
982 14 23.7 318 10 CB520780      CB520780 tigr-gss-
983 14 23.7 319 7  CO275849      CO275849 EK18937.
984 14 23.7 319 9  A2276485      A2276485 RPCI-23-1
985 14 23.7 319 10 CB764559      CB764559 tigr-gss-
986 14 23.7 320 2  BF748992      BF748992 MR2-BN038
987 14 23.7 320 9  CB0202925      CB0202925 tigr-gss-
988 14 23.7 320 9  CB129561      CB129561 tigr-gss-
989 14 23.7 320 9  CB220335      CB220335 tigr-gss-
990 14 23.7 320 10 CB403716      CB403716 tigr-gss-
991 14 23.7 320 10 CB435755      CB435755 tigr-gss-
992 14 23.7 321 9  CB056851      CB056851 tigr-gss-
993 14 23.7 321 10 CB548466      CB548466 tigr-gss-
994 14 23.7 321 10 CB584990      CB584990 tigr-gss-
995 14 23.7 321 10 CB759817      CB759817 tigr-gss-
996 14 23.7 322 9  CB103413      CB103413 tigr-gss-
997 14 23.7 322 9  CB140230      CB140230 tigr-gss-
998 14 23.7 322 9  CB153214      CB153214 tigr-gss-
999 14 23.7 322 10 CB579545      CB579545 tigr-gss-
1000 14 23.7 323 9  CB136783      CB136783 tigr-gss-

```

## ALIGNMENTS

```

RESULT 1          221 bp  DNA  linear  GSS 28-SEP-2003
CES16034          tigr-gss-dog-17000311663558 Dog Library Canis familiaris genomic,
LOCUS             genomic survey sequence.
ACCESSION         CES16034
VERSION           CES16034.1 GI:36832815
KEYWORDS          GSS.
SOURCE            Canis familiaris (dog)
ORGANISM          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
                  Canis.
REFERENCE         1 (bases 1 to 221)
AUTHORS           Kirkness,E.F., Batra,V., Halpern,A.L., Levy,S., Remington,K.,
                  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
                  Venter,J.C.
TITLE             The dog genome: survey sequencing and comparative analysis
JOURNAL           Science 301 (5641), 1898-1903 (2003)
PUBMED            14512627
COMMENT           Contact: Kirkness EF
                  The Institute for Genomic Research
                  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
                  Rockville, MD 20850, USA
                  Tel: 301-838-0200
                  Fax: 301-838-0208
                  Email: ekirkness@tigr.org
                  Class: shotgun
FEATURES          Location/Qualifiers
source            1..221
                  /organism="Canis familiaris"
                  /mol_type="genomic DNA"
                  /strain="Standard Poodle"
                  /db_xref="taxon:9615"
                  /clone_lib="Dog Library"
                  /note="Site 1: BstXI; Libraries were prepared from
                  peripheral blood"

```

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REFERENCE         1 (bases 1 to 221)
AUTHORS           Kirkness,E.F., Batra,V., Halpern,A.L., Levy,S., Remington,K.,
                  Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and
                  Venter,J.C.
TITLE             The dog genome: survey sequencing and comparative analysis
JOURNAL           Science 301 (5641), 1898-1903 (2003)
PUBMED            14512627
COMMENT           Contact: Kirkness EF
                  The Institute for Genomic Research
                  Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,
                  Rockville, MD 20850, USA
                  Tel: 301-838-0200
                  Fax: 301-838-0208
                  Email: ekirkness@tigr.org
                  Class: shotgun
FEATURES          Location/Qualifiers
source            1..221
                  /organism="Canis familiaris"
                  /mol_type="genomic DNA"
                  /strain="Standard Poodle"
                  /db_xref="taxon:9615"
                  /clone_lib="Dog Library"
                  /note="Site 1: BstXI; Libraries were prepared from
                  peripheral blood"
ORIGIN

```

```

Query Match          32.2% Score 19; DB 10; Length 221;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY              36 ATCCATTAGAAACGACTTAA 54
                |||||
Db              26 ATCCATTAGAAACGACTTAA 44

```

```

RESULT 2
CR067686/c        430 bp  DNA  linear  GSS 05-JUL-2004
LOCUS             Reverse strand read from insert in 3'HRT insertion targeting and
DEFINITION         chromosome engineering clone MHP293b05, genomic survey sequence.
ACCESSION         CR067686
VERSION           CR067686.1 GI:49801276
KEYWORDS          GSS; genome survey sequence; MICRR.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                  Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE         1 (bases 1 to 430)
AUTHORS           Adams,D.J., Biggs,P.J., Cox,A.V., Davis,R.M., van der Weyden,L.,
                  Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Nishijima,I., Yu,Y.,
                  Rogers,J. and Bradley,A.
TITLE             Direct Submission
JOURNAL           Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
                  CB10 1SA, UK. http://www.sanger.ac.uk/MICRR
FEATURES          Location/Qualifiers
source            1..430
                  /organism="Mus musculus"
                  /mol_type="genomic DNA"
                  /db_xref="taxon:10090"
                  /clone="MHP293b05"
                  /clone_lib="MHP"

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## ORIGIN

```

Query Match          32.2% Score 19; DB 11; Length 430;
Best Local Similarity 100.0%; Pred. No. 1.6;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY              23 GTTATCTAGTGCATCAT 41
                |||||
Db              103 GTTATCTAGTGCATCAT 85

```

```

RESULT 3
BH042558          518 bp  DNA  linear  GSS 17-JUL-2001
LOCUS             RPCI-24-360K1.TJ RPCI-24 Mus musculus genomic clone RPCI-24-360K1,
DEFINITION         genomic survey sequence.
ACCESSION         BH042558
VERSION           BH042558.1 GI:14823756
KEYWORDS          GSS.
SOURCE            Mus musculus (house mouse)
ORGANISM          Mus musculus
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
                  Sciurognathi; Murioidea; Muridae; Murinae; Mus.
REFERENCE         1 (bases 1 to 518)
AUTHORS           Zhao,S., Nierman,W., Malek,J., Shatman,S., Akinret,B., Levins,M.,
                  Tsengay,G., Geer,K., Krol,M., Shvartsbeyn,A., Gebregiorgis,E.,
                  Russell,D., de Jong,P. and Fraser,C.M.
TITLE             Mouse BAC End Sequences from Library RPCI-24
JOURNAL           Other GSSes: RPCI-24-360K1.TV
COMMENT           Contact: Shaying Zhao
                  Department of Eukaryotic Genomics
                  The Institute for Genomic Research
                  9712 Medical Center Dr., Rockville, MD 20850, USA
                  Tel: 301 838 0200
                  Fax: 301 838 0208
ORIGIN

```



Email: szhaoc@tigr.org  
 Clones are derived from the mouse BAC library RPCI-24. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 360 row: K column: 1  
 Seq primer: SP6  
 Class: BAC ends.

#### FEATURES

Source

Location/Qualifiers  
 1..518  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-24-360K1"  
 /sex="Male"  
 /cell\_type="Spleen/Brain"  
 /clone\_lib="RPCI-24"  
 /note="Vector: pTARBAC1; Site 1: BamHI; Site 2: BamHI; RPCI-24 Mouse BAC library produced by Pieter de Jong. The library was cloned in the pTARBAC1 cloning vector at the BamHI sites using MboI partially digested male C57BL/6J DNA."

#### ORIGIN

Query Match 32.2%; Score 19; DB 9; Length 518;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 23 GTTAATCTAGTATCCAT 41  
 |||||  
 Db 137 GTTAATCTAGTATCCAT 155

RESULT 4  
 LOCUS AO974432 664 bp DNA linear GSS 28-JAN-2000  
 DEFINITION RPCI-23-315P11.TU RPCI-23 Mus musculus genomic clone  
 ACCESSION AO974432  
 VERSION AO974432.1 GI:6804886  
 KEYWORDS GSS.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Zhao, S., Niernman, W., Feldlyum, T., Malek, J., Shatsman, S., Akincic, B., Levins, M., Megam, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P. and Fraser, C.M.  
 TITLE Mouse BAC End Sequences from Library RPCI-23  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhaoc@tigr.org

Clones are derived from the mouse BAC library RPCI-23. For BAC library availability, please contact Pieter de Jong (pjejong@mail.cho.org). Clones may be purchased from BACPAC Resources (<http://www.choi.org/bacpac/orderingframe.html>) or from Resea ch Genetics ([info@resgen.com](http://info@resgen.com)). BAC end page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
 Plate: 315 row: P column: 11  
 Seq primer: SP6  
 Class: BAC ends.

FEATURES  
 Source  
 Location/Qualifiers  
 1..664  
 /organism="Mus musculus"

/mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="RPCI-23-315P11"  
 /sex="Female"  
 /lab\_host="DH10B"  
 /clone\_lib="RPCI-23"  
 /note="Organ: Kidney/Brain; Vector: pBAC3.6; Site 1: EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or brain genomic DNA was isolated and partially digested with a combination of EcoRI and EcoRI Methylase. Site selected DNA was cloned into the pBAC3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies)."

#### ORIGIN

Query Match 32.2%; Score 19; DB 9; Length 664;  
 Best Local Similarity 100.0%; Pred. No. 1.6;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 23 GTTAATCTAGTATCCAT 41  
 |||||  
 Db 486 GTTAATCTAGTATCCAT 468

RESULT 5  
 LOCUS CX432289 660 bp mRNA linear EST 07-JAN-2005  
 DEFINITION JGI XZG62671.rev NIH XGC tropGa87 Xenopus tropicalis cDNA clone IMAGE:7576893 3', mRNA sequence.  
 ACCESSION CX432289  
 VERSION CX432289.1 GI:57248109  
 KEYWORDS EST.  
 SOURCE Xenopus tropicalis (western clawed frog)  
 ORGANISM Xenopus tropicalis

REFERENCE  
 AUTHORS Burkayota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae; Xenopodinae; Xenopus; Silurana.  
 1 (bases 1 to 660)  
 Richardson, P., Lucas, S., Rokhsar, D., Dettler, J.C., Ng, D.C., Brokstein, P. and Lindquist, E.A.  
 TITLE DOE Joint Genome Institute Xenopus tropicalis EST project  
 JOURNAL Unpublished (2004)  
 COMMENT Other\_ESTs: JGI XZG62671.fwd  
 Contact: Lindquist, E.A., Richardson, P.  
 DOE Joint Genome Institute  
 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 Tel: 925 296 5600  
 Fax: 925 296 5710

Email: cdna@jgi-psf.org  
 Tissue Procurement: Richard M. Harland Laboratory, University of California, Berkeley: <http://tropicalis.berkeley.edu/home>  
 cDNA Library Preparation: Richard M. Harland Laboratory, University of California, Berkeley  
 DNA Sequencing: DOE Joint Genome Institute: <http://www.jgi.doe.gov>  
 Clone Distribution: I.M.A.G.E. Consortium/LNLW:  
<http://image.llnl.gov>  
 Naming Conventions: EST name is generated by the concatenation of the JGI Clone id and the direction of sequencing. The suffix 'rev' indicates a reverse sequencing read of the insert. It does not necessarily reflect the orientation of the insert.  
 Poly-A: Based upon the presence of a run of 14 or more T residues at the beginning of the sequence, this clone was polyadenylated.  
 The resulting Poly-T sequence has been removed.  
 Plate: XZG 0653 row: m column: 19  
 High quality sequence stop: 563  
 POLYA=Yes.

FEATURES  
 Source  
 Location/Qualifiers  
 1..660  
 /organism="Xenopus tropicalis"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:8364"  
 /clone="IMAGE:7576893"



## ORIGIN

Query Match 30.5%; Score 18; DB 8; Length 660;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 29 CCTAGTATCCATTGAA 46  
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 DB 522 CCTAGTATCCATTGAA 505

"/tissue\_type="whole embryo"  
 /dev\_stage="Gastrula (St. 10.5-12.5)"  
 /lab\_host="E. coli XL1-Blue derivative, Stratagene  
 Electrogen-Blue"  
 /clone\_lib="NIH XGC tropGaet7"  
 /note="Vector: pCS108; Site 1: SalI; Site 2: NotI;  
 Gastrula library constructed by Russell B. Fletcher in R.  
 Harland's lab using poly A RNA and oligo dT primers  
 (Invitrogen Superscript Plasmid System for cDNA Synthesis  
 and Cloning). SalI (5' end) -NotI (3' end) cDNA was  
 inserted into vector pCS108  
 (http://mob.berkeley.edu/labs/harland/pages/plasmids.html)"

## RESULT 6

AZ400559/c 730 bp DNA linear GSS 03-OCT-2000  
 LOCUS 1M0166123R Mouse 10kb plasmid UUGC1M library Mus musculus genomic  
 DEFINITION clone UUGC1M0166123 R, genomic survey sequence.

ACCESSION AZ400559  
 VERSION AZ400559.1 GI:10515633  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Mus.  
 1 (bases 1 to 730)  
 Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamil, C.,  
 Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T.,  
 Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von  
 Niederhausern, A. and Wright, D., Weiss, R.

TITLE Mouse whole genome scaffolding with paired end reads from 10kb

JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert length: 10000 Std Error: 0.00  
 Plate: 0166 row: 1 column: 23  
 Seq primer: CACACAGAAACGCTATGACC  
 Class: plasmid ends  
 High quality sequence stop: 730.

## FEATURES

source

1..730  
 Location/Qualifiers  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGC1M0166123"  
 /sex="Male"  
 /lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_lib="Mouse 10kb plasmid UUGC1M library"  
 /note="Vector: PWD42nv, Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically sheared by repeated passage through a

## ORIGIN

Query Match 30.5%; Score 18; DB 9; Length 730;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 TTAATCCTAGTATCCAT 41  
 |||  
 DB 128 TTAATCCTAGTATCCAT 111

0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 ligated DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of pMD42 (g14732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

## RESULT 7

BZ267479/c 773 bp DNA linear GSS 15-OCT-2002  
 LOCUS CH230-315D4.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone  
 DEFINITION CH230-315D4, genomic survey sequence.

ACCESSION BZ267479  
 VERSION BZ267479.1 GI:23983044  
 KEYWORDS GSS.

SOURCE Rattus norvegicus (Norway rat)  
 ORGANISM Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridea; Muridae; Murinae; Rattus.  
 1 (bases 1 to 773)  
 Zhao, S., Shetty, J., Shatsman, S., Tsagaye, G., Geer, K.,  
 Shvartsbeyn, A., Gebregorgis, B., Overton, L., Russell, D., Chen, D.,  
 Riggs, F., de Jong, P. and Fraser, C.M.

TITLE Rat BAC End Sequences from Library CHORI-230 MboI segment  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Shaying Zhao  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850, USA  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: szhao@igr.org

Clones are derived from the rat BAC library CHORI-230  
 (http://www.chori.org/bacpac/rat230.htm). For BAC library  
 availability, please contact Pieter de Jong (pje@jngmail.cho.org).  
 Clones may be purchased from BACPAC Resources  
 (http://www.chori.org/bacpac/orering/information.html). BAC end  
 page: http://www.tigr.org/cdb/bac\_ends/rat/bac\_end\_intro.html  
 Plate: 315 row: D column: 4  
 Seq primer: 17  
 Class: BAC ends.  
 Location/Qualifiers

FEATURES  
 source

1..773  
 /organism="Rattus norvegicus"  
 /mol\_type="genomic DNA"  
 /strain="BN/SsNHsd/MCW"  
 /db\_xref="taxon:10116"  
 /clone="CH230-315D4"  
 /sex="Female"  
 /cell\_type="Brain"  
 /clone\_lib="CHORI-230 Segment 2"  
 /note="Vector: PTARBAC1.3; Site 1: MboI; Site 2: MboI;  
 CHORI-230 Rat (BN/SsNHsd/MCW) BAC library produced by  
 Pieter de Jong"



## ORIGIN

Query Match 30.5%; Score 18; DB 9; Length 773;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 GTTAATCCTAGTATCCA 40  
 |||||  
 DB 395 GTTAATCCTAGTATCCA 378

## RESULT 8

DR813392 775 bp mRNA linear EST 28-JUL-2005  
 LOCUS ZM\_BF0042118.r\_ZM\_BF0 Zea mays cDNA 5', mRNA sequence.  
 DEFINITION DR813392  
 ACCESSION DR813392.1 GI:71432342  
 VERSION DR813392.1  
 KEYWORDS EST.  
 SOURCE Zea mays  
 ORGANISM Zea mays

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 775)

## AUTHORS

Rao, K., Haller, K., Wiscocki, M., Smart, D., Kudrna, D., Muller, C.,  
 Kim, H., Collura, K., Wing, R., Soderlund, C., Walbot, V. and Yu, Y.

## TITLE

Maize Full-length cDNA Project  
 Unpublished (2005)

## JOURNAL

Contact: Yeliso Yu  
 Arizona Genomics Institute  
 The University of Arizona  
 Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
 Tel: 520 626 9585  
 Fax: 520 621 1259  
 Email: yeliso@genome.arizona.edu  
 Plate: 0042 row: 1 column: 18.

## COMMENT

Location/Qualifiers  
 1..775  
 /organism="Zea mays"  
 /mol\_type="mRNA"  
 /cultivar="B73"  
 /db\_xref="taxon:4577"  
 /tissue\_type="mixed (silks, husks, ears, pollen, shoot  
 tips, leaf, root tips, whole seed, embryo)"  
 /dev\_stage="varies by tissue"  
 /lab\_host="DH10B T1 phage resistant"  
 /clone\_id="ZM\_BF0"

## FEATURES

source

/note="Vector: PCMV-SPORT 6.1; Site 1: SCRV; Site 2:  
 NotI; Maize Full length cDNA library (3530 library)"  
 created by Invitrogen from multiple tissues; Organ: silks,  
 husks, ears, pollen, shoot tips, leaf, root tips, whole  
 seed, embryo. This is a Gateway compatible vector,  
 permitting clone movement to new vector backbones for  
 expression in diverse host cells using recombination  
 rather than restriction enzymes. poly(A) + mRNA was  
 prepared by Invitrogen, and equimolar amounts of RNA from  
 each of the 12 tissue samples were mixed together for  
 selection of mRNA with a 5' cap. After synthesis of cDNA,  
 a normalization step was conducted against the mixture of  
 RNA sources. Tissues prepared: 1. just emerging silks; 2.  
 inner husks from ears of sample #1; 3. 20 dap aleurone; 4.  
 immature tassels; stages from 1-2 mm to 1-2 cm; 5. 2 mm to  
 2 cm ears; 6. pollen; 7. 1 cm vegetative shoot tips from  
 15 day old seedlings; all leaves with an expanded or  
 partially expanded sheath were removed; 8. mature leaf  
 tissue; 9. 0.5 cm long root tips from 15 day old  
 seedlings; 10. 10 dap whole seed; 11. 12 dap endosperm and  
 embryo; 12. 17 dap endosperm and embryo. All of the  
 sequenced clones in Maize Full-length cDNA Project will be  
 archived at the University of Arizona. Clones, high  
 density filters and amplified library can be ordered from  
 the University of Arizona  
 (http://www.genome.arizona.edu/orders/)."

## ORIGIN

Query Match 30.5%; Score 18; DB 8; Length 775;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTAGAAACGACTTAA 55  
 |||||  
 DB 426 CCATTAGAAACGACTTAA 409

## RESULT 9

CC679999 853 bp DNA linear GSS 19-JUN-2003  
 LOCUS OGRAV88TH\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMWBMA0334008,  
 DEFINITION OGRAV88TH\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMWBMA0334008,  
 ACCESSION CC679999  
 VERSION CC679999.1 GI:32084775  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.  
 1 (bases 1 to 853)

## AUTHORS

Whitelaw, C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
 Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
 Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.

## TITLE

Consortium for Maize Genomics  
 Unpublished (2002)

## JOURNAL

Other GSSs: OGRAV88TH  
 Contact: Cathy Whitelaw

## COMMENT

TIGR  
 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whitelaw@tigr.org  
 Seq primer: TR  
 Class: methylation filtered.  
 Location/Qualifiers  
 1..853  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_id="ZMWBMA0334008"  
 /clone\_id="ZM\_0.7\_1.5\_KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## FEATURES

source

/organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_id="ZMWBMA0334008"  
 /clone\_id="ZM\_0.7\_1.5\_KB"  
 /note="Vector: pBCK-; Site 1: HincII; 0.7-1.5 kb  
 methylation filtered genomic DNA library"

## ORIGIN

Query Match 30.5%; Score 18; DB 9; Length 853;  
 Best Local Similarity 100.0%; Pred. No. 6.5;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTAGAAACGACTTAA 55  
 |||||  
 DB 503 CCATTAGAAACGACTTAA 486

## RESULT 10

BZ728527 891 bp DNA linear GSS 03-MAR-2003  
 LOCUS OGBU48TC\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMWBMA0223H24,  
 DEFINITION OGBU48TC\_ZM\_0.7\_1.5\_KB Zea mays genomic clone ZMWBMA0223H24,  
 ACCESSION BZ728527  
 VERSION BZ728527.1 GI:28701775  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays

## REFERENCE

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Zea.



REFERENCE 1 (bases 1 to 891)  
 AUTHORS WhiteLew,C.A., Quackenbush,J., Van Aken,S., Unterback,T.,  
 Renick,A., Fraser,C.M., Buddman,M.A., Bedell,J.A., Rohlfing,T.,  
 Citek,R.W., Numborg,A., Robbins,D. and Lakey,N.  
 TITLE Consortium for Maise Genomics  
 JOURNAL Unpublished (2002)  
 COMMENT Other GSSs: OGBJ48TM  
 Contact: Cathy WhiteLew  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteLew@tigr.org  
 Seq primer: TP  
 Class: methylation filtered.  
 Location/Qualifiers  
 source 1..891  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone="ZMMBMA023H24"  
 /clone\_lib="ZM 0\_7-1.5\_KB"  
 /note="Vector: pBCSK-; Site 1: HincII, 0.7-1.5 kb  
 methylation filtered genomic DNA library"

ORIGIN  
 Query Match 30.5%; Score 18; DB 9; Length 891;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 55  
 |||||  
 65 CCATTGAAACGACTTAA 82

RESULT 11  
 LOCUS CE296452 265 bp DNA linear GSS 26-SEP-2003  
 DEFINITION tigr-gss-dog-1700033908131 Dog Library Canis familiaris genomic.  
 accession CE296452  
 version CE296452.1 GI:36082022  
 keywords GSS.  
 source Canis familiaris (dog)  
 organism Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 265)  
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkness@tigr.org  
 Class: shotgun.  
 Location/Qualifiers  
 source 1..265  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 28.8%; Score 17; DB 10; Length 265;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 54  
 |||||  
 82 CCATTGAAACGACTTAA 98

RESULT 12  
 LOCUS CE776306 342 bp DNA linear GSS 30-SEP-2003  
 DEFINITION tigr-gss-dog-17000330631827 Dog Library Canis familiaris genomic.  
 accession CE776306  
 version CE776306.1 GI:37117069  
 keywords GSS.  
 source Canis familiaris (dog)  
 organism Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 342)  
 AUTHORS Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K.,  
 Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
 Venter,J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 COMMENT Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirkness@tigr.org  
 Class: shotgun.  
 Location/Qualifiers  
 source 1..342  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BstXI; Libraries were prepared from  
 peripheral blood"

ORIGIN  
 Query Match 28.8%; Score 17; DB 10; Length 342;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 54  
 |||||  
 82 CCATTGAAACGACTTAA 98

RESULT 13  
 LOCUS CE454063 388 bp DNA linear GSS 27-SEP-2003  
 DEFINITION tigr-gss-dog-17000339429317 Dog Library Canis familiaris genomic.  
 accession CE454063  
 version CE454063.1 GI:36747204  
 keywords GSS.  
 source Canis familiaris (dog)  
 organism Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

REFERENCE 1 (bases 1 to 388)



**AUTHORS** Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.  
**TITLE** The dog genome: survey sequencing and comparative analysis  
**JOURNAL** Science 301 (5641), 1898-1903 (2003)  
**PUBMED** 14512627  
**COMMENT** Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun

**FEATURES** Location/Qualifiers  
 source 1..388  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BcXI; Libraries were prepared from peripheral blood"

**ORIGIN**

Query Match 28.8%; Score 17; DB 10; Length 388;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 38 CCATTAGAAACGACTAA 54  
 |||||  
 Db 277 CCATTAGAAACGACTAA 261

**RESULT 14** CSE61277 390 bp DNA linear GSS 28-SEP-2003  
**LOCUS** tigr-gss-dog-17000327493349 Dog library Canis familiaris genomic,  
**DEFINITION** genomic survey sequence.  
**ACCESSION** CSE61277  
**VERSION** CSE61277.1 GI:36878058  
**KEYWORDS** GSS.  
**SOURCE** Canis familiaris (dog)  
**ORGANISM** Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

**REFERENCE** 1 (bases 1 to 390)  
**AUTHORS** Kirkness,E.F., Bafna,V., Halpern,A.L., Levy,S., Remington,K., Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and Venter,J.C.  
**TITLE** The dog genome: survey sequencing and comparative analysis  
**JOURNAL** Science 301 (5641), 1898-1903 (2003)  
**PUBMED** 14512627  
**COMMENT** Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun

**FEATURES** Location/Qualifiers  
 source 1..390  
 /organism="Canis familiaris"  
 /mol\_type="genomic DNA"  
 /strain="Standard Poodle"  
 /db\_xref="taxon:9615"  
 /clone\_lib="Dog Library"  
 /note="Site 1: BcXI; Libraries were prepared from peripheral blood"

**ORIGIN**

Query Match 28.8%; Score 17; DB 10; Length 390;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 38 CCATTAGAAACGACTAA 54  
 |||||  
 Db 142 CCATTAGAAACGACTAA 158

**RESULT 15** BF294016 443 bp mRNA linear EST 17-NOV-2000  
**LOCUS** BF294016/c  
**DEFINITION** WHE2162\_H05\_P1025 Triticum turgidum L. var. durum (durum wheat)  
 whole plant cDNA library Triticum turgidum cDNA clone  
 WHE2162\_H05\_P10, mRNA sequence.  
**ACCESSION** BF294016  
**VERSION** BF294016  
**KEYWORDS** BF294016.1 GI:11225080  
**SOURCE** EST.  
**ORGANISM** Triticum turgidum  
 Triticum turgidum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.

**REFERENCE** 1 (bases 1 to 443)  
**AUTHORS** Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Jazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D.  
**TITLE** The structure and function of the expressed portion of the wheat genomes - Whole plant cDNA library from Triticum turgidum L. var. durum  
**JOURNAL** Unpublished (2000)  
**COMMENT** Contact: Olin Anderson  
 US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center  
 800 Buchanan Street, Albany, CA 94710, USA  
 Tel: 5105595773  
 Fax: 5105595818  
 Email: oanderson@pw.usda.gov  
 Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20  
 Seq primer: Stragene SK primer.

**FEATURES** Location/Qualifiers  
 source 1..443  
 /organism="Triticum turgidum"  
 /mol\_type="mRNA"  
 /cultiivar="Langdon-16"  
 /db\_xref="taxon:4571"  
 /clone="WHE2162\_H05\_P10"  
 /tissue\_type="All tissues"  
 /dev\_stage="Different growth stages"  
 /lab\_host="E. coli SOLR"  
 /clone\_lib="Triticum turgidum L. var. durum (durum wheat)  
 whole plant cDNA library"

**note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site 1: EcoRI; Site 2: XhoI; Plants were grown in a growth chamber at North Dakota State University (Kianian, Otto, Simons). Tissues collected from seven-day etiolated seedling leaf, stem, root and seed; leaf from plant at fourth leaf stage; spike from pre-anthesis through 20 days after anthesis; flag leaf; leaf and stem tissue from tillers and root. Total RNA and poly(A) RNA were prepared from each tissue and then pooled, a cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagemids in the T7 Close lab (Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons, Zhang) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."**

**ORIGIN**

Query Match 28.8%; Score 17; DB 2; Length 443;  
 Best Local Similarity 100.0%; Pred. No. 26;



Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 AGCGGATAGCGCGGT 24  
 |||||  
 Db 164 AGCGGATAGCGCGGT 148

RESULT 16  
 AQ490035 446 bp DNA linear GSS 24-APR-1999  
 LOCUS RPCI-11-265017.TV RPCI-11 Homo sapiens genomic clone  
 DEFINITION RPCI-11-265017, genomic survey sequence.  
 ACCESSION AQ490035  
 VERSION AQ490035.1 GI:4675909  
 KEYWORDS GSS.  
 ORGANISM Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 446)  
 Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and  
 Venter,J.C.  
 Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
 Map Building (1997)  
 JOURNAL Unpublished  
 COMMENT Other GSSs: RPCI-11-265017.TJ  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850  
 Tel: 301 838 0200  
 Fax: 301 838 0208  
 Email: hbeet@igr.org  
 Clones are derived from the human BAC library RPCI-11. For BAC  
 library availability, please contact Pieter de Jong  
 (pieter@edj.med.buffalo.edu). Clones may be purchased from  
 BACRAC Resources (http://bacpac.med.buffalo.edu/ordering) or from  
 Research Genet cs (info@resgen.com). BAC end search page:  
 http://www.tigr.org/cdb/humgen/bac\_end\_search/bac\_end\_search.html.  
 Seq primer: T7  
 Class: BAC ends.  
 Location/Qualifiers  
 source  
 1..446  
 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="GDB:7601728"  
 /db\_xref="taxon:9606"  
 /clone="RPCI-11-265017"  
 /sex="Male"  
 /cell\_type="Lymphocytes"  
 /clone\_11b="RPCI-11"  
 /note="Vector: pBACe3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
 RCI11 Human Male BAC library"

Query Match 28.8%; Score 17; DB 9; Length 446;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 TCCTAGTATCCATTAG 44  
 |||||  
 Db 168 TCCTAGTATCCATTAG 184

RESULT 17  
 AZ653505 471 bp DNA linear GSS 14-DEC-2000  
 LOCUS IM0527008F Mouse 10kb plasmid UUGCIM library Mus musculus genomic  
 DEFINITION clone UUGCIM0527008 F, genomic survey sequence.  
 ACCESSION AZ653505  
 VERSION AZ653505.1 GI:11790651  
 KEYWORDS GSS.

SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 471)  
 Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,  
 Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T.,  
 Rellly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von  
 Niederhausern,A. and Wright,D., Weiss,R.  
 Mouse whole genome scaffolding with paired end reads from 10kb  
 plasmid inserts  
 JOURNAL Unpublished (2000)  
 COMMENT Contact: Robert B. Weiss  
 University of Utah Genome Center  
 University of Utah  
 Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT  
 84112, USA  
 Tel: 801 585 5606  
 Fax: 801 585 7177  
 Email: ddunn@genetics.utah.edu  
 Insert Length: 10000 Std Error: 0.00  
 Plate: 0527 row: 0 column: 08  
 Seq primer: CGTTGTAAACGACGCCAGT  
 Class: plasmid end  
 High quality sequence stop: 471.  
 Location/Qualifiers  
 1..471  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /strain="C57BL/6J"  
 /db\_xref="taxon:10090"  
 /clone="UUGCIM0527008"  
 /sex="Male"  
 /lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
 /clone\_11b="Mouse 10kb plasmid UUGCIM library"  
 /note="Vector: PMD42nv; Purified genomic DNA from M.  
 musculus C57BL/6J (male) was obtained from the Jackson  
 Laboratory Mouse DNA Resource  
 (http://www.jax.org/resources/documents/dnares/). The DNA  
 was hydrodynamically shared by repeated passage through a  
 0.005 inch orifice at constant velocity. The sheared DNA  
 was blunt end-repaired with T4 DNA polymerase and T4  
 polynucleotide kinase. Adaptor oligonucleotides were  
 ligated to the blunt ends in high molar excess. The  
 adaptor DNA was purified and size-selected for a 9.5 to  
 10.5 kb range using preparative agarose gel  
 electrophoresis. Vector DNA was prepared from a derivative  
 of PMD42 (g114732114|gb|AF129072.1), a copy-number  
 inducible derivative of plasmid R1. The vector was ligated  
 with adaptors complementary to the insert adaptors and  
 purified. The sheared, adaptor mouse DNA was annealed to  
 adaptor vector DNA, and transformed into  
 chemically-competent E. coli XL10-Gold (Stratagene) cells  
 and selected for ampicillin resistance."

ORIGIN

Query Match 28.8%; Score 17; DB 9; Length 471;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 40 ATTAGAAAGCTAAAC 56  
 |||||  
 Db 200 ATTAGAAAGCTAAAC 216

RESULT 18  
 AQ439149 516 bp DNA linear GSS 31-MAR-1999  
 LOCUS HS\_3051\_A1 D03 T7A RPCI-11 Human Male BAC library Homo sapiens  
 DEFINITION genomic clone Plate=627 Col=5 Row=G, genomic survey sequence.  
 ACCESSION AQ439149  
 VERSION AQ439149.1 GI:4550488



KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Homo.  
REFERENCE 1 (bases 1 to 516)  
AUTHORS Mahairas G.G., Wallace J.C., Smith K., Swartzell S., Holzman T.,  
Keller A., Shaker R., Furlong J., Young J., Zhao S., Adams M.D. and  
Hood L.  
TITLE Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
PUBMED 10449764  
COMMENT Contact: Mahairas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones are derived from the human BAC library RPCT-11. For BAC  
library availability, please contact Pieter de Jong  
(pieter@dejong.med.buffalo.edu). Clones may be purchased from  
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)  
or from Research Genetics (info@resgen.com). BAC end Web Server:  
http://www.hnsc.washington.edu  
Plate: 627 row: G column: 5  
Seq primer: T7  
Class: BAC ends  
High quality sequence stop: 516.  
FEATURES  
source location/Qualifiers  
1..516  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone="Plate=627 Col=5 Row=G"  
/sex="male"  
/clone\_lib="RPCT-11 Human Male BAC Library"  
/note="Vector: pBAC3.6; Site\_1: EcoRI; Site\_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBAC3.6 vector at EcoRI sites"  
ORIGIN  
Query Match 28.8%; Score 17; DB 9; Length 516;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 AGTGCATTCATTAGAAAC 48  
|||||  
Db 359 AGTGATCCATTAGAAAC 343  
|||||  
RESULT 19  
CNS07HW8/c 534 bp DNA linear GSS 03-OCT-2001  
LOCUS Anopheles gambiae GSS SP6 end of clone 31C02 of library Notredame1  
DEFINITION from strain PEST of Anopheles gambiae (African malaria mosquito),  
genomic survey sequence.  
ACCESSION AF611594.1 GI:15963017  
VERSION AF611594.1 GI:15963017  
KEYWORDS GSS.  
SOURCE Anopheles gambiae (African malaria mosquito)  
ORGANISM Anopheles gambiae  
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Prexygota;  
Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Culicidae; Anophelinae; Anopheles.  
REFERENCE 1 (bases 1 to 534)  
AUTHORS Genoscope.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-2001) Genoscope - Centre National de Sequencage :

BP 191 91006 EVRY cedex - FRANCE (E-mail : sequef@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
REFERENCE 2 (bases 1 to 534)  
AUTHORS Roth C.W., Brey P.T., Ke Z. and Collins F.H.  
TITLE Direct Submission  
JOURNAL Submitted (01-OCT-2001) BMVI, Institut Pasteur, 25, rue du Dr.  
Roux, Paris 75015, France  
COMMENT This clone is from an A. gambiae BAC library provided by F.H.  
Collins and sequenced by Genoscope in collaboration with the  
Laboratory of Biochem. and Biol. Molec. of Insects, Institut  
Pasteur.  
FEATURES  
source location/Qualifiers  
1..534  
/organism="Anopheles gambiae"  
/mol\_type="genomic DNA"  
/strain="PEST"  
/db\_xref="taxon:7165"  
/clone="31C02"  
/clone\_lib="Notredame1"  
/note="end : SP6"  
ORIGIN  
Query Match 28.8%; Score 17; DB 11; Length 534;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 35 GATCCATTAGAAACGAC 51  
|||||  
Db 451 GATCCATTAGAAACGAC 435  
|||||  
RESULT 20  
CE327120 602 bp DNA linear GSS 26-SEP-2003  
LOCUS tigr-gss-dog-1700033942130 Dog Library Canis familiaris genomic,  
genomic survey sequence.  
DEFINITION CE327120  
ACCESSION CE327120.1 GI:36139323  
VERSION CE327120.1 GI:36139323  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.  
REFERENCE 1 (bases 1 to 602)  
AUTHORS Kirkness E.F., Batina V., Halpern A.L., Levy S., Remington K.,  
Rusch D.B., Delcher A.L., Pop M., Wang W., Fraser C.M. and  
Venter J.C.  
TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: Shotgun.  
FEATURES  
source location/Qualifiers  
1..602  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"  
ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 602;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Oy 38 CCATTGAAACGACTTAA 54  
 |||||  
 Db 287 CCATTGAAACGACTTAA 303

## RESULT 21

CE655765/c  
 LOCUS CE655765/c  
 DEFINITION tigr-g98-dog-17000368373551 Dog Library Canis familiaris genomic,  
 genomic survey sequence.

ACCESSION CE655765  
 VERSION CE655765.1 GI:36974629  
 KEYWORDS GSS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
 Canis.

## REFERENCE

AUTHORS

1 (bases 1 to 624)  
 Kirkness E.F., Bafna V., Halpern A.L., Levy S., Remington K.,  
 Ruesch D.B., Delcher A.L., Pop M., Wang M., Fraser C.M. and  
 Venter J.C.  
 TITLE The dog genome: survey sequencing and comparative analysis  
 JOURNAL Science 301 (5641), 1898-1903 (2003)  
 PUBMED 14512627

## COMMENT

Contact: Kirkness EF  
 The Institute for Genomic Research  
 Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
 Rockville, MD 20850, USA  
 Tel: 301-838-0200  
 Fax: 301-838-0208  
 Email: ekirknes@tigr.org  
 Class: shotgun.

Location/Qualifiers

1..624

/organism="Canis familiaris"

/mol\_type="genomic DNA"

/strain="Standard Poodle"

/db\_xref="taxon:9615"

/clone\_lib="Dog Library"

/note="Site 1: BstXI; Libraries were prepared from

peripheral blood"

## ORIGIN

Query Match 28.8%; Score 17; DB 10; Length 624;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 38 CCATTGAAACGACTTAA 54  
 |||||  
 Db 383 CCATTGAAACGACTTAA 367

## RESULT 22

AV374156/c  
 LOCUS AV374156 648 bp mRNA linear EST 24-OCT-2001  
 DEFINITION AV374156 RIKEN full-length enriched, adult male cecum Mus musculus  
 cDNA clone 9130006K13 3', mRNA sequence.

ACCESSION AV374156  
 VERSION AV374156.2 GI:16397936  
 KEYWORDS EST.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus

## REFERENCE

AUTHORS

1 (bases 1 to 648)  
 Arakawa T., Carninci P., Fukuda S., Furuno M., Hanagaki T.,  
 Hara A., Hiramoto K., Horii F., Ishii Y., Ito M., Kawai J.,  
 Komano H., Kouda M., Koya S., Matsuyama T., Miyazaki A., Nomura K.,  
 Ohno M., Okazaki Y., Okido T., Saito R., Sakai C., Sakai K.,  
 Sano H., Sasaki D., Shibata K., Shingawa A., Shiraki T.,

TITLE  
 JOURNAL  
 COMMENT

Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F.,  
 Takeda Y., Tanaka T., Toya T., Muramatsu M. and Hayashizaki Y.  
 RIKEN Mouse ESTs (Arakawa T., et al. 2001)  
 Unpublished (2001)  
 On Nov 14, 1999 this sequence version replaced gi:6421803.

Contact: Yoshihide Hayashizaki  
 Laboratory for Genome Exploration Research Group, RIKEN Genomic  
 Sciences Center (GSC), Yokohama Institute  
 The Institute of Physical and Chemical Research (RIKEN)  
 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
 Tel: 81-45-503-9222  
 Fax: 81-45-503-9226

Email: genome-res@sc.riken.jp, URL: http://genome.gsc.riken.jp/  
 Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K.,  
 Itoh M., Komano H., Okazaki Y., Muramatsu M. and Hayashizaki Y.  
 Normalization and subtraction of cap-trapper-selected cDNAs to  
 prepare full-length cDNA libraries for rapid discovery of new  
 genes. Genome Res. 10 (10), 1617-1630 (2000)  
 wagi K., Fujiwara S., Inoue K., Togawa Y., Izawa M., Ohara E.,  
 Watabiki M., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T.,  
 Matsura S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A.  
 and Hayashizaki Y.

RIKEN integrated sequence analysis (RISA) system--384-format  
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.  
 10 (11), 1757-1771 (2000)  
 Komano H., Fukunishi Y., Shibata K., Itoh M., Carninci P.,  
 Sugahara Y. and Hayashizaki Y.

Computer-based methods for the mouse full-length cDNA  
 encyclopedia: real-time sequence clustering for construction of a  
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)  
 Kondo S., Shingawa A., Saito T., Kiyosawa H., Yamazaki I.,  
 Aizawa K., Fukuda S., Hara A., Itoh M., Kawai J., Shibata K. and  
 Hayashizaki Y.

Computational Analysis of Full-length Mouse cDNAs Compared with  
 Human Genome Sequences Mamm. Genome. 12, 673-677 (2001)  
 Please visit our web site (http://genome.gsc.riken.go.jp/) for  
 further details.

cDNA library was prepared and sequenced in Mouse Genome  
 Encyclopedia Project of Genome Exploration Research Group in Riken  
 Genomic Sciences Center and Genome Science Laboratory in Riken.  
 Division of Experimental Animal Research in Riken contributed to  
 prepare mouse tissues.

Location/Qualifiers

1..648

/organism="Mus musculus"

/mol\_type="mRNA"

/strain="C57BL/6J"

/db\_xref="taxon:10090"

/clone="9130006K13"

/sex="male"

/tissue\_type="cecum"

/dev\_stage="adult"

/lab\_host="DH10B"

/clone\_lib="RIKEN full-length enriched, adult male cecum"

/note="Site 1: SalI; Site 2: BamHI; cDNA library was

prepared and sequenced in Mouse Genome Encyclopedia

Project of Genome Exploration Research Group in Riken

Genomic Sciences Center and Genome Science Laboratory in

RIKEN. Division of Experimental Animal Research in Riken

contributed to prepare mouse tissues. 1st strand cDNA was

primed with a primer [5'

GAGAGAGAGAGATCCAGAGCTCTTTTCTTTTCTTTTCTTTVN 3'], cDNA was

prepared by using trehalose thermo-activated reverse

transcriptase and subsequently enriched for full-length by

cap-trapper. cDNA went through one round of normalization

to Rot = 10.0 and subtraction to Rot = 185.0. Second

strand cDNA was prepared with the primer adapter of

sequence [5' GAGAGAGAGATCCAGAGTATTAATTAATCCCCCCCCCC

3']. cDNA was cloned into the XhoI and BamHI sites.

Vector: a modified plucscript KS(+) after bulk excision

from Lambda PLoC I. Cloning sites, 5' end: SalI; 3' end:

BamHI"

## ORIGIN



Query Match 28.8%; Score 17; DB 1; Length 648;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCTAGTATCCATTAG 44  
|||||  
Db 104 TCTAGTATCCATTAG 88

RESULT 23  
LOCUS CM975216 652 bp DNA linear GSS 21-DEC-2004  
DEFINITION A1AA-aaa84a08.b1 Ancylostoma caninum whole genome shotgun library (A1AAGSS 001) Ancylostoma caninum genomic, genomic survey sequence.  
ACCESSION CM975216  
KEYWORDS CM975216.1 GI:56779529  
SOURCE GSS.  
ORGANISM Ancylostoma caninum (dog hookworm)  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Strongylida; Ancylostomatoidea; Ancylostomatidae; Ancylostomatinae; Ancylostoma.  
REFERENCE 1 (bases 1 to 652)  
AUTHORS Mitreva,M., McCarter,J.P., Pape,D., Ritzer,E., Tsagareishvili,R., Rorko,I., Martin,J., Wylie,T., Dante,M., Meyer,R., Messina,D., Wareston,R.H., Clifton,S.W. and Wilson,R.  
TITLE Genome Survey sequences from the parasitic nematode Ancylostoma caninum  
JOURNAL Unpublished (2004)  
COMMENT Contact: Mitreva M  
Washington University in St. Louis  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: nematode@watson.wustl.edu  
Genomic DNA provided by John Hawdon (mtmjnb@wumc.edu) DNA sequenced by Washington University Genome Sequencing Center  
Class: shotgun.  
Location/Qualifiers  
source 1..652  
/organism="Ancylostoma caninum"  
/mol\_type="genomic DNA"  
/strain="Baltimore"  
/db\_xref="taxon:29170"  
/dev\_stage="Adult"  
/lab\_host="G510"  
/clone\_lib="Ancylostoma caninum whole genome shotgun library (A1AAGSS 001)"  
/note="Vector: pOTW13; Site 1: BstXI; Site 2: BstXI; Ancylostoma caninum genomic DNA was randomly sheared, end-repaired and size fractionated to enrich for 2-4 kb fragments. Genomic DNA was provided by John Hawdon (mtmjnb@wumc.edu) at George Washington University. Sequencing by Washington University Genome Sequencing Center, St. Louis, MO."

ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 652;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTGAAGGCGGATAG 17  
|||||  
Db 482 GGTGAAGGCGGATAG 498

RESULT 24  
LOCUS AZ351768 654 bp DNA linear GSS 29-SEP-2000  
DEFINITION IM0090A04F Mouse 10kb plasmid U06C1M library Mus musculus genomic clone U06C1M0090A04 F, genomic survey sequence.  
ACCESSION AZ351768

VERSION AZ351768.1 GI:10431005  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.  
REFERENCE 1 (bases 1 to 654)  
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,B., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Weiss,R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts  
JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah  
University of Utah  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLIC, UT 84112, USA  
Tel: 801 585 5606  
Fax: 801 585 7177  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0090 row: A column: 04  
Seq primer: CGTTGTAAACGACGCCACGT  
Class: plasmid ends  
High quality sequence stop: 654.  
Location/Qualifiers  
source 1..654  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="U06C1M0090A04"  
/sex="Male"  
/lab\_host="E. Coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid U06C1M library"  
/note="Vector: pWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adapted DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (g1[473114]gb[AF129072.1]), a copy-number inducible derivative of plasmid 81. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adapted mouse DNA was annealed to adapted vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

ORIGIN  
Query Match 28.8%; Score 17; DB 9; Length 654;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 TCTAGTATCCATTAG 44  
|||||  
Db 81 TCTAGTATCCATTAG 97

RESULT 25  
LOCUS CE047792 694 bp DNA linear GSS 24-SEP-2003  
DEFINITION t1gr-gss-dog-17000357492075 Dog library Canis familiaris genomic, genomic survey sequence.



ACCESSION CE047792  
VERSION GI:35066807  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 694)  
AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

FEATURES  
source Location/Qualifiers  
1..694  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN  
Query Match 28.8%; Score 17; DB 9; Length 694;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 54  
|||||  
Db 610 CCATTGAAACGACTTAA 594

RESULT 26  
CE068977/c 730 bp DNA linear GSS 24-SEP-2003  
LOCUS tigr-gss-dog-17000322906371 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
CE068977  
ACCESSION CE068977.1 GI:35128705  
VERSION  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 730)  
AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

FEATURES  
source Location/Qualifiers  
1..730

/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN  
Query Match 28.8%; Score 17; DB 9; Length 730;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 54  
|||||  
Db 490 CCATTGAAACGACTTAA 506

RESULT 28  
CG293819 743 bp DNA linear GSS 25-AUG-2003  
LOCUS OXKBH59TH ZM.0.7.1.5\_KB Zee may's genomic clone ZMMBMA0628122,  
DEFINITION genomic survey sequence.  
CG293819  
ACCESSION CG293819.1 GI:34208033  
VERSION

FEATURES  
source Location/Qualifiers  
1..741  
/organism="Canis familiaris"  
/mol\_type="genomic DNA"  
/strain="Standard Poodle"  
/db\_xref="taxon:9615"  
/clone\_lib="Dog Library"  
/note="Site 1: BstXI; Libraries were prepared from  
peripheral blood"

ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 741;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 38 CCATTGAAACGACTTAA 54  
|||||  
Db 490 CCATTGAAACGACTTAA 506

RESULT 27  
CE427878 741 bp DNA linear GSS 27-SEP-2003  
LOCUS tigr-gss-dog-17000362873821 Dog Library Canis familiaris genomic,  
DEFINITION genomic survey sequence.  
CE427878  
ACCESSION CE427878.1 GI:3638692  
VERSION  
KEYWORDS GSS.  
SOURCE Canis familiaris (dog)  
ORGANISM Canis familiaris  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;  
Canis.

REFERENCE 1 (bases 1 to 741)  
AUTHORS Kirkness,E.F., Batina,V., Halpern,A.L., Levy,S., Remington,K.,  
Rusch,D.B., Delcher,A.L., Pop,M., Wang,W., Fraser,C.M. and  
Venter,J.C.  
The dog genome: survey sequencing and comparative analysis  
Science 301 (5641), 1898-1903 (2003)

TITLE The dog genome: survey sequencing and comparative analysis  
JOURNAL Science 301 (5641), 1898-1903 (2003)  
PUBMED 14512627  
COMMENT Contact: Kirkness EF  
The Institute for Genomic Research  
Department of Eukaryotic Genomics, TIGR, 9712 Medical Center Drive,  
Rockville, MD 20850, USA  
Tel: 301-838-0200  
Fax: 301-838-0208  
Email: ekirkness@tigr.org  
Class: shotgun.

FEATURES  
source Location/Qualifiers  
1..741



KEYWORDS GSS.  
SOURCE Zea mays  
ORGANISM Zea mays

REFERENCE  
AUTHORS White, C.A., Quackenbush, J., Van Aken, S., Uteerback, T., Resnick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T., Citek, R.W., Numborg, A., Robbins, D. and Lakey, N.  
Consortium for Maize Genomics  
Unpublished (2002)  
Other GSSs: OX8H59TV  
Contact: Cathy Whitelaw  
TIGR

9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whitelaw@tigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
1..743  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMMB0628122"  
/clone\_1lb="ZM 0.7.1.5\_KB"  
/note="Vector: pBSCSK-1; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN

Query Match 28.8%; Score 17; DB 10; Length 743;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 7 AAGGCGATAGCGGCGG 23  
|||||  
660 AAGGCGATAGCGGCGG 676

RESULT 29  
AO894668 748 bp DNA linear GSS 10-NOV-1999  
LOCUS HS\_3148\_A2\_H12\_MR CIT Approved Human Genomic Sperm Library D Homo  
DEFINITION sapiens genomic clone Plate=3148 Col=24 Row=O, genomic survey  
sequence.  
ACCESSION AO894668  
VERSION AO894668.1 GI:6350858  
KEYWORDS GSS.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominiidae; Homo  
1 (bases 1 to 748)  
Mahaitas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T.,  
Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and  
Hood, L.  
Sequence-tagged connectors: A sequence approach to mapping and  
scanning the human genome  
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)  
10449764  
Contact: Mahaitas GG, Wallace JC, Hood L  
High Throughput Sequencing Center  
University of Washington  
401 Queen Anne Avenue North, Seattle, WA 98109, USA  
Tel: (206) 616-3618  
Fax: (206) 616-3887  
Email: jwallace@u.washington.edu  
Clones may be purchased from Research Genetics (info@resgen.com).  
BAC end Web Server: <http://www.htsec.washington.edu>

Plate: 3148 row: 0 column: 24  
Seq primer: M13 Reverse  
Class: BAC ends  
High quality sequence stop: 748.  
Location/Qualifiers  
1..748  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/clone\_plate=3148 Col=24 Row=O"  
/sex="male"  
/clone\_1lb="CIT Approved Human Genomic Sperm Library D"  
/note="Organ: sperm; Vector: pBelOBAC11; BAC clones in  
E-Coli DH10B"

ORIGIN

Query Match 28.8%; Score 17; DB 9; Length 748;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 28 TCTTAGTATCATTAG 44  
|||||  
248 TCTTAGTATCATTAG 264

RESULT 30  
AZ883925/c 749 bp DNA linear GSS 05-MAR-2001  
LOCUS RPCI-23-204010.TV RPCI-23 Mus musculus genomic clone  
DEFINITION RPCI-23-204010, genomic survey sequence.  
ACCESSION AZ883925  
VERSION AZ883925.1 GI:13202870  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 749)  
Zhao, S., Nierman, W., Feldblum, T., Malek, J., Shatman, S.,  
Akuret, B., Levins, M., McGann, S., Teegaye, G., Geer, K., Krol, M., de  
Jong, P. and Fraser, C.M.  
Mouse BAC End Sequences from Library RPCI-23  
Unpublished (1999)  
Other GSSs: RPCI-23-204010.TV  
Contact: Shaying Zhao  
Department of Eukaryotic Genomics  
The Institute for Genomic Research  
9712 Medical Center Dr., Rockville, MD 20850, USA  
Tel: 301 838 0200  
Fax: 301 838 0208  
Email: szhao@tigr.org  
Clones are derived from the mouse BAC library RPCI-23. For BAC  
library availability, please contact Pieter de Jong  
(pdejong@mail.cho.org). Clones may be purchased from BACPAC  
resources (<http://www.choi.org/bacpac/orderingframe.html>). BAC end  
page: [http://www.tigr.org/tdb/bac\\_ends/mouse/bac\\_end\\_intro.html](http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html)  
Plate: 204 row: 0 column: 10  
Seq primer: T7  
Class: BAC ends.  
Location/Qualifiers  
1..749  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone\_plate=3148 Col=24 Row=O"  
/sex="female"  
/lab\_host="DH10B"  
/clone\_1lb="RPCI-23"  
/note="Organ: Kidney/Brain; Vector: pBACe3.6; Site 1:  
EcoRI; Site 2: EcoRI; Female C57BL/6J mouse kidney and/or  
brain genomic DNA was isolated and partially digested



with a combination of EcoRI and EcoRI Methylase. Size selected DNA was cloned into the pBac3.6 vector at the EcoRI sites. The ligation products were transformed into DH10B electrocompetent cells (BRL Life Technologies). "

## ORIGIN

Query Match 28.8%; Score 17; DB 9; Length 749;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 TCGTAGTATCCATTAG 44  
|||||  
Db 630 TCGTAGTATCCATTAG 614

RESULT 31  
A2992510 792 bp DNA linear GSS 27-APR-2001  
LOCUS 2M0277N08F Mouse 10kb plasmid UUGC2M library Mus musculus genomic  
DEFINITION clone UUGC2M0277N08 F, genomic survey sequence.

ACCESSION A2992510 GI:13863737  
VERSION A2992510.1  
KEYWORDS GSS.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Dunn, D., Aoyagi, A., Barber, M., Beacorn, T., Duval, B., Hamill, C., Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Reilly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.  
TITLE Mouse whole genome scaffolding with paired end reads from 10kb plasmid inserts

JOURNAL Unpublished (2000)  
COMMENT Contact: Robert B. Weiss  
University of Utah Genome Center  
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT 84112, USA

FEATURES  
source  
Email: ddunn@genetics.utah.edu  
Insert Length: 10000 Std Error: 0.00  
Plate: 0277 Row: N Column: 08  
Seq primer: CGTTGTAAACGACGGCCAGT  
Class: plasmid ends  
High quality sequence stop: 792.  
Location/Qualifiers  
1..792

/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/strain="C57BL/6J"  
/db\_xref="taxon:10090"  
/clone="UUGC2M0277N08"  
/sex="Female"  
/lab\_host="E. coli strain XL10-Gold, T1-resistant, F-"  
/clone\_lib="Mouse 10kb plasmid UUGC2M library"  
/note="Vector: pMD42nv; Purified genomic DNA from M. musculus C57BL/6J (female) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pMD42 (g14732114|gb|AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated

with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."

## ORIGIN

Query Match 28.8%; Score 17; DB 9; Length 792;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 TCGTAGTATCCATTAG 44  
|||||  
Db 578 TCGTAGTATCCATTAG 594

RESULT 32  
CP451309 801 bp mRNA linear EST 04-SEP-2003  
LOCUS EST687654 normalized cDNA library of onion Allium cepa cDNA clone  
DEFINITION ACADP29, mRNA sequence.

ACCESSION CP451309 GI:34474011  
VERSION CP451309.1  
KEYWORDS EST.  
SOURCE Allium cepa (onion)  
ORGANISM Allium cepa

REFERENCE Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae; Allium.  
AUTHORS Hayey, M.J., Cheung, F., Van Aken, S., Uterback, T. and Town, C.D.  
TITLE Expressed Sequence Tags from a normalized library of mixed onion tissues (Allium cepa)  
JOURNAL Unpublished (2003)  
COMMENT Contact: Hayey MJ  
Department of Horticulture  
USDA-ARS and University of Wisconsin  
1575 Linden Drive, Madison, WI 53706, USA  
Tel: 608-262-1830  
Fax: 608-262-4743  
Email: mjhayey@facstaff.wisc.edu  
TIGR sequence name ACADP29TR. For more information:  
http://hayeylab.hort.wisc.edu  
Seq primer: CAG GAA ACA GCT ATG ACC.

FEATURES  
source  
Location/Qualifiers  
1..801

/organism="Allium cepa"  
/mol\_type="mRNA"  
/cultivar="Red Creole(bulbs), unknown(callus), Ebano & Texas Legend(roots)"  
/db\_xref="taxon:4679"  
/clone="ACADP29"  
/clone\_lib="Callus, roots, and young bulbs"  
/clone\_lib="normalized cDNA library of onion"  
/note="Vector: PCMVSPORT-1-cdb (Invitrogen); Site 1: EcoRV (5'); Site 2: NotI (3'); Equal molar amounts of mRNA from callus, roots, and young bulbs were combined to synthesize the library. Normalization to enrich for low-copy transcripts was performed by proprietary techniques of Invitrogen."

## ORIGIN

Query Match 28.8%; Score 17; DB 6; Length 801;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 TAGTGATCCATTAGAA 47  
|||||  
Db 604 TAGTGATCCATTAGAA 588

RESULT 33  
CR221675



LOCUS CR221675 816 bp DNA linear GSS 06-JUL-2004  
 DEFINITION Reverse strand read from insert in 5'HPT insertion targeting and chromosome engineering clone MHPN160117, genomic survey sequence.  
 ACCESSION CR221675  
 VERSION CR221675.1 GI:50000524  
 KEYWORDS GSS; genome survey sequence; MICR.  
 SOURCE Mus musculus (house mouse)  
 ORGANISM Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 REFERENCE 1 (bases 1 to 816)  
 AUTHORS Adams,D.J., Biggs,P.J., Cox,A.V., Davies,R.M., van der Weyden,L., Jonkers,J., Smith,J., Plumb,R.W., Taylor,R.G., Niehijima,I., Yu,Y., Rogers,J. and Bradley,A.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire, CB10 1SA, UK. <http://www.sanger.ac.uk/MICR>  
 FEATURES  
 SOURCE location/Qualifiers  
 1..816  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /clone\_1fb="MHPN160117"  
 /clone\_1fb="MHPN"

ORIGIN  
 Query Match 28.8%; Score 17; DB 11; Length 816;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 40 ATTGAACGACTAAC 56  
 ||||||||||||||||  
 Db 130 ATTGAACGACTAAC 146

RESULT 34  
 LOCUS BZ702421 846 bp DNA linear GSS 19-FEB-2003  
 DEFINITION POCDD13TD ZM 0.6\_1.0\_KB Zea mays genomic clone ZMMBTA19C02, genomic survey sequence.  
 ACCESSION BZ702421  
 VERSION BZ702421.1 GI:28422656  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 846)  
 AUTHORS Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Frazer,C.M., Yuan,Y., San Miguel,P., Ma,J. and Bennezen,J.  
 TITLE Maize Genomics Consortium  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Cathy Whiteaw  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteaw@tigr.org  
 Seq primer: TP  
 Class: sheared ends.  
 FEATURES  
 SOURCE location/Qualifiers  
 1..846  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1fb="ZMMBTA19C02"  
 /clone\_1fb="ZM 0.6\_1.0\_KB"  
 /note="Vector: PCR4-ROPO; Site 1: EcoRI; 0.6-1.0 kb high Cor selected genomic DNA library"

ORIGIN  
 Query Match 28.8%; Score 17; DB 9; Length 846;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 26 AATCTAGTATCCATT 42  
 ||||||||||||||||  
 Db 820 AATCTAGTATCCATT 804

RESULT 35  
 LOCUS CG262429 848 bp DNA linear GSS 25-AUG-2003  
 DEFINITION OGMAS53TV ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0522J09, genomic survey sequence.  
 ACCESSION CG262429  
 VERSION CG262429.1 GI:34174024  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.  
 REFERENCE 1 (bases 1 to 848)  
 AUTHORS Whiteaw,C.A., Quackenbush,J., Van Aken,S., Uterback,T., Resnick,A., Frazer,C.M., Budiman,M.A., Bedell,J.A., Rohlfing,T., Citek,R.W., Nuneberg,A., Robbins,D. and Lakey,N.  
 TITLE Consortium for Maize Genomics  
 JOURNAL Unpublished (2002)  
 COMMENT Other\_GSSs: OGMAS53TH  
 CONTACT: Cathy Whiteaw  
 TIGR 9712 Medical Center Drive, Rockville, MD 20850, USA  
 Tel: 301-838-5843  
 Fax: 301-838-0208  
 Email: whiteaw@tigr.org  
 Seq primer: TP  
 Class: methylation filtered.  
 FEATURES  
 SOURCE location/Qualifiers  
 1..848  
 /organism="Zea mays"  
 /mol\_type="genomic DNA"  
 /strain="B73"  
 /db\_xref="taxon:4577"  
 /clone\_1fb="ZMMBMA0522J09"  
 /clone\_1fb="ZM 0.7\_1.5\_KB"  
 /note="Vector: DBCSK-; Site 1: HincII; 0.7-1.5 kb methylation filtered genomic DNA library"

ORIGIN  
 Query Match 28.8%; Score 17; DB 10; Length 848;  
 Best Local Similarity 100.0%; Pred. No. 27;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 AAGCGGATAGCGCGG 23  
 ||||||||||||||||  
 Db 396 AAGCGGATAGCGCGG 412

RESULT 36  
 LOCUS CG305394 918 bp DNA linear GSS 25-AUG-2003  
 DEFINITION OGB3BC16TH ZM 0.7\_1.5\_KB Zea mays genomic clone ZMMBMA0767C07, genomic survey sequence.  
 ACCESSION CG305394  
 VERSION CG305394.1 GI:34219608  
 KEYWORDS GSS.  
 SOURCE Zea mays  
 ORGANISM Zea mays  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoideae; Andropogoneae; Zea.



REFERENCE 1 (bases 1 to 918)  
AUTHORS WhiteLaw C.A., Quackenbush, J., Van Aken, S., Utterback, T.,  
Remick, A., Fraser, C.M., Budiman, M.A., Bedell, J.A., Rohlfing, T.,  
Citek, R.W., Nunez, A., Robbins, D. and Lakey, N.  
TITLE Consortium for Maize Genomics  
JOURNAL Unpublished (2002)  
COMMENT Other GSSs: OG3BCL6TV  
Contact: Cathy WhiteLaw  
TIGR Medical Center Drive, Rockville, MD 20850, USA  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-838-5843  
Fax: 301-838-0208  
Email: whiteLaw@cigr.org  
Seq primer: TR  
Class: methylation filtered.  
Location/Qualifiers  
1..918  
/organism="Zea mays"  
/mol\_type="genomic DNA"  
/strain="B73"  
/db\_xref="taxon:4577"  
/clone\_lib="ZMBA076C07"  
/clone\_1lb="ZM\_0.7-1.5\_KB"  
/note="Vector: pBCSK-; Site 1: HincII; 0.7-1.5 kb  
methylation filtered genomic DNA library"

ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 918;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGCGGATAGCGCGG 23  
Db 309 AAGCGGATAGCGCGG 325

RESULT 37 1042 bp DNA linear GSS 16-SEP-2003  
CG431663 Glomus intraradices Bgl II library (in pBK-CMV strataGene)  
LOCUS Glomus intraradices genomic clone Bgl156-T3, genomic survey  
DEFINITION sequence.  
ACCESSION CG431663  
VERSION CG431663.1 GI:34766529  
KEYWORDS GSS  
SOURCE Glomus intraradices  
ORGANISM Glomus intraradices  
Eukaryota; Fungi; Glomeromycota; Glomeromycetes; Glomerales;  
Glomeraceae; Glomus.  
1 (bases 1 to 1042)  
Lammere, P.J., Ratanaka, S., Rehner, C. and Jun, J.  
Genomic sequence from Glomus intraradices spore tissue  
Unpublished (2003)  
Contact: Peter Lammere  
New Mexico State University  
BOX 30001, 3MLS, Las Cruces, NM 88003, USA  
Tel: 505-646-3918  
Fax: 505-646-6846  
Email: plammere@nmsu.edu  
Result of blast search of NCBI non-redundant protein database,  
June 2003: Highest scoring result, with an E-value of 1e-07 was  
g1280655|pir||A38420 antifreeze glycoprotein precursor - black  
rockcod  
Seq primer: T3  
Class: plasmid ends  
High quality sequence stop: 1042.  
Location/Qualifiers  
1..1042  
/organism="Glomus intraradices"  
/mol\_type="genomic DNA"  
/strain="DAOM 197198, Biosystematic Research Center,  
Ottawa"  
/db\_xref="taxon:4876"

FEATURES  
source

/clone="Bgl156-T3"  
/issue\_type="Spores"  
/lab\_host="E. coli XLR Blue"  
/clone\_1lb="Glomus intraradices Bgl II library (in pBK-CMV  
strataGene)"  
/note="Vector: pBK-CMV; genomic DNA isolated from spores;  
complete Bgl II digest of gDNA; cloned into BamHI site of  
pBK-CMV"

ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 1042;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 CATTGAAGAGCTAAA 55  
Db 263 CATTGAAGAGCTAAA 279

RESULT 38 1346 bp DNA linear GSS 02-NOV-2001  
AG052577 Pan troglodytes DNA, clone: PTB-036H04.F, genomic survey sequence.  
LOCUS Pan troglodytes DNA, clone: PTB-036H04.F, genomic survey sequence.  
DEFINITION AG052577  
ACCESSION AG052577  
VERSION AG052577.1 GI:16590020  
KEYWORDS GSS.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homnidae; Pan.  
1  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Torok, Y., Matanabe, H. and Sakaki, Y.  
BAC end sequences of library PTB  
Unpublished  
2 (bases 1 to 1346)  
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,  
Torok, Y., Matanabe, H. and Sakaki, Y.  
Direct Submission  
Submitted (02-AUG-2001) Aaso Fujiyama, The Institute of Physical  
and Chemical Research (RIKEN), Genomic Sciences Center (GSC), Japan  
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan  
(E-mail: chimbee@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,  
Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
Clones are derived from the chimpanzee BAC library PTB. This BAC end  
was generated during the Red process and may have higher chance of  
clone tracking errors.  
PRIMERS  
Sequencing: -21M13  
LIBRARY  
Vector : pKS145  
R.Site 1 : SacI  
R.Site 2 : SacI.  
Location/Qualifiers  
1..1346  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/clone="PTB-036H04.F"  
/sex="male"  
/cell\_type="lymphoblast"  
/clone\_1lb="PTB Chimpanzee Male BAC library"

ORIGIN  
Query Match 28.8%; Score 17; DB 10; Length 1346;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 AAGCGGATAGCGCGG 23  
Db 894 AAGCGGATAGCGCGG 878



RESULT 39  
AK035963  
LOCUS  
DEFINITION  
AK035963 3783 bp mRNA linear HTC 03-APR-2004  
Mus musculus 16 days neonate cerebellum cDNA, RIKEN full-length  
enriched library, clone:9630021F01 product:SH3 domain protein D19,  
full insert sequence.

ACCESSION  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
AK035963  
AK035963.1 GI:26084929  
HTC; CAP trapper.  
Mus musculus (house mouse)  
Mus musculus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciuromorphi; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
10349636

2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,  
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Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watanabe, M.,  
Okazaki, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J.,  
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PUBMED  
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AUTHORS  
Adachi, J., Aizawa, K., Akimura, T., Arawaka, T., Bono, H., Carninci, P.,  
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Genomic Sciences Center and Genome Science Laboratory in RIKEN.  
Division of Experimental Animal Research in Riken contributed to  
prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://genome.gsc.riken.jp/.  
Location/Qualifiers

FEATURES  
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

7 AAGCGGATGACGGCGG 23  
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RESULT 40  
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LOCUS  
DEFINITION  
Single read from an extremity of a full-length cDNA clone made from  
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Anopheles gambiae  
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Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae;  
Culicidae; Anophelinae; Anopheles.  
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Gomez, S.M., Eglmeier, K., Seguren, B., Dehoux, P., Couloux, A.,  
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Genoscope.  
Direct Submission  
Submitted (06-JAN-2003) Genoscope - Centre National de Sequencage :  
BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
- Web : www.genoscope.cns.fr)  
Location/Qualifiers  
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Job time : 870.351 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 688.017 Seconds

(without alignments)  
9253.359 Million cell updates/sec

Title: US-10-712-654-25

Perfect score: 112

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Scoring table: OLIGO NUC

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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4	112	100.0	96231	1	AF188935
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6	30	26.8	30	6	AX743807
7	26	23.2	26	6	AX743817
8	25	22.3	25	6	AX743816
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21	19	17.0	203914	14	AC148941	AC148941 Pan trogl
22	19	17.0	211310	8	AC147334	AC147334 Pan trogl
23	19	17.0	212365	8	AC147687	AC147687 Pan trogl
24	19	17.0	219991	8	BS000547	BS000547 Pan trogl
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26	18	16.1	4050	9	BX322535	BX322535 Mouse DNA
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C 135	16	14.3	2691	15	AK072057	Oryza sat	C 208	16	14.3	110000	15	AP008208_267	Continuation (268
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C 146	16	14.3	12810	1	AB007536	Clostridi	C 219	16	14.3	120545	14	AC158846	AC158846 Bos tauru
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C 153	16	14.3	24427	2	AF100675	Caenorhab	C 226	16	14.3	130907	15	AP003848	AP003848 Oryza sat
C 154	16	14.3	35985	2	AF016668	Caenorhab	C 227	16	14.3	131855	5	BX901910	BX901910 Zebrafish
C 155	16	14.3	37400	15	SC08119	S. cerevisia	C 228	16	14.3	132900	14	AC166637	AC166637 Braa may
C 156	16	14.3	45300	15	AC136350	Homo sapi	C 229	16	14.3	137697	15	AC155338	AC155338 Brea may
C 157	16	14.3	50886	8	AL450107	Human DNA	C 230	16	14.3	138416	15	AP004379	AP004379 Oryza sat
C 158	16	14.3	54269	14	AC157718	Xenopus t	C 231	16	14.3	141300	9	AC120559	AC120559 Homo sapi
C 159	16	14.3	59510	14	AC126384	Homo sapi	C 232	16	14.3	142265	8	AC091173	AC091173 Homo sapi
C 160	16	14.3	61618	9	AY143165	Mus muscu	C 233	16	14.3	144126	14	AC079368	AC079368 Mus muscu
C 161	16	14.3	61828	14	AC144504	Medicago	C 234	16	14.3	144488	9	AC145841	AC145841 Macropus
C 162	16	14.3	64260	14	AC100900	Mus muscu	C 235	16	14.3	145246	9	AC115906	AC115906 Mus muscu
C 163	16	14.3	68984	14	AC103797	Homo sapi	C 236	16	14.3	146364	15	AP004883	AP004883 Oryza sat
C 164	16	14.3	79137	14	AC163383	Medicago	C 237	16	14.3	147114	8	AC008600	AC008600 Homo sapi



C 238	16	14.3	147267	14	AC099317	AC099317 Felis cat	311	16	14.3	188020	8	CNS01RIA	AL163051 Human chr
C 239	16	14.3	148263	8	AC091988	AC091988 Homo sapi	C 312	16	14.3	189738	16	AC011851	AC011851 Homo sapi
C 240	16	14.3	148818	14	AC098700	AC098700 Rellis cat	C 313	16	14.3	191676	9	AL844609	AL844609 Mouse DNA
C 241	16	14.3	148887	15	AP003448	AP003448 Oryza sat	C 314	16	14.3	195254	14	AC117934	AC117934 Papio anu
C 242	16	14.3	150671	2	AC007862	AC007862 Trypanoso	C 315	16	14.3	195873	9	AL805944	AL805944 Mouse DNA
C 243	16	14.3	150788	14	AC011832	AC011832 Homo sapi	C 316	16	14.3	196303	9	AC101349	AC101349 Mus muscu
C 244	16	14.3	152287	14	AC067795	AC067795 Homo sapi	C 317	16	14.3	196490	14	AC005507	AC005507 Plasmodiu
C 245	16	14.3	152869	8	AC073165	AC073165 Homo sapi	C 318	16	14.3	196774	14	AC010640	AC010640 Homo sapi
C 246	16	14.3	153035	14	AC144914	AC144914 Mus muscu	C 319	16	14.3	198450	14	AC149880	AC149880 Xenopus t
C 247	16	14.3	154334	14	AC162892	AC162892 Mus muscu	C 320	16	14.3	198942	8	AC008517	AC008517 Homo sapi
C 248	16	14.3	155435	14	CR974437	CR974437 Danio rer	C 321	16	14.3	200393	14	AC150994	AC150994 Bos tauru
C 249	16	14.3	155977	9	AC140211	AC140211 Mus muscu	C 322	16	14.3	201296	14	CR548628	CR548628 Danio rer
C 250	16	14.3	160168	8	CNS05TDM	AL356679 Human chr	C 323	16	14.3	202214	9	AC124556	AC124556 Mus muscu
C 251	16	14.3	160345	14	AC067870	AC067870 Homo sapi	C 324	16	14.3	202267	8	DJ293M10	DJ293M10 Homo sapi
C 252	16	14.3	160455	14	BX571776	BX571776 Zebrafish	C 325	16	14.3	202736	14	AC151256	AC151256 Bos tauru
C 253	16	14.3	160736	14	AL162383	AL162383 Oryza sat	C 326	16	14.3	204151	14	AC145140	AC145140 Homo sapi
C 254	16	14.3	160989	15	OSJN00089	AL606683 Oryza sat	C 327	16	14.3	204662	8	CNS01RHQ	AL162191 Human chr
C 255	16	14.3	161195	14	AC159932	AC159932 Papio anu	C 328	16	14.3	205053	14	AC159285	AC159285 Mus muscu
C 256	16	14.3	161218	14	AC011171	AC011171 Homo sapi	C 329	16	14.3	205954	14	AC118829	AC118829 Rattus no
C 257	16	14.3	161710	9	AC128736	AC128736 Mus muscu	C 330	16	14.3	206289	14	BX284682	BX284682 Zebrafish
C 258	16	14.3	161831	14	AC073078	AC073078 Homo sapi	C 331	16	14.3	206867	5	AC162166	AC162166 Mus muscu
C 259	16	14.3	162381	15	AP005072	AP005072 Oryza sat	C 332	16	14.3	208711	14	AC152264	AC152264 Bos tauru
C 260	16	14.3	164051	8	AP006892	AC106892 Homo sapi	C 333	16	14.3	209394	14	AC094731	AC094731 Rattus no
C 261	16	14.3	164266	5	BX321906	BX321906 Zebrafish	C 334	16	14.3	210028	14	AC149743	AC149743 Bos tauru
C 262	16	14.3	165175	14	AC019277	AC019277 Homo sapi	C 335	16	14.3	211028	14	AC161848	AC161848 Bos tauru
C 263	16	14.3	165594	8	AC025524	AC025524 Homo sapi	C 336	16	14.3	212080	14	AC098433	AC098433 Rattus no
C 264	16	14.3	165720	14	AC025524	AC025524 Homo sapi	C 337	16	14.3	212685	5	BX294380	BX294380 Zebrafish
C 265	16	14.3	165757	14	AC113980	AC113980 Mus muscu	C 338	16	14.3	212888	8	AL513325	AL513325 Human DNA
C 266	16	14.3	166637	8	AC008657	AC008657 Homo sapi	C 339	16	14.3	212936	14	AC020970	AC020970 Mus muscu
C 267	16	14.3	167065	14	AC150567	AC150567 Bos tauru	C 340	16	14.3	213113	9	AC124807	AC124807 Mus muscu
C 268	16	14.3	167126	14	AC115471	AC115471 Rattus no	C 341	16	14.3	214483	8	AP001830	AP001830 Homo sapi
C 269	16	14.3	167174	8	AC013492	AC013492 Homo sapi	C 342	16	14.3	214877	14	CT009720	CT009720 Mus muscu
C 270	16	14.3	167222	15	AC118132	AC118132 Oryza sat	C 343	16	14.3	217288	14	AC097947	AC097947 Rattus no
C 271	16	14.3	168354	9	AC124382	AC124382 Mus muscu	C 344	16	14.3	217746	5	CR161005	CR161005 Pan trogl
C 272	16	14.3	168488	14	CR925877	CR925877 Danio rer	C 345	16	14.3	217987	8	CR792443	CR792443 Zebrafish
C 273	16	14.3	169566	8	AC021518	AC021518 Homo sapi	C 346	16	14.3	218180	9	AC107642	AC107642 Mus muscu
C 274	16	14.3	170072	8	AC116329	AC116329 Mus muscu	C 347	16	14.3	219903	14	AC098309	AC098309 Rattus no
C 275	16	14.3	170189	14	AC027615	AC027615 Homo sapi	C 348	16	14.3	220177	14	CR354597	CR354597 Danio rer
C 276	16	14.3	170299	8	AC021523	AC021523 Homo sapi	C 349	16	14.3	220468	9	AC101004	AC101004 Mus muscu
C 277	16	14.3	170799	8	AC107204	AC107204 Homo sapi	C 350	16	14.3	222236	14	AC096440	AC096440 Rattus no
C 278	16	14.3	171392	9	AC079933	AC079933 Trypanoso	C 351	16	14.3	223940	14	AC087567	AC087567 Mus muscu
C 279	16	14.3	171652	12	AC160306	AC160306 Bos tauru	C 352	16	14.3	223940	14	AC139632	AC139632 Bos tauru
C 280	16	14.3	171710	14	AC068049	AC068049 Homo sapi	C 353	16	14.3	224721	14	AC163304	AC163304 Bos tauru
C 281	16	14.3	171969	14	AC027756	AC027756 Homo sapi	C 354	16	14.3	224809	14	AC099690	AC099690 Mus muscu
C 282	16	14.3	172043	8	AC026797	AC026797 Homo sapi	C 355	16	14.3	225655	9	AC095549	AC095549 Rattus no
C 283	16	14.3	172097	15	AP006057	AP006057 Oryza sat	C 356	16	14.3	226967	14	AC113654	AC113654 Rattus no
C 284	16	14.3	172746	2	AC018484	AC018484 Drosophil	C 357	16	14.3	227763	14	AC126518	AC126518 Rattus no
C 285	16	14.3	172769	9	AC158529	AC158529 Mus muscu	C 358	16	14.3	228933	9	AL645669	AL645669 Mouse DNA
C 286	16	14.3	173054	9	AC139240	AC139240 Mus muscu	C 359	16	14.3	230432	14	BX890558	BX890558 Danio rer
C 287	16	14.3	173414	8	AC012535	AC012535 Homo sapi	C 360	16	14.3	231382	14	AC095549	AC095549 Rattus no
C 288	16	14.3	174067	9	AC119590	AC119590 Mus muscu	C 361	16	14.3	231490	5	CR854945	CR854945 Mouse DNA
C 289	16	14.3	176392	14	AC135954	AC135954 Papio anu	C 362	16	14.3	232491	14	AC093043	AC093043 Mus muscu
C 290	16	14.3	176940	9	AC133331	AC133331 Mus muscu	C 363	16	14.3	233864	9	AC122860	AC122860 Mus muscu
C 291	16	14.3	177080	5	BX323984	BX323984 Zebrafish	C 364	16	14.3	236130	14	AC120064	AC120064 Rattus no
C 292	16	14.3	177265	14	AC147758	AC147758 Macropus	C 365	16	14.3	237705	8	AP215845	AP215845 Homo sapi
C 293	16	14.3	178545	8	AC093301	AC093301 Homo sapi	C 366	16	14.3	237821	14	CR855879	CR855879 Danio rer
C 294	16	14.3	178930	14	AC023109	AC023109 Homo sapi	C 367	16	14.3	237974	14	AC094771	AC094771 Rattus no
C 295	16	14.3	179085	5	BX510959	BX510959 Zebrafish	C 368	16	14.3	238921	14	AC112356	AC112356 Rattus no
C 296	16	14.3	180189	14	AC018864	AC018864 Homo sapi	C 369	16	14.3	240105	14	AC115207	AC115207 Rattus no
C 297	16	14.3	180836	14	CR925859	CR925859 Danio rer	C 370	16	14.3	241507	5	BX571803	BX571803 Zebrafish
C 298	16	14.3	180927	14	AC017105	AC017105 Homo sapi	C 371	16	14.3	241708	5	BX571803	BX571803 Zebrafish
C 299	16	14.3	181524	9	AC153883	AC153883 Mus muscu	C 372	16	14.3	245182	14	AC164145	AC164145 Bos tauru
C 300	16	14.3	182559	8	AC096590	AC096590 Homo sapi	C 373	16	14.3	245698	14	AC124841	AC124841 Rattus no
C 301	16	14.3	183543	9	AL670360	AL670360 Mouse DNA	C 374	16	14.3	245976	14	AC112593	AC112593 Rattus no
C 302	16	14.3	184043	8	AC097502	AC097502 Homo sapi	C 375	16	14.3	246235	14	AC129432	AC129432 Rattus no
C 303	16	14.3	185786	15	AC079372	AC079372 Mus muscu	C 376	16	14.3	249046	14	AC158066	AC158066 Bos tauru
C 304	16	14.3	185858	15	AP004765	AP004765 Oryza sat	C 377	16	14.3	250421	2	AE014849	AE014849 Plasmodiu
C 305	16	14.3	185866	5	AC109510	AC109510 Mus muscu	C 378	16	14.3	250739	14	AC095992	AC095992 Rattus no
C 306	16	14.3	186123	5	BX640592	BX640592 Zebrafish	C 379	16	14.3	251432	14	AC115545	AC115545 Rattus no
C 307	16	14.3	186304	8	AC090136	AC090136 Homo sapi	C 380	16	14.3	251780	14	AC130912	AC130912 Rattus no
C 308	16	14.3	186726	9	AC133351	AC133351 Mus muscu	C 381	16	14.3	253134	14	AC160458	AC160458 Mus muscu
C 309	16	14.3	186935	2	AC013351	AC013351 Drosophil	C 382	16	14.3	254630	14	AC108269	AC108269 Rattus no
C 310	16	14.3	187069	9	AC153533	AC153533 Mus muscu	C 383	16	14.3	259862	14	AC153256	AC153256 Bos tauru



C 384	16	14.3	260296	14	AC130745	AC10745	Rattus no	457	15	13.4	352	2	AY593678	AY593678	Tylopelta
C 385	16	14.3	260711	14	AC099272	AC099272	Rattus no	458	15	13.4	352	2	AY593679	AY593679	Kronides
C 386	16	14.3	262374	14	AC095433	AC095433	Rattus no	459	15	13.4	352	2	AY593682	AY593682	Erethopoma
C 387	16	14.3	262930	14	AC113753	AC113753	Rattus no	460	15	13.4	352	2	AY593683	AY593683	Campylenc
C 388	16	14.3	276376	14	AC097979	AC097979	Rattus no	461	15	13.4	352	2	AY593684	AY593684	Campylenc
C 389	16	14.3	278984	14	AC143016	AC143016	Maccaca mu	462	15	13.4	352	2	AY593685	AY593685	Campylenc
C 390	16	14.3	287833	1	AB017267	AB017267	Bacillus	463	15	13.4	352	2	AY593704	AY593704	Stalocypa
C 391	16	14.3	296571	14	AC152586	AC152586	Bos taurus	464	15	13.4	352	2	AY593705	AY593705	Stalocypa
C 392	16	14.3	300029	15	AB017065	AB017065	Oryza sat	465	15	13.4	352	2	AY593710	AY593710	Alchime
C 393	16	14.3	300162	1	AB016929	AB016929	Bacteroid	466	15	13.4	352	2	AY593719	AY593719	Alchime
C 394	16	14.3	304186	14	AC112438	AC112438	Rattus no	467	15	13.4	352	2	AY593721	AY593721	Alchime
C 395	16	14.3	304186	14	AC112438	AC112438	Rattus no	468	15	13.4	357	6	CQ486631	CQ486631	Sequence
C 396	16	14.3	304725	14	AC122592	AC122592	Rattus no	469	15	13.4	370	6	CQ679387	CQ679387	Sequence
C 397	16	14.3	317131	14	AC107111	AC107111	Rattus no	470	15	13.4	381	6	CQ743367	CQ743367	Sequence
C 398	16	14.3	326606	14	AC110839	AC110839	Rattus no	471	15	13.4	400	1	ECX9GAS	ECX9GAS	Sequence
C 399	16	14.3	345730	1	BX957219	BX957219	Methanoco	472	15	13.4	403	6	BD028807	BD028807	Sequence
C 400	16	14.3	349648	1	BX957220	BX957220	Methanoco	473	15	13.4	403	6	AX887197	AX887197	Sequence
C 401	15	13.4	100	6	AX990129	AX990129	Sequence	474	15	13.4	421	6	AX371151	AX371151	Sequence
C 402	15	13.4	100	6	AX990130	AX990130	Sequence	475	15	13.4	426	6	CQ516442	CQ516442	Sequence
C 403	15	13.4	169	2	AY498520	AY498520	Polyglypt	476	15	13.4	426	9	AF087469	AF087469	Mus muscu
C 404	15	13.4	214	2	AY498523	AY498523	Polycopel	477	15	13.4	431	6	CQ051613	CQ051613	Sequence
C 405	15	13.4	237	4	AY355848	AY355848	Carls fam	478	15	13.4	431	6	CQ066670	CQ066670	Sequence
C 406	15	13.4	237	10	G67725	G67725	MSURDA79 po	479	15	13.4	431	6	CQ093716	CQ093716	Sequence
C 407	15	13.4	250	6	BD270301	BD270301	Human nuc	480	15	13.4	431	6	CQ132491	CQ132491	Sequence
C 408	15	13.4	250	6	AX035238	AX035238	Sequence	481	15	13.4	431	6	CQ171061	CQ171061	Sequence
C 409	15	13.4	250	6	AX342092	AX342092	Sequence	482	15	13.4	431	6	CQ200199	CQ200199	Sequence
C 410	15	13.4	250	6	AX342152	AX342152	Sequence	483	15	13.4	431	6	CQ215691	CQ215691	Sequence
C 411	15	13.4	250	6	AX441155	AX441155	Sequence	484	15	13.4	431	6	CQ254287	CQ254287	Sequence
C 412	15	13.4	254	2	AY498479	AY498479	Cladonota	485	15	13.4	431	6	CQ291308	CQ291308	Sequence
C 413	15	13.4	255	6	AB520711	AB520711	Sequence	486	15	13.4	431	6	CQ328415	CQ328415	Sequence
C 414	15	13.4	262	2	AY498495	AY498495	Emya sp.	487	15	13.4	461	2	DME569677	DME569677	Sequence
C 415	15	13.4	271	2	AY498484	AY498484	Cyrtolobu	488	15	13.4	461	2	DME569655	DME569655	Sequence
C 416	15	13.4	299	6	BD138446	BD138446	Mammalian	489	15	13.4	462	2	DME569666	DME569666	Sequence
C 417	15	13.4	299	6	AX017224	AX017224	Sequence	490	15	13.4	462	2	DME569699	DME569699	Sequence
C 418	15	13.4	307	6	AY498531	AY498531	Membracin	491	15	13.4	462	2	DME569710	DME569710	Sequence
C 419	15	13.4	319	2	AY498483	AY498483	Cyrtolobu	492	15	13.4	462	2	DME569732	DME569732	Sequence
C 420	15	13.4	319	2	AY498489	AY498489	Cyrtolobu	493	15	13.4	462	2	DME569743	DME569743	Sequence
C 421	15	13.4	319	2	AY498494	AY498494	Eufairmai	494	15	13.4	462	2	DME569754	DME569754	Sequence
C 422	15	13.4	319	2	AY498515	AY498515	Ophiderma	495	15	13.4	462	2	DME569765	DME569765	Sequence
C 423	15	13.4	320	2	AY498480	AY498480	Cyrtolobu	496	15	13.4	462	2	DME569776	DME569776	Sequence
C 424	15	13.4	320	2	AY498533	AY498533	Tylopelta	497	15	13.4	462	2	DME569787	DME569787	Sequence
C 425	15	13.4	320	2	AY498475	AY498475	Antianthe	498	15	13.4	462	2	DME569798	DME569798	Sequence
C 426	15	13.4	321	2	AY498485	AY498485	Cyrtolobu	499	15	13.4	462	2	DME569809	DME569809	Sequence
C 427	15	13.4	321	2	AY498486	AY498486	Carynota	500	15	13.4	462	2	DME569820	DME569820	Sequence
C 428	15	13.4	321	2	AY498490	AY498490	Cymbomorp	501	15	13.4	462	2	DME569831	DME569831	Sequence
C 429	15	13.4	321	2	AY498496	AY498496	Glossonot	502	15	13.4	462	2	DME569842	DME569842	Sequence
C 430	15	13.4	321	2	AY498499	AY498499	Guayaquil	503	15	13.4	462	2	DME569853	DME569853	Sequence
C 431	15	13.4	321	2	AY498508	AY498508	Methelisa	504	15	13.4	462	2	DME569864	DME569864	Sequence
C 432	15	13.4	321	2	AY498513	AY498513	Ophiderma	505	15	13.4	462	2	DME569875	DME569875	Sequence
C 433	15	13.4	321	2	AY498514	AY498514	Ophiderma	506	15	13.4	462	2	DME569886	DME569886	Sequence
C 434	15	13.4	321	2	AY498516	AY498516	Telamona	507	15	13.4	462	2	DME569897	DME569897	Sequence
C 435	15	13.4	321	2	AY498529	AY498529	Xantholob	508	15	13.4	462	2	DME569908	DME569908	Sequence
C 436	15	13.4	321	2	AY498536	AY498536	Sequence	509	15	13.4	462	2	DME569919	DME569919	Sequence
C 437	15	13.4	321	2	AR346719	AR346719	Sequence	510	15	13.4	462	2	DME569930	DME569930	Sequence
C 438	15	13.4	321	6	AR498516	AR498516	Sequence	511	15	13.4	462	2	DME569941	DME569941	Sequence
C 439	15	13.4	330	6	TT1388426	TT1388426	Sequence	512	15	13.4	462	2	DME569952	DME569952	Sequence
C 440	15	13.4	331	6	AX524275	AX524275	Sequence	513	15	13.4	462	2	DME569963	DME569963	Sequence
C 441	15	13.4	332	6	AR505339	AR505339	Sequence	514	15	13.4	462	2	DME569974	DME569974	Sequence
C 442	15	13.4	332	6	AR505339	AR505339	Sequence	515	15	13.4	462	2	DME569985	DME569985	Sequence
C 443	15	13.4	349	2	AY593707	AY593707	Platycoel	516	15	13.4	462	2	DME569996	DME569996	Sequence
C 444	15	13.4	349	2	AY593707	AY593707	Platycoel	517	15	13.4	462	2	DME569997	DME569997	Sequence
C 445	15	13.4	352	2	AY593676	AY593676	Smerdalea	518	15	13.4	462	2	DME569998	DME569998	Sequence
C 446	15	13.4	352	2	AY593635	AY593635	Cymbomorp	519	15	13.4	462	2	DME569999	DME569999	Sequence
C 447	15	13.4	352	2	AY593639	AY593639	Stictopel	520	15	13.4	462	2	DME569999	DME569999	Sequence
C 448	15	13.4	352	2	AY593642	AY593642	Acutalis	521	15	13.4	462	2	DME569999	DME569999	Sequence
C 449	15	13.4	352	2	AY593649	AY593649	Cladonota	522	15	13.4	462	2	DME569999	DME569999	Sequence
C 450	15	13.4	352	2	AY593650	AY593650	Cladonota	523	15	13.4	462	2	DME569999	DME569999	Sequence
C 451	15	13.4	352	2	AY593662	AY593662	Guayaquil	524	15	13.4	462	2	DME569999	DME569999	Sequence
C 452	15	13.4	352	2	AY593663	AY593663	Guayaquil	525	15	13.4	462	2	DME569999	DME569999	Sequence
C 453	15	13.4	352	2	AY593665	AY593665	Guayaquil	526	15	13.4	462	2	DME569999	DME569999	Sequence
C 454	15	13.4	352	2	AY593670	AY593670	Bolbonota	527	15	13.4	462	2	DME569999	DME569999	Sequence
C 455	15	13.4	352	2	AY593674	AY593674	Tritropid	528	15	13.4	462	2	DME569999	DME569999	Sequence
C 456	15	13.4	352	2	AY593676	AY593676	Erechthia	529	15	13.4	462	2	DME569999	DME569999	Sequence
C 457	15	13.4	352	2	AY593677	AY593677	Erechthia	530	15	13.4	462	2	DME569999	DME569999	Sequence



530	15	13.4	537	6	AX607323	AX607323 Sequence	c 603	15	13.4	926	6	CQ180938	CQ180938 Sequence
531	15	13.4	539	10	BV038413	BV038413 S208P6188	c 604	15	13.4	926	6	CQ205303	CQ205303 Sequence
532	15	13.4	540	8	HCM2D46F01	AP086283 Homo sapi	c 605	15	13.4	926	6	CQ228692	CQ228692 Sequence
533	15	13.4	545	10	AB164832	AB164832 Bos tauru	c 606	15	13.4	926	6	CQ266851	CQ266851 Sequence
534	15	13.4	549	6	AR545048	AR545048 Sequence	c 607	15	13.4	926	6	CQ303812	CQ303812 Sequence
535	15	13.4	552	6	AR588079	AR588079 Sequence	c 608	15	13.4	926	6	CQ341132	CQ341132 Sequence
536	15	13.4	559	10	BV068719	BV068719 S212P6108	c 609	15	13.4	935	15	AK106805	AK106805 Oryza sat
537	15	13.4	564	6	CQ740200	CQ740200 Sequence	c 610	15	13.4	947	10	BV520372	BV520372 G591P6491
538	15	13.4	568	10	BV095723	BV095723 RPAMSE00	c 611	15	13.4	959	10	BV524680	BV524680 G591P6048
539	15	13.4	573	2	DME276419	AJ726419 Drosophill	c 612	15	13.4	969	1	PM053213	PM053213 Sequence
540	15	13.4	613	3	AF461626	AF461626 Unculture	c 613	15	13.4	972	1	AY593150	AY593150 Lina snlh
541	15	13.4	616	5	AJ969128	AJ969128 Lepomis g	c 614	15	13.4	1001	15	AK121760	AK121760 Oryza sat
542	15	13.4	623	10	BV332139	BV332139 S230P6472	c 615	15	13.4	1140	5	MITTCY0B	Y10451 T. tinca mt
543	15	13.4	624	2	BV375800	BV375800 S231P6174	c 616	15	13.4	1159	6	AR193777	AR193777 Sequence
544	15	13.4	632	10	DME243836	AJ743836 Drosophill	c 617	15	13.4	1181	8	AY459393	AY459393 Gorilla g
545	15	13.4	633	10	BV444039	BV444039 S237P6318	c 618	15	13.4	1227	3	AY991998	AY991998 Unculture
546	15	13.4	637	6	CQ577482	CQ577482 Sequence	c 619	15	13.4	1263	15	AK073719	AK073719 Oryza sat
547	15	13.4	640	10	BV541022	BV541022 G591P5254	c 620	15	13.4	1281	1	TAU55996	TAU55996 Sequence
548	15	13.4	649	6	CS137122	CS137122 Sequence	c 621	15	13.4	1281	6	E30474	E30474 Process for
549	15	13.4	653	10	G76934	G76934 S209P6447RC	c 622	15	13.4	1281	6	E30477	E30477 Liquid reas
550	15	13.4	654	10	BV544234	BV544234 qym80h03.	c 623	15	13.4	1284	6	AR198373	AR198373 Sequence
551	15	13.4	655	2	AY118419	AY118419 Drosophill	c 624	15	13.4	1284	6	E30475	E30475 Process for
552	15	13.4	655	6	AR379553	AR379553 Sequence	c 625	15	13.4	1284	6	E30478	E30478 Liquid reas
553	15	13.4	671	15	AY425073	AY425073 Ochma sp.	c 626	15	13.4	1284	6	AR198374	AR198374 Sequence
554	15	13.4	673	10	BV609434	BV609434 S215P6233	c 627	15	13.4	1295	15	BT017022	BT017022 Zea mays
555	15	13.4	682	15	AY425072	AY425072 Ochma mul	c 628	15	13.4	1331	3	AY992995	AY992995 Unculture
556	15	13.4	687	8	AB115267	AB115267 Homo sapi	c 629	15	13.4	1343	3	AY992501	AY992501 Unculture
557	15	13.4	695	10	BV269120	BV269120 S235P6523	c 630	15	13.4	1435	2	AK115812	AK115812 Clona int
558	15	13.4	695	10	AF458321	AF458321 Hemibagru	c 631	15	13.4	1441	5	CR761602	CR761602 Xenopus t
559	15	13.4	711	10	BV597837	BV597837 S217P6888	c 632	15	13.4	1458	1	AY040215	AY040215 Lactobaci
560	15	13.4	723	15	AF351014	AF351014 Pterandra	c 633	15	13.4	1458	6	AR262708	AR262708 Sequence
561	15	13.4	732	10	BV526330	BV526330 G591P6083	c 634	15	13.4	1469	1	ECOPDXA	ECOPDXA E. coli pyri
562	15	13.4	735	15	AF351013	AF351013 Acmanther	c 635	15	13.4	1491	13	AY044842	AY044842 White spo
563	15	13.4	738	15	AF351010	AF351010 Diacidia	c 636	15	13.4	1499	2	DMU93032	DMU93032 Drosophila
564	15	13.4	741	15	AF351012	AF351012 Coleostac	c 637	15	13.4	1503	1	D64125	D64125 Bacillus su
565	15	13.4	742	3	AY820227	AY820227 Unculture	c 638	15	13.4	1524	6	AX820690	AX820690 Sequence
566	15	13.4	744	15	AF351011	AF351011 Byrsotima	c 639	15	13.4	1524	6	AX831720	AX831720 Sequence
567	15	13.4	756	15	AF351008	AF351008 Biepharan	c 640	15	13.4	1632	13	AF493145	AF493145 Shrimp wh
568	15	13.4	763	10	BV660049	BV660049 S216P6209	c 641	15	13.4	1635	6	AK151473	AK151473 Sequence
569	15	13.4	770	2	DME243837	AJ743837 Drosophill	c 642	15	13.4	1648	6	CQ609717	CQ609717 Sequence
570	15	13.4	771	3	AY820205	AY820205 Unculture	c 643	15	13.4	1655	6	CQ577605	CQ577605 Sequence
571	15	13.4	785	8	HS8341821	AJ341821 Homo sapi	c 644	15	13.4	1659	6	AX654429	AX654429 Sequence
572	15	13.4	787	15	BT018092	BT018092 Zea mays	c 645	15	13.4	1664	8	AF131855	AF131855 Homo sapi
573	15	13.4	790	5	AY549725	AY549725 Pica pica	c 646	15	13.4	1674	6	CQ647916	CQ647916 Sequence
574	15	13.4	791	10	BV026793	BV026793 S212P6316	c 647	15	13.4	1677	5	AX607113	AX607113 Sequence
575	15	13.4	797	8	HS8342533	AJ324533 Homo sapi	c 648	15	13.4	1692	2	AY118747	AY118747 Drosophill
576	15	13.4	798	5	AY549726	AY549726 Pica pica	c 649	15	13.4	1714	15	ZMOC5BR	ZMOC5BR z. mays OBF3
577	15	13.4	800	4	AF401453	AF401453 Myotis da	c 650	15	13.4	1716	15	BT015924	BT015924 Arabidops
578	15	13.4	800	4	AF401454	AF401454 Myotis da	c 651	15	13.4	1795	15	BT020538	BT020538 Arabidops
579	15	13.4	812	5	AY129262	AY129262 Pica pica	c 652	15	13.4	1815	15	AY621539	AY621539 Triticum
580	15	13.4	812	5	AY129263	AY129263 Pica pica	c 653	15	13.4	1847	6	CQ849582	CQ849582 Sequence
581	15	13.4	812	5	AY129264	AY129264 Pica pica	c 654	15	13.4	1847	6	AK126606	AK126606 Homo sapi
582	15	13.4	812	5	AY129265	AY129265 Pica pica	c 655	15	13.4	1924	15	BT005735	BT005735 Arabidops
583	15	13.4	812	5	AY129266	AY129266 Pica pica	c 656	15	13.4	1943	1	AB061541	AB061541 Desulfovi
584	15	13.4	812	5	AY129267	AY129267 Pica mutt	c 657	15	13.4	1952	8	BC015319	BC015319 Homo sapi
585	15	13.4	812	5	AY129268	AY129268 Pica mutt	c 658	15	13.4	1957	2	DME309489	DME309489 Drosophill
586	15	13.4	812	5	AY129269	AY129269 Pica huds	c 659	15	13.4	1962	8	BC006972	BC006972 Homo sapi
587	15	13.4	812	5	AY129270	AY129270 Pica huds	c 660	15	13.4	1964	8	CQ776552	CQ776552 Sequence
588	15	13.4	814	10	BV370169	BV370169 S231P6398	c 661	15	13.4	1965	2	AY069659	AY069659 Homo sapi
589	15	13.4	821	10	BV520792	BV520792 G591P6274	c 662	15	13.4	1973	15	AF307145	AF307145 Drosophill
590	15	13.4	825	15	AY167409	AY167409 Batroneall	c 663	15	13.4	1977	8	CS118496	CS118496 Sequence
591	15	13.4	825	15	AF435070	AF435070 Trichoder	c 664	15	13.4	1977	8	BC018528	BC018528 Homo sapi
592	15	13.4	826	15	AK064169	AK064169 Oryza sat	c 665	15	13.4	1989	2	AY119159	AY119159 Drosophill
593	15	13.4	826	15	AY515130	AY515130 Batroneall	c 666	15	13.4	1999	5	BC080148	BC080148 Xenopus t
594	15	13.4	885	1	AY515131	AY515131 Batroneall	c 667	15	13.4	2000	6	AX461171	AX461171 Sequence
595	15	13.4	910	15	AK121755	AK121755 Oryza sat	c 668	15	13.4	2001	6	AX059449	AX059449 Glycine m
596	15	13.4	914	5	TTI555551	TTI555551 Tinca tin	c 669	15	13.4	2009	15	AY439099	AY439099 Glycine m
597	15	13.4	914	5	TTI555552	TTI555552 Tinca tin	c 671	15	13.4	2047	15	AK070648	AK070648 Oryza sat
598	15	13.4	926	6	CQ056584	CQ056584 Sequence	c 672	15	13.4	2064	5	BT009245	BT009245 Gallus ga
599	15	13.4	926	6	CQ075861	CQ075861 Sequence	c 673	15	13.4	2068	15	AJ719631	AJ719631 Gallus ga
600	15	13.4	926	6	CQ106841	CQ106841 Sequence	c 674	15	13.4	2112	1	AF270374	AF270374 Staphyloc
601	15	13.4	926	6	CQ145494	CQ145494 Sequence	c 675	15	13.4	2112	6	AR486328	AR486328 Sequence



C 676	15	13.4	2112	6	AX145692	AX145692 Sequence	749	15	13.4	5818	6	AX416836	AX416836 Sequence
677	15	13.4	2117	6	AX835126	AX835126 Sequence	750	15	13.4	5900	5	AF109305	AF109305 Sequence
678	15	13.4	2117	8	AK097973	AK097973 Homo sapi	751	15	13.4	6070	5	AF085746	AF085746 Homo sapi
679	15	13.4	2122	9	BC051134	BC051134 Mus muscu	752	15	13.4	6172	14	AC017968	AC017968 Homo sapi
680	15	13.4	2135	9	NMPABPTI	XI75959 M. musculus	753	15	13.4	6302	8	BC049379	BC049379 Homo sapi
681	15	13.4	2150	9	CGU38620	U98620 Gallus gall	754	15	13.4	6661	6	AX329748	AX329748 Sequence
C 682	15	13.4	2232	9	MMY09086	Y09086 Mus musculu	C 755	15	13.4	6661	8	HSU61500	HSU61500 Sequence
C 683	15	13.4	2370	6	AX415037	AX415037 Sequence	C 756	15	13.4	6697	6	CO592400	CO592400 Sequence
C 684	15	13.4	2396	1	ECAPAH	X04711 E. coli apa	C 757	15	13.4	7189	8	AB058753	AB058753 Homo sapi
C 685	15	13.4	2453	3	CQ601409	CQ601409 Sequence	C 758	15	13.4	7190	6	BD183486	BD183486 Homo sapi
C 686	15	13.4	2461	5	AJ720633	AJ720633 Gallus ga	C 759	15	13.4	7204	2	CERK971	CERK971 Sequence
C 687	15	13.4	2533	2	AY372529	AY372529 Trypanoso	C 760	15	13.4	7554	13	AF266697	AF266697 Helicover
C 688	15	13.4	2567	6	AX416733	AX416733 Sequence	C 761	15	13.4	7701	13	BSU011483	BSU011483 Homo sapi
C 689	15	13.4	2618	2	SPNPKGSD	Y13102 S. dominica	C 762	15	13.4	7774	1	L02630	L02630 Xanthomora
C 690	15	13.4	2661	2	AK116950	AK116950 Ciona int	C 763	15	13.4	8107	5	CR753882	CR753882 Sequence
C 691	15	13.4	2686	1	AF473821	AF473821 Bartonell	C 764	15	13.4	8606	1	STU43676	STU43676 Sequence
C 692	15	13.4	2696	6	CO577481	CO577481 Sequence	C 765	15	13.4	9077	1	AE06726	AE06726 Sulfolobu
C 693	15	13.4	2704	2	DMU05240	U05240 Drosophila	C 766	15	13.4	9077	1	AE06726	AE06726 Sulfolobu
C 694	15	13.4	2724	2	CO573438	CO573438 Sequence	C 767	15	13.4	9077	1	AE06726	AE06726 Sulfolobu
C 695	15	13.4	2796	2	AY147013	AY147013 Leishmani	C 768	15	13.4	9077	1	AE06726	AE06726 Sulfolobu
C 696	15	13.4	2872	6	E16359	E16359 Thermus aqu	C 769	15	13.4	9306	6	CO588953	CO588953 Sequence
C 697	15	13.4	2872	6	E30473	E30473 Process for	C 770	15	13.4	9613	6	CO573437	CO573437 Sequence
C 698	15	13.4	2872	6	E30476	E30476 Liquid reas	C 771	15	13.4	10335	1	AE015024	AE015024 Sequence
C 699	15	13.4	2872	6	AR198372	AR198372 Sequence	C 772	15	13.4	10759	1	BACRPLP	BACRPLP Sequence
C 700	15	13.4	2917	6	CO577889	CO577889 Sequence	C 773	15	13.4	10894	1	AE010233	AE010233 Sequence
C 701	15	13.4	2918	15	AK110027	AK110027 Oryza sat	C 774	15	13.4	10898	1	AE015642	AE015642 Pyrococcu
C 702	15	13.4	2939	6	CO573588	CO573588 Sequence	C 775	15	13.4	10898	1	AE015642	AE015642 Pyrococcu
C 703	15	13.4	3016	6	CO577475	CO577475 Sequence	C 776	15	13.4	10982	15	AB003364	AB003364 Homo sapi
C 704	15	13.4	3050	6	CO584637	CO584637 Sequence	C 777	15	13.4	11061	14	TANN13	TANN13 Sequence
C 705	15	13.4	3126	1	AF270331	AF270331 Staphyloc	C 778	15	13.4	11068	1	AE007336	AE007336 Homo sapi
C 706	15	13.4	3126	6	AR486285	AR486285 Sequence	C 779	15	13.4	11149	1	AE012165	AE012165 Homo sapi
C 707	15	13.4	3126	6	AX145649	AX145649 Sequence	C 780	15	13.4	11416	1	AE007819	AE007819 Clostridi
C 708	15	13.4	3156	8	AB056821	AB056821 Macaca fa	C 781	15	13.4	11659	6	CO788974	CO788974 Sequence
C 709	15	13.4	3302	1	AF269976	AF269976 Staphyloc	C 782	15	13.4	11831	6	AR218833	AR218833 Sequence
C 710	15	13.4	3302	6	AR485930	AR485930 Sequence	C 783	15	13.4	11831	6	BD003745	BD003745 Polynucle
C 711	15	13.4	3302	6	AX145294	AX145294 Sequence	C 784	15	13.4	11831	6	AE013004	AE013004 Thermoma
C 712	15	13.4	3319	15	AY230444	AY230444 Gibberell	C 785	15	13.4	12020	1	AE007524	AE007524 Clostridi
C 713	15	13.4	3409	6	CO577778	CO577778 Sequence	C 786	15	13.4	12676	6	CO600236	CO600236 Sequence
C 714	15	13.4	3424	9	AF001290	AF001290 Mus muscu	C 787	15	13.4	12794	8	MMCOL18A07	MMCOL18A07 Homo sapi
C 715	15	13.4	3482	15	AK121200	AK121200 Oryza sat	C 788	15	13.4	13292	8	AE014305_6	AE014305_6 Homo sapi
C 716	15	13.4	3581	8	CO842360	CO842360 Sequence	C 789	15	13.4	13522	2	L16560	L16560 Caenorhabdi
C 717	15	13.4	3581	8	AK125320	AK125320 Homo sapi	C 790	15	13.4	14141	6	CO579716	CO579716 Sequence
C 718	15	13.4	3723	6	CO577604	CO577604 Sequence	C 791	15	13.4	14222	1	AE004401	AE004401 Vibrio ch
C 719	15	13.4	3723	6	CO599483	CO599483 Sequence	C 792	15	13.4	14557	6	BD193773	BD193773 Enterococ
C 720	15	13.4	3777	2	BT001629	BT001629 Drosophi	C 793	15	13.4	14914	1	AE000714	AE000714 Aquifex a
C 721	15	13.4	3780	5	AB063101	AB063101 Cyprinid	C 794	15	13.4	14914	1	AE015466	AE015466 Shewanell
C 722	15	13.4	3864	6	CO577613	CO577613 Sequence	C 795	15	13.4	14987	1	AE015466	AE015466 Shewanell
C 723	15	13.4	3864	6	AB045378	AB045378 Rattus no	C 796	15	13.4	16397	6	AR354087	AR354087 Sequence
C 724	15	13.4	3906	6	CO581690	CO581690 Sequence	C 797	15	13.4	16397	6	AR354087	AR354087 Sequence
C 725	15	13.4	4029	8	BC094799	BC094799 Homo sapi	C 798	15	13.4	17064	5	AY687385	AY687385 Pelodiscu
C 726	15	13.4	4029	2	IOU10338	U10338 Ilyanassa o	C 799	15	13.4	17064	5	BX296523	BX296523 Mouse DNA
C 727	15	13.4	4085	2	AY060287	AY060287 Drosophi	C 800	15	13.4	20532	14	AC017605	AC017605 Drosophi
C 728	15	13.4	4088	8	HS69P20	U61520 Human GT334	C 801	15	13.4	20532	14	AE014194	AE014194 Sequence
C 729	15	13.4	4116	6	CO599903	CO599903 Sequence	C 802	15	13.4	20925	14	AC015205	AC015205 Sequence
C 730	15	13.4	4156	5	AF348156	AF348156 Danio rer	C 803	15	13.4	22012	14	AC014468	AC014468 Sequence
C 731	15	13.4	4173	6	AR070559	AR070559 Sequence	C 804	15	13.4	22012	14	AC020042	AC020042 Sequence
C 732	15	13.4	4173	6	AR310595	AR310595 Sequence	C 805	15	13.4	22892	1	AE008697	AE008697 Salmonell
C 733	15	13.4	4212	6	AR411665	AR411665 Sequence	C 806	15	13.4	23617	1	AB014266	AB014266 Streptoco
C 734	15	13.4	4212	6	CO588954	CO588954 Sequence	C 807	15	13.4	24227	6	CO573587	CO573587 Sequence
C 735	15	13.4	4260	6	CO736590	CO736590 Sequence	C 808	15	13.4	24227	6	AC139617	AC139617 Homo sapi
C 736	15	13.4	4517	1	AF354273	AF354273 Lactobaci	C 809	15	13.4	25901	8	AX276384	AX276384 Sequence
C 737	15	13.4	4562	1	TAPYRCIUS	Y09536 T. aquaticus	C 810	15	13.4	27324	2	CERF5A11	CERF5A11 Sequence
C 738	15	13.4	4586	1	BC065335	BC065335 Danio rer	C 811	15	13.4	27598	2	AC023735	AC023735 Drosophi
C 739	15	13.4	4764	15	CAHYRIGN	Z50123 Candida alb	C 812	15	13.4	28538	14	AC023735	AC023735 Drosophi
C 740	15	13.4	4846	2	AY069695	AY069695 Drosophi	C 813	15	13.4	28627	2	DROZFP	DROZFP Sequence
C 741	15	13.4	5059	9	AF289091	AF289091 Rattus no	C 814	15	13.4	29106	14	AC015530	AC015530 Homo sapi
C 742	15	13.4	5166	9	AK122563	AK122563 Mus muscu	C 815	15	13.4	32273	14	DMC2588	DMC2588 Sequence
C 743	15	13.4	5192	6	BC059209	BC059209 Mus muscu	C 816	15	13.4	33246	2	U64855	U64855 Caenorhabdi
C 744	15	13.4	5205	6	CQ609716	CQ609716 Sequence	C 817	15	13.4	34657	2	CER0961	CER0961 Sequence
C 745	15	13.4	5259	6	BC060378	BC060378 Mus muscu	C 818	15	13.4	35734	14	AC019974	AC019974 Drosophi
C 746	15	13.4	5390	1	XCXPSGRN	X59079 X. campestr	C 819	15	13.4	35898	14	AC162777	AC162777 Macropus
C 747	15	13.4	5591	9	MMSKELINA	Z22866 M. musculus	C 820	15	13.4	35898	14	AC162777	AC162777 Macropus
C 748	15	13.4	5645	9	MMU012072	AJ012072 Mus muscu	C 821	15	13.4	35898	14	AC162777	AC162777 Macropus



C 822	15	13.4	35162	15	SPAC2G11	254354 S.pombe chr	895	15	13.4	87302	8	AC027313	AC027313 Homo sapi
823	15	13.4	35776	15	SPAC4G8	256272 S.pombe chr	896	15	13.4	87819	5	BX510338	BX510338 Zebrafish
C 824	15	13.4	38449	8	AC005204	AC005204 Homo sapi	C 897	15	13.4	88011	15	ATT1614	AL079344 Arabidops
C 825	15	13.4	38828	15	AY485644_4	Continuation (5 of	C 898	15	13.4	88013	15	NCB1K11	AL669998 Neurospor
826	15	13.4	39640	14	AC014099	AC014099 Drosophila	C 899	15	13.4	88672	14	AC014992	AC014992 Drosophila
C 827	15	13.4	40070	2	DWC87B1	Z99269 Drosophila	C 900	15	13.4	89139	14	AC109980	AC109980 Rattus no
C 828	15	13.4	40766	6	CG612512	CG612512 Sequence	C 901	15	13.4	89370	11	AE015945	AE015945 Clostridi
C 829	15	13.4	42429	6	CO596348	CO596348 Sequence	C 902	15	13.4	89885	2	AC004368	AC004368 Drosophila
C 830	15	13.4	43051	8	AB001517	AB001517 Homo sapi	C 903	15	13.4	90349	15	AB023036	AB023036 Arabidops
C 831	15	13.4	43219	14	AC100163	AC100163 Mus muscu	C 904	15	13.4	90525	5	BX510955	BX510955 Zebrafish
C 832	15	13.4	43504	15	SC9150	Z28125 S.cerevisia	C 905	15	13.4	92384	8	AL137125	AL137125 Human DNA
833	15	13.4	44145	6	AX602195	AX602195 Sequence	C 906	15	13.4	92520	14	TANN1_25	Continuation (26 o
834	15	13.4	47410	16	AC166417	AC166417 Bos tauru	C 907	15	13.4	92520	14	TANN1_25	Continuation (26 o
C 835	15	13.4	48823	14	AC017217	AC017217 Drosophila	C 908	15	13.4	92852	14	AL671485	AL671485 Neurospor
C 836	15	13.4	49101	14	AC017923	AC017923 Drosophila	C 909	15	13.4	93143	9	AP007379	AP007379 Human DNA
C 837	15	13.4	49148	5	AB092842	AB092842 Gallus ga	C 910	15	13.4	93872	15	CNS08C78	AL731743 Oryza sat
838	15	13.4	49688	14	AC090162	AC090162 Homo sapi	C 911	15	13.4	93880	14	OSIG00043	AL733343 Oryza sat
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C 840	15	13.4	50969	1	AY046276	AY046276 Incn plas	C 913	15	13.4	96467	15	CT009545	CT009545 M.truncat
C 841	15	13.4	52811	14	AC099978	AC099978 Mus muscu	C 914	15	13.4	96745	14	AC074219	AC074219 Mus muscu
C 842	15	13.4	52874	14	AC151519	AC151519 Dario rer	C 915	15	13.4	96959	8	AC016142	AC016142 Homo sapi
843	15	13.4	53791	14	AF172272	AF172272 Homo sapi	C 916	15	13.4	96987	8	AC096573	AC096573 Homo sapi
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847	15	13.4	55610	14	AC105198	AC105198 Homo sapi	C 920	15	13.4	100939	13	AF270937	AF270937 Plutella
848	15	13.4	56319	14	AC100535	AC100535 Mus muscu	C 921	15	13.4	101305	15	AC007508	AC007508 Genomic s
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C 850	15	13.4	57000	8	AP005020	AP005020 Homo sapi	C 923	15	13.4	101678	14	CT009608	AP007743 Oryza cor
851	15	13.4	57685	14	AC111020	AC111020 Mus muscu	C 924	15	13.4	101708	14	AP007435	AC161616 Mus muscu
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C 853	15	13.4	57818	14	AC017287	AC017287 Drosophila	C 926	15	13.4	102591	14	AC165023	AL606702 Zebrafish
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C 858	15	13.4	64035	14	AC067822	AC067822 Homo sapi	C 931	15	13.4	106013	8	AC012607	AC012607 Homo sapi
C 859	15	13.4	66066	15	AC149486	AC149486 Populus t	C 932	15	13.4	106323	8	AL513477	AL513477 Human DNA
860	15	13.4	66831	14	AC137730	AC137730 Homo sapi	C 933	15	13.4	106449	8	AC096949	AC096949 Homo sapi
C 861	15	13.4	66811	6	AX702596	AX702596 Sequence	C 934	15	13.4	106494	14	BX537124_3	Continuation (4 of
C 862	15	13.4	69017	6	HS41018	AL031732 Human DNA	C 935	15	13.4	106724	9	AF130357	AF130357 Mus muscu
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C 864	15	13.4	71544	8	AC093792	AC093792 Homo sapi	C 937	15	13.4	107137	8	AC011292	AC011292 Homo sapi
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C 867	15	13.4	72645	14	AC112672	AC112672 Mus muscu	C 940	15	13.4	109123	15	AC105318	AC105318 Oryza sat
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872	15	13.4	77227	14	AC134350	AC134350 Homo sapi	C 945	15	13.4	110000	1	AB005674_00	AB005674 Shigella
C 873	15	13.4	77296	14	AC165761	AC165761 Bos tauru	C 946	15	13.4	110000	1	CP000091_15	Continuation (16 o
C 874	15	13.4	77506	14	AC165844	AC165844 Bos tauru	C 947	15	13.4	110000	1	CR522870_00	CR522870 Desulfoc
875	15	13.4	77568	14	AC139418	AC139418 Homo sapi	C 948	15	13.4	110000	1	CR626927_08	Continuation (9 of
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878	15	13.4	79470	14	AL391000	AL391000 Homo sapi	C 951	15	13.4	110000	1	AB013598_13	Continuation (14 o
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881	15	13.4	81677	15	AB025629	AB025629 Arabidops	C 954	15	13.4	110000	1	AB017220_00	AB017220 Salmo
C 882	15	13.4	82288	14	AC164698	AC164698 Bos tauru	C 955	15	13.4	110000	1	AB017245_0	AB017245 Mycoplasma
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886	15	13.4	85000	8	AP003056	AP003056 Homo sapi	C 959	15	13.4	110000	1	AP006716_08	Continuation (9 of
C 887	15	13.4	85101	8	AL450244	AL450244 Human DNA	C 960	15	13.4	110000	1	AP006716_13	Continuation (14 o
C 888	15	13.4	85762	5	CR388368	CR388368 Zebrafish	C 961	15	13.4	110000	1	AP006716_24	Continuation (25 o
C 889	15	13.4	86183	14	AP008145	AP008145 Lotus cor	C 962	15	13.4	110000	1	AP006841_08	Continuation (9 of
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## ALIGNMENTS

RESULT 1  
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LOCUS B.anthraxis encapsulation protein genes (capA, capB, and capC),  
DEFINITION complete cds.  
ACCESSION M24150  
VERSION M24150.1 GI:142630  
KEYWORDS encapsulation protein; membrane-associated protein.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1 (bases 1 to 3244)  
AUTHORS Makino,S., Uchida,I., Terakado,N., Sasakawa,C. and Yoshikawa,M.  
TITLE Molecular characterization and protein analysis of the cap region,  
JOURNAL which is essential for encapsulation in Bacillus anthracis  
PUBMED J. Bacteriol. 171 (2), 722-730 (1989)  
COMMENT 2536679

ORIGINAL source text: B.anthraxis (strain TE702; isolate pCAP1)  
DNA.  
Draft entry and computer-readable sequence for [1] kindly provided  
by I.Uchida, 01-MAY-1989.  
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## CDS

ORIGIN 748 bp upstream of HindIII site.

Query Match 100.0%; Score 112; DB 1; Length 3244;  
Best local similarity 100.0%; Pred. No. 1,8e-55;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGTACATCTGGCGGAGATGATATATTGTTTACTGACGAGGACCAACGATTAAAGCCCGT 60  
DB 477 GGTACATCTGGCGGAGATGATATATTGTTTACTGACGAGGACCAACGATTAAAGCCCGT 536  
QY 61 AAAGAGGTCCTAATATGCTGAGCAACGCGGAGTACTTAAGAGCGTGGC 112  
DB 537 AAAGAGGTCCTAATATGCTGAGCAACGCGGAGTACTTAAGAGCGTGGC 588

## RESULT 2

AE011191/c 94829 bp DNA circular BCT 14-JUN-2002  
LOCUS Bacillus anthracis str. A2012 plasmid pXO2, complete sequence.  
DEFINITION AE011191  
ACCESSION AE011191  
VERSION AE011191.1 GI:20520280  
KEYWORDS  
SOURCE Bacillus anthracis str. A2012  
ORGANISM Bacillus anthracis str. A2012  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.

REFERENCE 1 (bases 1 to 94829)  
AUTHORS Read,T.D., Salzberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapple,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Comparative genome sequencing for discovery of novel polymorphisms  
JOURNAL in Bacillus anthracis  
PUBMED Science 296 (5575), 2028-2033 (2002)  
12004073

REFERENCE 2 (bases 1 to 94829)  
AUTHORS Read,T.D., Salzberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapple,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Direct Submission  
JOURNAL Submitted (09-May-2002) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
FEATURES  
Location/Qualifiers  
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Best Local Similarity 100.0%; Pred. No. 1,4e-55;
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db      56597 GGTACATCGCGCGAATGATATGTTTACTGACGAGCAACGATTAGCGCGCT 56538
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Db      56537 AAGAAGGCTCTAATATCGTGTGACGACGAGGTATTAAAGAGCTGCTG 56486

RESULT 3
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DEFINITION Bacillus anthracis str. 'Ames Ancestor' plasmid pX02, complete
sequence.
ACCESSION  AB017335
VERSION     AB017335
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS    1 (bases 1 to 94830)
           Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
           Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,
           Salzberg,S. and Fraser,C.M.
TITLE      Bacillus anthracis comparative genomics
JOURNAL
REFERENCE
AUTHORS    2 (bases 1 to 94830)
           Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
           Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,
           Salzberg,S. and Fraser,C.M.
TITLE      Direct Submission
JOURNAL
REFERENCE
AUTHORS    Submitted (17-May-2004) Microbial Genomics, The Institute for
           Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850,
           USA
           3 (bases 1 to 94830)
           Ravel,J., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
           Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,
           Salzberg,S. and Fraser,C.M.
TITLE      Direct Submission
JOURNAL
REFERENCE
AUTHORS    Submitted (09-JUL-2004) Microbial Genomics, The Institute for
           Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850,

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REMARK      USA
COMMENT      Sequence update by submitter
            On Jul 9, 2004 this sequence version replaced gi:47552342.
FEATURES
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DB	56597	GGTCACTCTGGCGCAATGATATATATGGTTTACTGACGAGCAACCGATTAAAGCGCGCT	56533	
QY	61	AAAGAAGTCTTATATCGGTGAGCAACGAGGCTAGTTAAAGAGCTGCTG	112	
DB	56537	AAAGAAGTCTTATATCGGTGAGCAACGAGGCTAGTTAAAGAGCTGCTG	56486	
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DEFINITION	Bacillus anthracis plasmid pX02, complete sequence.			
ACCESSION	AF188935			
VERSION	AF188935.1	GI:6470151		
KEYWORDS				
SOURCE				
ORGANISM	Bacillus anthracis			
REFERENCE	Bacillus anthracis			
AUTHORS	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.			
	1 (bases 1 to 96231)			
	Okimura, R.T., Cloud, K., Hampton, O., Hill, K.K., Keim, P., Lamke, G., Kumano, S., Manter, D., Martinez, Y., Svensson, R., Tatam, L.R., Brown, A.E. and Jackson, P. J.			
TITLE	Direct Submission			
JOURNAL	Submitted (01-NOV-1999) Bioscience Division, Los Alamos National Laboratory, M888, Los Alamos, NM 87545, USA			
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CDs

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FPLDKDAGNDPASFIIKGLFVALFVLVIMIGIRITIOHKPPRFKSVGNILIMIG  
LLGGLNELMDQMSTDPFSEITNTSKADGLAMDVOKMTADLIYLSKGFEPDQS  
KKEHEPAISSTDSKPKGMSKDIPLKOLGQVTVPKYIEMLTGKODIPKETEYLVYKI  
TNDGKETVERKINDSVNPFMDKPRGGVVRPMNFGTIFMGLLALGVAVLETFVVFPM

Query Match 100.0%; Score 112; DB 1; Length 96231;  
Best Local Similarity 100.0%; Pred. No. 1.4e-55;  
Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGATCATCTGGCGAATGATATATTGGTTTACTGACGAGGACCAACGATTAAAGCGCGT 60  
Db 57087 GGATCATCTGGCGAATGATATATTGGTTTACTGACGAGGACCAACGATTAAAGCGCGT 57028

Qy 61 AAAGAAAGTCTCTAATATCGGTGACCAACGAGGTAAGTAAAGGCTGCTG 112  
Db 57027 AAAGAAAGTCTCTAATATCGGTGACCAACGAGGTAAGTAAAGGCTGCTG 56976

RESULT 5  
AX743806 32 bp DNA linear PAT 14-MAY-2003  
LOCUS Sequence 3 from Patent EP1304387.  
ACCESSION AX743806  
VERSION AX743806.1 GI:30722558  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
AUTHORS  
TITLE  
Detection of Bacillus anthracis  
Patent: EP 1304387-A 3 23-APR-2003;  
JOURNAL  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
Location/Qualifiers  
FEATURES  
source 1..32  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

ORIGIN  
Query Match 28.6%; Score 32; DB 6; Length 32;  
Best Local Similarity 100.0%; Pred. No. 1.8e-07;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 47 CGATTAAAGCGCGTAAAGAGTCTAATATC 78  
Db 1 CGATTAAAGCGCGTAAAGAGTCTAATATC 32

RESULT 6  
AX743807 30 bp DNA linear PAT 14-MAY-2003  
LOCUS Sequence 4 from Patent EP1304387.  
ACCESSION AX743807

VERSION AX743807.1 GI:30722559  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
AUTHORS  
TITLE  
Detection of Bacillus anthracis  
Patent: EP 1304387-A 4 23-APR-2003;  
JOURNAL  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
Location/Qualifiers  
FEATURES  
source 1..30  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

ORIGIN  
Query Match 26.8%; Score 30; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred. No. 2.9e-06;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 80 GTGAGCAACGCGGTAAGTAAAGGCTG 109  
Db 1 GTGAGCAACGCGGTAAGTAAAGGCTG 30

RESULT 7  
AX743817 26 bp DNA linear PAT 14-MAY-2003  
LOCUS Sequence 14 from Patent EP1304387.  
ACCESSION AX743817  
VERSION AX743817.1 GI:30722569  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
AUTHORS  
TITLE  
Detection of Bacillus anthracis  
Patent: EP 1304387-A 14 23-APR-2003;  
JOURNAL  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
Location/Qualifiers  
FEATURES  
source 1..26  
/organism="synthetic construct"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide"

ORIGIN  
Query Match 23.2%; Score 26; DB 6; Length 26;  
Best Local Similarity 100.0%; Pred. No. 0.00072;  
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 81 TGAGCAACGCGGTAAGTAAAGG 106  
Db 1 TGAGCAACGCGGTAAGTAAAGG 26

RESULT 8  
AX743816 25 bp DNA linear PAT 14-MAY-2003  
LOCUS Sequence 13 from Patent EP1304387.  
ACCESSION AX743816  
VERSION AX743816.1 GI:30722568  
KEYWORDS  
SOURCE  
ORGANISM  
synthetic construct  
other sequences; artificial sequences.  
REFERENCE  
1 Bell,C.A., Uhl,J.R. and Cockerill,F.R.



**TITLE** Detection of *Bacillus anthracis*  
**JOURNAL** Patent: EP 1304387-A 13 23-APR-2003;  
 Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
 and Research (US)  
**FEATURES** Location/Qualifiers  
 source 1..25  
 /organism="synthetic construct"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:32630"  
 /note="Oligonucleotide"  
**ORIGIN**  
 Query Match 22.3%; Score 25; DB 6; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.0029;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 55 CGCCGTAAGAAGGTCCTAATATCG 79  
 1 CGCCGTAAGAAGGTCCTAATATCG 25  
**RESULT 9**  
 BV454344 901 bp DNA linear STS 06-APR-2005  
 LOCUS sop38c12.b1 Clint Pan troglodytes versus STS genomic, sequence  
 DEFINITION tagged site.  
 accession BV454344  
 version BV454344.1 GI:62213772  
 keywords STS.  
 source Pan troglodytes versus  
 organism Pan troglodytes versus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Pan.  
 1 (bases 1 to 901)  
 Mikkelson,T.S., Hillier,W.L., Eichler,E.E., Zody,M.C. and  
 Jaffe,D.B.  
**REFERENCE** Initial Sequence of the Chimpanzee Genome and Comparison with the  
 Human Genome  
 unpublished (2005)  
**TITLE**  
**JOURNAL**  
**COMMENT**  
 Contact: Michael C. Zody  
 Broad Institute of MIT and Harvard  
 320 Charles Street, Cambridge, MA 02141, USA  
 Tel: 6172580933  
 Fax: 6172580903  
 Email: mczody@broad.mit.edu  
 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 901  
 Protocol:  
 23,021,928 chimpanzee whole genome shotgun reads were aligned to  
 the Human genome NCBI  
 Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,  
 including Clint (Pan  
 troglodytes verus), 3 other Pan troglodytes verus chimps  
 (Donald,Karlén,Yvonne), 3 Pan  
 troglodytes troglodytes chimps (Noemie,Masuku,Clara) and 2 chimps  
 of unknown origin  
 (Gon,Unknown Chimp). Common names: Pan troglodytes verus is the  
 western chimp and Pan  
 troglodytes troglodytes is the central chimp. To be included in  
 chimpanzee SNP discovery, a  
 read must be at least 500bp in length, at least 50% of its base  
 calls must have Phred  
 score >= 20, at least 30% of its base calls must satisfy  
 SNQs(30,25)(single strand NQS, the  
 base in question has Phred score >= 30, the surrounding 10 bases in  
 the read have Phred  
 score >= 25), and the read must have at least 200 bp SNQs(30,25)  
 bases. Reads not uniquely  
 placed in the genome and read pairs whose two ends were not  
 consistently placed were

discarded. After above filtering, NQS(30,25) standard was applied  
 to all pairs of  
 overlapping reads to call NQS bases and SNPs. Alignments (between  
 two reads) with less  
 than 100 NQS bases or with SNP rate > 0.01 were discarded. To  
 exclude alignment between two  
 copies of a single read, comparisons between two reads that share  
 95% of their genome  
 alignments (>=95% bases of read A and >=95% bases of read B were  
 placed at the same locus  
 of human genome) were discarded.  
**FEATURES** Location/Qualifiers  
 source 1..901  
 /organism="Pan troglodytes verus"  
 /mol\_type="genomic DNA"  
 /sub\_species="verus"  
 /db\_xref="taxon:37012"  
 /clone\_id="Clint"  
 <1..>901  
**ORIGIN**  
 STS  
 Query Match 17.0%; Score 19; DB 10; Length 901;  
 Best Local Similarity 100.0%; Pred. No. 8.8;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 15 AATGATATATGTTTACT 33  
 817 AATGATATATGTTTACT 835  
**RESULT 10**  
 AC161017 101021 bp DNA linear HTG 05-MAY-2005  
 LOCUS Pan troglodytes chromosome Y clone CH251-157N1, WORKING DRAFT  
 DEFINITION  
 SEQUENCE, 8 unordered pieces.  
 accession AC161017  
 version AC161017.1 GI:63028373  
 keywords HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_FULLTOP.  
 source Pan troglodytes (chimpanzee)  
 organism Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Pan.  
 1 (bases 1 to 101021)  
 Wilson,R.K.  
**REFERENCE** The sequence of Pan troglodytes clone  
 Unpublished  
 2 (bases 1 to 101021)  
 Wilson,R.K.  
**REFERENCE** Submitted (05-MAY-2005) Genetics, Genome Sequencing Center, 4444  
 Forest Park Parkway, St. Louis, MO 63108, USA  
**TITLE**  
**JOURNAL**  
**COMMENT**  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu  
 Contact: submissions@wustl.edu  
 Project Information -----  
 Center project name: C\_AB0157N01  
 ----- Summary Statistics -----  
 Sequencing vector: M13, 0%  
 Sequencing vector: plasmid, 100%  
 Chemistry: Dye-terminator Big Dye, 100% of reads  
 Assembly program: Phrap; Version 0.990319  
 Consensus quality: 99387 bases at least Q40  
 Consensus quality: 99605 bases at least Q20  
 -----  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 8 contigs. The true order of the pieces



\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence.  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1227: contig of 1227 bp in length  
1228 1327: gap of unknown length  
1328 2900: contig of 1573 bp in length  
2901 3000: gap of unknown length  
3001 4736: contig of 1736 bp in length  
4737 4836: gap of unknown length  
4837 9906: contig of 5070 bp in length  
9907 10007: gap of unknown length  
10007 17896: contig of 7890 bp in length  
17897 17997: gap of unknown length  
17997 40486: contig of 22490 bp in length  
40487 40587: gap of unknown length  
40587 99657: contig of 59071 bp in length  
99658 99757: gap of unknown length  
99758 101021: contig of 1264 bp in length.

## FEATURES

## Source

1. .101021  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="Y"  
/clone="CH251-157N1"  
1. .1227  
/note="assembly\_name:Contig17"

## misc\_feature

1228. .1327  
/estimated\_length=unknown

## misc\_feature

1328. .2900  
/note="assembly\_name:Contig18"

## gap

2901. .3000  
/estimated\_length=unknown

## misc\_feature

3001. .4736  
/note="assembly\_name:Contig20"

## gap

4737. .4836  
/estimated\_length=unknown

## misc\_feature

4837. .9906  
/note="assembly\_name:Contig21"

## gap

9907. .10006  
/estimated\_length=unknown

## misc\_feature

10007. .17896  
/note="assembly\_name:Contig22"

## gap

17897. .17996  
/estimated\_length=unknown

## misc\_feature

17997. .40486  
/note="assembly\_name:Contig23"

## gap

40487. .40586  
/estimated\_length=unknown

## misc\_feature

40587. .99657  
/note="assembly\_name:Contig24"

## gap

99658. .99757  
vector\_side:right"

## misc\_feature

99758. .101021  
/estimated\_length=unknown

## ORIGIN

99758. .101021  
/note="assembly\_name:Contig5"

## Query Match

17.0%; Score 19; DB 14; Length 101021;  
Best Local Similarity 100.0%; Pred. No. 6.4;

## Matches

19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

15 AATGATATATGTTTACT 33

## Db

66252 AATGATATATGTTTACT 66270

## RESULT 11

AB005174\_20

## WPCOMMENT

Sequence split into 56 fragments LOCUS AB005174 Accession AB005174

Fragment Name

AB005174\_00

AB005174\_01

AB005174\_02

AB005174\_03

AB005174\_04

AB005174\_05

AB005174\_06

AB005174\_07

AB005174\_08

AB005174\_09

AB005174\_10

AB005174\_11

AB005174\_12

AB005174\_13

AB005174\_14

AB005174\_15

AB005174\_16

AB005174\_17

AB005174\_18

AB005174\_19

AB005174\_20

AB005174\_21

AB005174\_22

AB005174\_23

AB005174\_24

AB005174\_25

AB005174\_26

AB005174\_27

AB005174\_28

AB005174\_29

AB005174\_30

AB005174\_31

AB005174\_32

AB005174\_33

AB005174\_34

AB005174\_35

AB005174\_36

AB005174\_37

AB005174\_38

AB005174\_39

AB005174\_40

AB005174\_41

AB005174\_42

AB005174\_43

AB005174\_44

AB005174\_45

AB005174\_46

AB005174\_47

AB005174\_48

AB005174\_49

AB005174\_50

AB005174\_51

AB005174\_52

AB005174\_53

AB005174\_54

AB005174\_55

AB005174\_56

AB005174\_57

AB005174\_58

AB005174\_59

AB005174\_60

AB005174\_61

AB005174\_62

AB005174\_63

AB005174\_64

AB005174\_65

AB005174\_66

AB005174\_67

AB005174\_68

Begin End

1 110000

210000

310000

410000

510000

610000

710000

810000

910000

1010000

1110000

1210000

1310000

1410000

1510000

1610000

1710000

1810000

1910000

2010000

2100000

2210000

2310000

2410000

2510000

2610000

2710000

2810000

2910000

3010000

3110000

3210000

3310000

3410000

3510000

3610000

3710000

3810000

3910000

4010000

4110000

4210000

4310000

4410000

4510000

4610000

4710000

4810000

4910000

5010000

5110000

5210000

5310000

5410000

5510000

5528445

Continuation (21 of 56) of AB005174 from base 2000001 (AB005174 Escherichia coli O157

Query Match 17.0%; Score 19; DB 1; Length 110000;

Best Local Similarity 100.0%; Pred. No. 6.4;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Qy

58 CGTAAAGAGCTCTATA 76

## Db

76177 CGTAAAGAGCTCTATA 76195

## RESULT 12

BA000007 20/c  
WPCOMMENT



Sequence split into 55 fragments LOCUS BA000007 Accession BA000007

Fragment Name	Begin	End
BA000007_00	1	110000
BA000007_01	100001	210000
BA000007_02	200001	310000
BA000007_03	300001	410000
BA000007_04	400001	510000
BA000007_05	500001	610000
BA000007_06	600001	710000
BA000007_07	700001	810000
BA000007_08	800001	910000
BA000007_09	900001	1010000
BA000007_10	1000001	1110000
BA000007_11	1100001	1210000
BA000007_12	1200001	1310000
BA000007_13	1300001	1410000
BA000007_14	1400001	1510000
BA000007_15	1500001	1610000
BA000007_16	1600001	1710000
BA000007_17	1700001	1810000
BA000007_18	1800001	1910000
BA000007_19	1900001	2010000
BA000007_20	2000001	2110000
BA000007_21	2100001	2210000
BA000007_22	2200001	2310000
BA000007_23	2300001	2410000
BA000007_24	2400001	2510000
BA000007_25	2500001	2610000
BA000007_26	2600001	2710000
BA000007_27	2700001	2810000
BA000007_28	2800001	2910000
BA000007_29	2900001	3010000
BA000007_30	3000001	3110000
BA000007_31	3100001	3210000
BA000007_32	3200001	3310000
BA000007_33	3300001	3410000
BA000007_34	3400001	3510000
BA000007_35	3500001	3610000
BA000007_36	3600001	3710000
BA000007_37	3700001	3810000
BA000007_38	3800001	3910000
BA000007_39	3900001	4010000
BA000007_40	4000001	4110000
BA000007_41	4100001	4210000
BA000007_42	4200001	4310000
BA000007_43	4300001	4410000
BA000007_44	4400001	4510000
BA000007_45	4500001	4610000
BA000007_46	4600001	4710000
BA000007_47	4700001	4810000
BA000007_48	4800001	4910000
BA000007_49	4900001	5010000
BA000007_50	5000001	5110000
BA000007_51	5100001	5210000
BA000007_52	5200001	5310000
BA000007_53	5300001	5410000
BA000007_54	5400001	5498450

Continuation (21 of 55) of BA000007 from base 2000001 (BA000007 Escherichia coli O157:H7)

Query Match 17.0%; Score 19; DB 1; Length 110000;  
 Best Local Similarity 100.0%; Pred. No. 6.4;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

58 CGTAAAGAGGTCCTAATA 76  
 DB 12301 CGTAAAGAGGTCCTAATA 12283

RESULT 13 AC148285 161266 bp DNA 1linear HTG 05-JUN-2004  
 LOCUS AC148285/c Rhinolophus ferrumequinum clone VMC7-21917, WORKING DRAFT  
 DEFINITION SEQUENCE, 6 ordered pieces.

AC148285  
 AC148285.4 GI:48311464  
 HTG: HTGS PHASE2; HTGS DRAFT.  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Rhinolophus ferrumequinum (greater horseshoe bat)  
 Rhinolophus ferrumequinum  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Chiroptera; Microchiroptera;  
 Rhinolophidae; Rhinolophinae; Rhinolophus.  
 1 (bases 1 to 161266)  
 AUTHORS  
 Antonellis A., Ayele K., Benjamin B., Blakesley R.W.,  
 Bouffard G.G., Brinkley C., Brooks S., Chu G., Coleman B.,  
 Coleman H., Daki N., Engle J., Guan X., Gupta J., Haghighi P.,  
 Han J., Hansen N., Ho S.-D., Hu P., Hurtle B., Idol J.R., Jones C.,  
 Karins E., Kim H., Kwong P., Latic P., Larson S., Lee-Lin S.-Q.,  
 Legaspi R., Madden M., Maduro Q.L., Maduro V.B., Margules B.H.,  
 Masiello C., Maskeri B., McDowell J., Mullikin J.C., Paguiragan C.,  
 Park M., Portnoy M.E., Prasad A., Puti O., Reddi-Dugue N.,  
 Schandler K., Schueler M.G., Shah K., Sison C., Stamtrop S.,  
 Thomas J.W., Thomas P.J., Tsipouri V., Vogt J.L., Wetherby K.D.,  
 Young A. and Green E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 161266)  
 Green E.D.  
 Direct Submission  
 Submitted (19-FEB-2004) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 3 (bases 1 to 161266)  
 Green E.D.  
 Direct Submission  
 Submitted (05-JUN-2004) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 On Jun 5, 2004 this sequence version replaced gi:47026462.  
 ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc.zoo@nhgri.nih.gov](mailto:nisc.zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: gch  
 Center clone name: 219107

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies; the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990119  
 Consensus quality: 160115 bases at least Q40  
 Consensus quality: 160437 bases at least Q30  
 Consensus quality: 160628 bases at least Q20  
 Insert size: 109000; agarose-fp  
 Insert size: 160766; sum-of-contigs  
 Quality coverage: 13.64X in Q20 bases; agarose-fp  
 Quality coverage: 9.25X in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 6 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced



```

* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1 33209: contig of 33209 bp in length
* 32210 32309: gap of unknown length
* 32310 35490: contig of 3181 bp in length
* 35491 35590: gap of unknown length
* 35591 48271: contig of 12681 bp in length
* 48272 48371: gap of unknown length
* 48372 122673: contig of 74302 bp in length
* 122674 122773: gap of unknown length
* 122774 126289: contig of 3516 bp in length
* 126290 126389: gap of unknown length
* 126390 161266: contig of 34877 bp in length.
*
FEATURES
    source
        1..161266
            /organism="Rhizophus ferrugineum"
            /mol_type="genomic DNA"
            /db_xref="taxon:59479"
            /clone="VMRC7-21917"
            /clone_id="VMRC7"
            /note="BAC resource: http://bacpac.chori.org/"
    misc_feature
        1..33209
            /note="assembly_fragment
            missing clone end on 5' end of insert"
    gap
        33210..33309
            /estimated_length=unknown
    misc_feature
        33310..35490
            /note="assembly_fragment"
    gap
        35491..35590
            /estimated_length=unknown
    misc_feature
        35591..48271
            /note="assembly_fragment"
    gap
        48272..48371
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    misc_feature
        48372..122673
            /note="assembly_fragment"
    gap
        122674..122773
            /estimated_length=unknown
    misc_feature
        122774..126289
            /note="assembly_fragment"
    gap
        126290..126389
            /estimated_length=unknown
    misc_feature
        126390..161266
            /note="assembly_fragment
            clone_end:SP6
            vector_side:right"
    misc_feature
        128974..161266
            /note="clone overlaps with GenBank Accession Number
            AC148286 clone VMRC7-266121 (center project name gcl)"
ORIGIN
    Query Match 17.0%; Score 19; DB 14; Length 161266;
    Best Local Similarity 100.0%; Pred. No. 6.2;
    Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
    Qy 60 TAAAGAGCTCCTAATATC 78
    Db 19249 TAAAGAGCTCCTAATATC 19231

```

```

AUTHORS
    TITLE
        JOURNAL
    REFERENCE
        2 (bases 1 to 169143)
        Wilson,R.K.
        Direct Submission
        Submitted (04-NOV-2003) Genetics, Genome Sequencing Center, 4444
        Forest Park Parkway, St. Louis, MO 63108, USA
    REFERENCE
        3 (bases 1 to 169143)
        Wilson,R.K.
        Direct Submission
        Submitted (07-JUN-2004) Genetics, Genome Sequencing Center, 4444
        Forest Park Parkway, St. Louis, MO 63108, USA
    REFERENCE
        4 (bases 1 to 169143)
        Wilson,R.K.
        Direct Submission
        Submitted (19-MAY-2004) Washington University School of Medicine,
        Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
        63108, USA
    COMMENT
        On Jan 7, 2004 this sequence version replaced gi:38154206.
        ----- Genome Center
        Center: Washington University Genome Sequencing Center
        Center code: WUGSC
        Web site: http://genome.wustl.edu
        Contact: submissions@watson.wustl.edu
        ----- Summary Statistics
        Center project name: C_AB0410H20
        -----
    NOTICE:
        This sequence was finished as follows unless otherwise noted:
        all regions were double stranded, sequenced with an alternate
        chemistry, or covered by high quality data (i.e., phred quality >=
        30); an attempt was made to resolve all sequencing problems, such
        as compressions and repeats; all regions were covered by sequence
        from more than one subclone; and the assembly was confirmed by
        restriction digest.
    MAPPING INFORMATION:
        The position of this clone was established as part of a
        collaboration between the Chimpanzee Chromosome Y Mapping Project
        (Jennifer F. Hughes, Tatyana Pyntikova, Helen Skalecky, Steve
        Rozen, and David C. Page at the Whitehead Institute for Biomedical
        Research, Cambridge MA) and the Washington University Genome
        Sequencing Center, St. Louis MO.
    SOURCE INFORMATION:
        The CHORI-251 Chimpanzee BAC library has been constructed at the
        Children's Hospital Oakland Research Institute, BACPAC Resources,
        by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained
        from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0471;
        birthdate:6-6-80). The clone and detailed information can be
        obtained from Pletter de Jong and co-workers at
        http://www.bacpac.chori.org.
    NEIGHBORING SEQUENCE INFORMATION:
        This sequence is the entire insert of the clone. This clone is
        overlapped by AC147338.
    FEATURES
        source
            1..169143
                /organism="Pan troglodytes"
                /mol_type="genomic DNA"
                /db_xref="taxon:9598"
                /chromosome="Y"
                /map="Y"
                /clone="CH251-410H20"
                /clone_id="CHOR1251"
                1..42629
                /note="Unresolved duplication."
ORIGIN
    Query Match 17.0%; Score 19; DB 8; Length 169143;

```



Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATTGGTTTACT 33  
Db 76822 AATGATATATTGGTTTACT 76840

# RESULT 15

AC147338/c 173967 bp DNA linear PRI 03-JAN-2004  
LOCUS AC147338  
DEFINITION Pan troglodytes BAC clone CH251-61P8 from Y, complete sequence.  
ACCESSION AC147338  
VERSION AC147338.2 GI:40286624  
KEYWORDS HTG.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.

REFERENCE 1 (bases 1 to 173967)  
AUTHORS Trani, L., Cotton, M. and Bielicki, L.  
TITLE The sequence of Pan troglodytes BAC clone CH251-61P8  
JOURNAL Unpublished (2001)  
REFERENCE 2 (bases 1 to 173967)  
AUTHORS Wilson, R.  
TITLE Sequencing of Pan troglodytes  
JOURNAL Unpublished (2001)  
REFERENCE 3 (bases 1 to 173967)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (07-NOV-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
4 (bases 1 to 173967)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (21-DEC-2003) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
5 (bases 1 to 173967)  
AUTHORS Wilson, R.  
TITLE Direct Submission  
JOURNAL Submitted (03-JAN-2004) Department of Genetics, Washington  
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
On Dec 21, 2003 this sequence version replaced gi:38198892.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)  
----- Summary Statistics  
-----  
Center project name: C\_AB0061P08

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a collaboration between the Chimpanzee Chromosome Y Mapping Project (Jennifer F. Hughes, Tatyana Pyntikova, Helen Skalecky, Steve Rozen, and David C. Page at the Whitehead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.

## FEATURES

source  
Location/Qualifiers  
1. 173967  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="Y"  
/map="Y"  
/clone="CH251-61P8"  
/clone\_1b="CHOR1251"  
21011. 21102  
/note="Sequence derived from one plasmid subclone."  
84969. 85167  
/note="Sequence derived from one plasmid subclone."  
85350. 85380  
/note="Sequence derived from one plasmid subclone."  
157453. 157517  
/note="Sequence derived from one plasmid subclone."

## ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 173967;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATTGGTTTACT 33  
Db 138290 AATGATATATTGGTTTACT 138272

# RESULT 16

AC148875 182437 bp DNA linear PRI 18-AUG-2004  
LOCUS AC148875  
DEFINITION Pan troglodytes BAC clone CH251-198111 from Y, complete sequence.  
ACCESSION AC148875  
VERSION AC148875.2 GI:50204609  
KEYWORDS HTG.  
SOURCE Pan troglodytes (chimpanzee)  
ORGANISM Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.

REFERENCE 1 (bases 1 to 182437)  
AUTHORS Trani, L., Haglund, K. and Cordum, H.  
TITLE The sequence of Pan troglodytes BAC clone CH251-198111  
JOURNAL Unpublished (2001)  
REFERENCE 2 (bases 1 to 182437)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (16-APR-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 182437)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (24-APR-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
4 (bases 1 to 182437)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (10-JUN-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
5 (bases 1 to 182437)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
JOURNAL Submitted (18-AUG-2004) Washington University School of Medicine,  
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
63108, USA  
On Jul 10, 2004 this sequence version replaced gi:46395454.  
----- Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>



Contact: submissions@watson.wustl.edu  
 ----- Summary Statistics  
 Center project name: C\_ABO198111  
 -----

## NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a  
 collaboration between the Chimpanzee Chromosome Y Mapping Project  
 (Jennifer F. Hughes, Tatyana Pynlikova, Helen Skaletsky, Steve  
 Rozen, and David C. Page at the Whitehead Institute for Biomedical  
 Research, Cambridge MA) and the Washington University Genome  
 Sequencing Center, St. Louis MO.

## SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the  
 Children's Hospital Oakland Research Institute, BACPAC Resources,  
 by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained  
 from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0477;  
 birthdate:6-6-80). The clone and detailed information can be  
 obtained from Pieter de Jong and co-workers at  
 http://www.bacpac.chori.org.

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

Location/Qualifiers

1..182437  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /chromosome="Y"

## FEATURES

source  
 1..97762  
 /note="Unresolved inverted repeat."  
 50616..50956  
 /note="Sequence derived from PCR product of project DNA."  
 51062..51228  
 /note="Sequence derived from one plasmid subclone."

## ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 182437;  
 Best Local Similarity 100.0%; Pred. No. 6.1;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 15 AATGATATATGCTTACT 33  
 |||  
 Db 104379 AATGATATATGCTTACT 104397

## RESULT 17

AC148937 184818 bp DNA linear PRI 18-AUG-2004  
 DEFINITION Pan troglodytes BAC clone CH251-48517 from Y, complete sequence.  
 ACCESSION AC148937  
 VERSION AC148937.2 GI:50204573  
 KEYWORDS HTG.  
 SOURCE Pan troglodytes (chimpanzee)  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan.

REFERENCE 1 (bases 1 to 184818)

AUTHORS  
 TITLE Trani, L., Haglund, K. and Cordum, H.  
 JOURNAL The sequence of Pan troglodytes BAC clone CH251-48517  
 REFERENCE Unpublished (2001)  
 2 (bases 1 to 184818)  
 AUTHORS Wilson, R.K.  
 JOURNAL Direct Submission  
 Submitted (27-APR-2004) Genetics, Genome Sequencing Center, 4444  
 Forest Park Parkway, St. Louis, MO 63108, USA  
 3 (bases 1 to 184818)  
 AUTHORS Wilson, R.K.  
 JOURNAL Direct Submission  
 Submitted (10-JUL-2004) Genetics, Genome Sequencing Center, 4444  
 Forest Park Parkway, St. Louis, MO 63108, USA  
 4 (bases 1 to 184818)  
 AUTHORS Wilson, R.K.  
 JOURNAL Direct Submission  
 Submitted (18-AUG-2004) Washington University School of Medicine,  
 Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
 63108, USA  
 On Jul 10, 2004 this sequence version replaced gi:46576166.

## REFERENCE

1. 177870  
 /note="Unresolved inverted repeat."  
 86612..86648  
 /note="Sequence derived from one plasmid subclone."  
 86724..87238  
 /note="Sequence derived from PCR product of project DNA."

## COMMENT

----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu  
 Contact: submissions@watson.wustl.edu  
 ----- Summary Statistics  
 Center project name: C\_ABO485107  
 -----

## NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a  
 collaboration between the Chimpanzee Chromosome Y Mapping Project  
 (Jennifer F. Hughes, Tatyana Pynlikova, Helen Skaletsky, Steve  
 Rozen, and David C. Page at the Whitehead Institute for Biomedical  
 Research, Cambridge MA) and the Washington University Genome  
 Sequencing Center, St. Louis MO.

## SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the  
 Children's Hospital Oakland Research Institute, BACPAC Resources,  
 by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained  
 from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0477;  
 birthdate:6-6-80). The clone and detailed information can be  
 obtained from Pieter de Jong and co-workers at  
 http://www.bacpac.chori.org.

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

Location/Qualifiers

1..184818  
 /organism="Pan troglodytes"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9598"  
 /chromosome="Y"

## FEATURES

source  
 1..177870  
 /note="Unresolved inverted repeat."  
 86612..86648  
 /note="Sequence derived from one plasmid subclone."  
 86724..87238  
 /note="Sequence derived from PCR product of project DNA."



## ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 184818;  
 Best Local Similarity 100.0%; Pred. No. 6.1;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AATGATATATTGTTTACT 33  
 |||||

Db 144451 AATGATATATTGTTTACT 144469

## RESULT 18

AC148937/c

DEFINITION Pan troglodytes BAC clone CH251-48517 from Y, complete sequence.

AC148937.2 GI:50204573

HTG.

Pan troglodytes (chimpanzee)

SOURCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan.

1 (bases 1 to 184818)

Triani, L., Haglund, K. and Cordum, H.

The sequence of Pan troglodytes BAC clone CH251-48517

2 (bases 1 to 184818)

Wilson, R.K.

Direct Submission

Submitted (27-APR-2004) Genetics, Genome Sequencing Center, 4444

Forest Park Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 184818)

Wilson, R.K.

Direct Submission

Submitted (10-JUL-2004) Genetics, Genome Sequencing Center, 4444

Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 184818)

Wilson, R.K.

Direct Submission

Submitted (18-AUG-2004) Washington University School of Medicine,  
 Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
 63108, USA

On Jul 10, 2004 this sequence version replaced gi:46576166.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>

Contact: [submissions@wustl.edu](mailto:submissions@wustl.edu)

----- Summary Statistics

Center project name: C\_AB0485107

-----

NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by  
 restriction digest.

## MAPPING INFORMATION:

The position of this clone was established as part of a  
 collaboration between the Chimpanzee Chromosome Y Mapping Project  
 (Jennifer F. Hughes, Tatyana Pyntikova, Helen Skaltsky, Steve  
 Rozen, and David C. Page at the Whitehead Institute for Biomedical  
 Research, Cambridge MA) and the Washington University Genome  
 Sequencing Center, St. Louis MO.

## SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the

Children's Hospital Oakland Research Institute, BACPAC Resources,  
 by Dr. Baoji Zhu. DNA was isolated from white blood cells obtained  
 from a male chimpanzee (Pan troglodytes, 'Clint', Yerkis #C0471;  
 birthdate:6-6-80). The clone and detailed information can be  
 obtained from Pieter de Jong and co-workers at  
<http://www.bacpac.chori.org>.

## NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

## FEATURES

location/Qualifiers

1..184818

/organism="Pan troglodytes"

/mol\_type="genomic DNA"

/db\_xref="taxon:9598"

/chromosome="Y"

/map="Y"

/clone="CH251-48517"

/clone\_id="CHOR1251"

1..177870

/note="Unresolved inverted repeat."

86612..86648

/note="Sequence derived from one plasmid subclone."

86724..87238

/note="Sequence derived from PCR product of project DNA."

## ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 184818;  
 Best Local Similarity 100.0%; Pred. No. 6.1;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AATGATATATTGTTTACT 33  
 |||||

Db 33443 AATGATATATTGTTTACT 33425

## RESULT 19

AC155319

LOCUS

DEFINITION

Pan troglodytes BAC clone CH251-770A15 from chromosome Y, complete  
 sequence.

AC155319.2 GI:58197803

HTG.

Pan troglodytes (chimpanzee)

SOURCE

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan.

1 (bases 1 to 185385)

Tomlinson, C., Kozlowski, A. and Bielicki, L.

The sequence of Pan troglodytes BAC clone CH251-770A15

2 (bases 1 to 185385)

Wilson, R.K.

Direct Submission

Submitted (14-JAN-2005) Genetics, Genome Sequencing Center, 4444

Forest Park Parkway, St. Louis, MO 63108, USA

3 (bases 1 to 185385)

Wilson, R.K.

Direct Submission

Submitted (26-JAN-2005) Genetics, Genome Sequencing Center, 4444

Forest Park Parkway, St. Louis, MO 63108, USA

4 (bases 1 to 185385)

Wilson, R.K.

Direct Submission

Submitted (27-APR-2005) Washington University School of Medicine,  
 Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO  
 63108, USA

On Jan 26, 2005 this sequence version replaced gi:57790264.

----- Genome Center

Center: Washington University Genome Sequencing Center

Center code: WUGSC

Web site: <http://genome.wustl.edu>







Db 2166 AATGATATATTGTTTACT 2184

RESULT 21  
AC148941/c

LOCUS  
DEFINITION  
SEQUENCE, 10 unordered pieces.

AC148941 203914 bp DNA linear HTG 01-OCT-2004  
Pan troglodytes chromosome Y clone CH251-41G22, WORKING DRAFT

AC148941.2 GI:53386941  
HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.

KEYWORDS  
SOURCE  
ORGANISM  
Pan troglodytes  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominae; Pan.  
Wilson, R.K.  
1 (bases 1 to 203914)  
The sequence of Pan troglodytes clone  
Unpublished  
2 (bases 1 to 203914)  
Wilson, R.K.  
Direct Submission  
Submitted (27-APR-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
3 (bases 1 to 203914)  
Wilson, R.K.  
Direct Submission  
Submitted (01-OCT-2004) Genetics, Genome Sequencing Center, 4444  
Forest Park Parkway, St. Louis, MO 63108, USA  
On Oct 1, 2004 this sequence version replaced gi:46576171.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu  
Contact: submissions@watson.wustl.edu  
----- Project Information -----  
Center project name: C\_AB0041G22  
----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-primer; 0% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 200498 bases at least Q40  
Consensus quality: 201045 bases at least Q30  
Consensus quality: 201438 bases at least Q20  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 10 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
\*  
1 1451: contig of 1451 bp in length  
\* 1452 1551: gap of unknown length  
\* 1552 3154: contig of 1603 bp in length  
\* 3155 3254: gap of unknown length  
\* 3255 6335: contig of 3081 bp in length  
\* 6336 6435: gap of unknown length  
\* 6436 8267: contig of 1832 bp in length  
\* 8268 8367: gap of unknown length  
\* 8368 11604: contig of 3237 bp in length  
\* 11605 11704: gap of unknown length  
\* 11705 19880: contig of 8176 bp in length  
\* 19881 19980: gap of unknown length  
\* 19981 37249: contig of 17269 bp in length  
\* 37250 37349: gap of unknown length  
\* 37350 49206: contig of 11857 bp in length

FEATURES  
source

\* 49207 49306: gap of unknown length  
\* 49307 81671: contig of 32365 bp in length  
\* 81672 81771: gap of unknown length  
\* 81772 203914: contig of 122143 bp in length.  
Location/Qualifiers  
1. 203914  
/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="Y"  
/clone="CH251-41G22"  
1. 1451  
/note="assembly\_name:Contig20"  
1452. 1551  
/estimated\_length=unknown  
1552. 3154  
/note="assembly\_name:Contig31"  
3155. 3254  
/estimated\_length=unknown  
3255. 6335  
/note="assembly\_name:Contig32"  
6336. 6435  
/estimated\_length=unknown  
6436. 8267  
/note="assembly\_name:Contig33"  
8268. 8367  
/estimated\_length=unknown  
8368. 11604  
/note="assembly\_name:Contig34"  
11605. 11704  
/estimated\_length=unknown  
11705. 19880  
/note="assembly\_name:Contig35"  
19881. 19980  
/estimated\_length=unknown  
19981. 37249  
/note="assembly\_name:Contig36"  
37250. 37349  
/estimated\_length=unknown  
37350. 49206  
/note="assembly\_name:Contig37"  
49207. 49306  
/estimated\_length=unknown  
49307. 81671  
/note="assembly\_name:Contig38"  
81672. 81771  
/estimated\_length=unknown  
81772. 203914  
/note="assembly\_name:Contig39  
clone\_end:SP6  
vector\_side:right"

ORIGIN

Query Match 17.0%; Score 19; DB 14; Length 203914;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTTACT 33  
|||||  
Db 28698 AATGATATATTGTTTACT 28680

RESULT 22  
AC147334/c

LOCUS  
DEFINITION  
SEQUENCE.

AC147334 211310 bp DNA linear PRI 27-APR-2005  
Pan troglodytes BAC clone CH251-372D20 from chromosome Y, complete

AC147334.4 GI:53386695  
HTG.  
KEYWORDS  
SOURCE  
ORGANISM  
Pan troglodytes  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;



```

REFERENCE Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
AUTHORS Homidae; Pan.
TITLE 1 (bases 1 to 211310)
JOURNAL Kruchowski, S. and Cotton, M.
REFERENCE The sequence of Pan troglodytes BAC clone CH251-372D20
AUTHORS Unpublished (2001)
TITLE 2 (bases 1 to 211310)
JOURNAL Wilson, R.K.
REFERENCE Direct Submission
AUTHORS Submitted (07-NOV-2003) Genetics, Genome Sequencing Center, 4444
TITLE Forest Park Parkway, St. Louis, MO 63108, USA
JOURNAL 3 (bases 1 to 211310)
AUTHORS Wilson, R.K.
REFERENCE Direct Submission
AUTHORS Submitted (24-APR-2004) Genetics, Genome Sequencing Center, 4444
TITLE Forest Park Parkway, St. Louis, MO 63108, USA
JOURNAL 4 (bases 1 to 211310)
AUTHORS Wilson, R.K.
REFERENCE Direct Submission
AUTHORS Submitted (01-OCT-2004) Genetics, Genome Sequencing Center, 4444
TITLE Forest Park Parkway, St. Louis, MO 63108, USA
JOURNAL 5 (bases 1 to 211310)
AUTHORS Wilson, R.K.
REFERENCE Direct Submission
AUTHORS Submitted (27-APR-2005) Washington University School of Medicine,
TITLE Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
JOURNAL 63108, USA
COMMENT On Oct 1, 2004 this sequence version replaced gl:46395451.
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUSGC
Web site: http://genome.wustl.edu
Contact: submissions@watson.wustl.edu
----- Summary Statistics
Center project name: C_AB0372D20

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:
The position of this clone was established as part of a
collaboration between the Chimpanzee Chromosome Y Mapping Project
(Jennifer F. Hughes, Tatyana Pyntkova, Helen Skaltsky, Steve
Rosen, and David C. Page at the Whithead Institute for Biomedical
Research, Cambridge MA) and the Washington University Genome
Sequencing Center, St. Louis MO.

SOURCE INFORMATION:
The CHORI-251 Chimpanzee BAC library has been constructed at the
Children's Hospital Oakland Research Institute, BACPAC Resources,
by Dr. Baoli Zhu. DNA was isolated from white blood cells obtained
from a male chimpanzee (Pan troglodytes, 'Cint', Yerkes #C0471;
bitchate:6-6-80). The clone and detailed information can be
obtained from Pieter de Jong and co-workers at
http://www.bacpac.chori.org.

FEATURES
source
This sequence is the entire insert of the clone.
Location/Qualifiers
1..211310
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/chromosome="Y"
/clone="CH251-372D20"
/clone_1fb="CHORI251"

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misc_feature      5791..5792
/note="Bacterial transposon insertion in clone excised here"
unsure           69778..69921
/note="Sequence derived from one plasmid subclone."
unsure          82462..82481
/note="Sequence derived from one plasmid subclone."
unsure          106326..106349
/note="Sequence derived from one plasmid subclone."
unsure          116732..116768
/note="Sequence derived from one plasmid subclone."
unsure          149226..149228
/note="Sequence derived from one plasmid subclone."
unsure          158528..211310
/note="Unresolved inverted repeat."

ORIGIN
Query Match      17.0%; Score 19; DB 8; Length 211310;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy              15 AATGATATATTGGTTTACT 33
|||||
Db              129422 AATCATATATTGGTTTACT 129404

RESULT 23
LOCUS       AC147687             212365 bp    DNA     linear   PRI 19-MAY-2004
DEFINITION Pan troglodytes BAC clone CH251-95K2 from Y, complete sequence.
ACCESSION   AC147687
VERSION     AC147687.2   GI:40786756
KEYWORDS    HTG.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM    Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Euarchontia; Euarchontoglires; Primates; Catarrhini;
Hominoidea; Pan.
REFERENCE   1 (bases 1 to 212365)
AUTHORS    Levy A. and Bielicki L.
TITLE      The sequence of Pan troglodytes BAC clone CH251-95K2
JOURNAL     Unpublished (2001)
REFERENCE   2 (bases 1 to 212365)
AUTHORS    Wilson R.K.
TITLE      Direct Submission
JOURNAL     Submitted (23-DEC-2003) Genetec, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE   3 (bases 1 to 212365)
AUTHORS    Wilson R.K.
TITLE      Direct Submission
JOURNAL     Submitted (09-JUN-2004) Genetec, Genome Sequencing Center, 4444
Forest Park Parkway, St. Louis, MO 63108, USA
REFERENCE   4 (bases 1 to 212365)
AUTHORS    Wilson R.K.
TITLE      Direct Submission
JOURNAL     Submitted (19-MAY-2004) Washington University School of Medicine,
Genome Sequencing Center, 4444 Forest Park Parkway, St. Louis, MO
63108, USA
COMMENT     On Jan 9, 2004 this sequence version replaced gi:40316905.
-----
Center: Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: http://genome.wustl.edu
Contact: submissions@wustl.edu
-----
Center project name: C_AB0095K02
-----

NOTICE:
This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >=
```



30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

#### MAPPING INFORMATION:

The position of this clone was established as part of a collaboration between the Chimpanzee Chromosome Y Mapping Project (Jennifer F. Hughes, Tatyana Pyntikova, Helen Skaletsky, Steve Rosen, and David C. Page at the Whitehead Institute for Biomedical Research, Cambridge MA) and the Washington University Genome Sequencing Center, St. Louis MO.

#### SOURCE INFORMATION:

The CHORI-251 Chimpanzee BAC library has been constructed at the Children's Hospital Oakland Research Institute, BACPAC Resources, by Dr. Baoji Zhu. DNA was isolated from white blood cells obtained from a male chimpanzee (Pan troglodytes, 'Clint', Yerkes #C0472; birthdate:6-6-80). The clone and detailed information can be obtained from Pieter de Jong and co-workers at <http://www.bacpac.chori.org>.

#### NEIGHBORING SEQUENCE INFORMATION:

This sequence is the entire insert of the clone.

Location/Qualifiers  
1..212365

/organism="Pan troglodytes"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="Y"  
/map="Y"  
/clone="CH251-95K2"  
/clone\_lib="CHORI251"

#### ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 212365;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 AATGATATATTGGTTTACT 33

Db 36834 AATGATATATTGGTTTACT 36852

RESULT 24  
BS000547 219991 bp DNA linear PRI 17-MAR-2004  
LOCUS  
DEFINITION Pan troglodytes chromosome Y clone:PTB-212N08, complete sequences.  
ACCESSION BS000547  
VERSION BS000547.1 GI:45504147  
KEYWORDS  
SOURCE

ORGANISM  
Homo sapiens  
Pan troglodytes (chimpanzee)  
Pan troglodytes  
Pan troglodytes  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Hominoidea; Pan.

#### REFERENCE

1 The Chimpanzee Chromosome Y Sequencing Consortium.

TITLE DNA sequence of chimpanzee chromosome Y and its evolutionary implications

#### JOURNAL

#### REFERENCE

#### AUTHORS

#### TITLE

#### JOURNAL

Submitted (15-MAR-2004) Masahira Hattori, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsukuba, Ibaraki, Japan  
(E-mail:hattori@sc.riken.jp, URL:<http://hpg.gsc.riken.jp/>,  
Tel:81-45-503-9111, Fax:81-45-503-9170)  
Location/Qualifiers  
1..219991  
/organism="Pan troglodytes"

FEATURES  
source

/mol\_type="genomic DNA"  
/db\_xref="taxon:9598"  
/chromosome="Y"  
/clone="PTB-212N08"

#### ORIGIN

Query Match 17.0%; Score 19; DB 8; Length 219991;  
Best Local Similarity 100.0%; Pred. No. 6.1;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

15 AATGATATATTGGTTTACT 33

Db 2405 AATGATATATTGGTTTACT 2423

#### RESULT 25

#### LOCUS

AF120171/c 534 bp DNA linear PLN 26-APR-2000

DEFINITION Aegilops longissima RAPD-generated marker sequence amplified with OPE09.

#### ACCESSION

AF120171

#### VERSION

AF120171.1 GI:7648534

#### KEYWORDS

SOURCE

#### ORGANISM

Aegilops longissima

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Pooidae; Triticeae; Aegilops.

1 (bases 1 to 534)  
Lin,X., Wang,R.R.-C., Jia,J. and Dong,Y.

REFERENCE  
2 (bases 1 to 534)  
Lin,X. and Wang,R.R.-C.

AUTHORS  
TITLE  
JOURNAL

Submitted (14-JAN-1999) FRRL, USDA-ARS, 695 N 1100 E, Logan, UT  
84322-6300, USA

#### FEATURES

source

misc\_feature

1..534  
/organism="Aegilops longissima"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4486"

1..534  
/note="RAPD-generated marker sequence; specific to  
Aegilops longissima, Aegilops sharonense, and Aegilops  
searsii; amplified with OPE09"

Query Match 16.1%; Score 18; DB 15; Length 534;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

16 ATGATATATTGGTTTACT 33

Db 159 ATGATATATTGGTTTACT 142

#### RESULT 26

#### LOCUS

BX322535/c 4050 bp DNA linear ROD 13-MAY-2003

DEFINITION Mouse DNA sequence from clone RP23-83A14 on chromosome 2, complete  
sequence.

ACCESSION BX322535

VERSION BX322535.5 GI:30722323

KEYWORDS  
HTG.

SOURCE  
Mus musculus (house mouse)

ORGANISM  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
1 (bases 1 to 4050)



**AUTHORS** Tracey, A.  
**TITLE** Direct Submission  
**JOURNML** Submitted (13-May-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

**COMMENT**

On May 14, 2003 this sequence version replaced gi:30524809. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-83A14 is from the RPCI-23 Mouse BAC library constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6.

**FEATURES****source**

Location/Qualifiers  
 1..4050  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone="RP23-83A14"  
 /clone\_1id="RPCI-23"

**ORIGIN**

Query Match 16.1%; Score 18; DB 9; Length 4050;  
 Best Local Similarity 100.0%; Pred. No. 32;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 59 GTAAAGAAGTCTTATA 76  
 ||||||||||||||||  
 Db 3448 GTAAAGAAGTCTTATA 3431

**RESULT 27**  
 AL928965/c 92250 bp DNA linear ROD 01-FEB-2005  
**LOCUS** Mouse DNA sequence from clone RP23-60M5 on chromosome 2, complete  
**DEFINITION** sequence.  
**ACCESSION** AL928965  
**VERSION** AL928965.35 GI:58418404  
**KEYWORDS** HTG.

**SOURCE** Mus musculus (house mouse)  
**ORGANISM**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
**REFERENCE** 1 (bases 1 to 92250)  
**AUTHORS** Sycamore, N.

**TITLE** Direct Submission  
**JOURNML** Submitted (01-FEB-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk

**COMMENT**

On Feb 1, 2005 this sequence version replaced gi:58330877. Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [humquery@sanger.ac.uk](mailto:humquery@sanger.ac.uk)

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at [http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) RP23-60M5 is from the RPCI-23 Mouse BAC library constructed by the group of Pieter de Jong.

For further details see <http://www.chori.org/bacpac/home.htm>  
 VECTOR: pBAC3.6.

**FEATURES****source**

Location/Qualifiers  
 1..92250  
 /organism="Mus musculus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:10090"  
 /chromosome="2"  
 /clone="RP23-60M5"  
 /clone\_1id="RPCI-23"

**ORIGIN**

Query Match 16.1%; Score 18; DB 9; Length 92250;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 59 GTAAAGAAGTCTTATA 76  
 ||||||||||||||||  
 Db 1398 GTAAAGAAGTCTTATA 1381

**RESULT 28**  
 AP008209\_008  
**WPCOMMENT** Sequence split into 362 fragments LOCUS AP008209 Accession AP008209

Fragment Name	Begin	End
AP008209_001	1	110000
AP008209_002	100001	210000
AP008209_003	200001	310000
AP008209_004	300001	410000
AP008209_005	400001	510000
AP008209_006	500001	610000
AP008209_007	600001	710000
AP008209_008	700001	810000
AP008209_009	800001	910000
AP008209_010	900001	1010000
AP008209_011	1000001	1110000



AP008209\_011 1100001 1210000  
AP008209\_012 1200001 1310000  
AP008209\_013 1300001 1410000  
AP008209\_014 1400001 1510000  
AP008209\_015 1500001 1610000  
AP008209\_016 1600001 1710000  
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AP008209\_019 1900001 2010000  
AP008209\_020 2000001 2110000  
AP008209\_021 2100001 2210000  
AP008209\_022 2200001 2310000  
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AP008209_192	19200001	19310000
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AP008209_194	19400001	19510000
AP008209_195	19500001	19610000
AP008209_196	19600001	19710000

Query Match	16.1%;	Score 18;	DB 15;	Length 110000;
Best Local Similarity	100.0%;	Pred. No. 25;		

18 GATATATTGGTTACTGA 35

Db 86869 GATATATGGTTACTGA 86886

RESULT 29  
AC138786/c

**DEFINITION** *Sus scrofa* clone RP44-332G22, WORKING DRAFT SEQUENCE, 5 unordered pieces.

ACCESSION	AC138786
VERSION	AC138786.1
	GI:27777585

KEYWORDS	HTG; HTGS_PHASE1; HTGS_DRAFT
SOURCE	Sub scrofa (pig)

ORGANISM  
Sus scrofa  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae  
Sus.

REFERENCE  
1 (pages 1 to 133877)  
Achter, N., Antonellis, A., Ayala, K., Beckstrom-Sternberg, S. M.,

Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S., Cariga, K., Coleman, B., Engle, J., Granite, S., Guan, X., Gupta, J.,

Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
Laric, P., Lee-Lin, S.-Q., Legaspi, R., Maduro, Q.L., Maduro, V.B.,

Margulies, E.H., Masiello, C., Maskeri, B., McDowell, J.,  
Paguitigan, C., Pearson, R., Portnoy, M.E., Prasad, A.,

Reddix-Dugue, N., Schandler, K., Schueler, M. G., Sison, C.,  
Stantipop, S., Thomas, J. W., Thomas, P. J., Touchman, J. W.,  
Vogt, J. L.,

```

TITLE
Weatherly, K.D., Wiggins, L., Young, A. and Green, E.D.
JOURNAL
NISC Comparative Sequencing Initiative
REFERENCE
2 (bases 1 to 133877)
AUTHORS
Green, E.D.
JOURNAL
Direct Submission
Submitted (17-JAN-2003) NIH Intramural Sequencing Center,
Grovetmont Circle, Gaithersburg, MD 20877, USA
COMMENT
----- Genome Center
Center: NIH Intramural Sequencing Center
Center code: NISC
Web site: http://www.nisc.nih.gov
Contact: nisc_zoo@ngri.nih.gov
----- Project Information
Center project name: dbv
Center clone name: 332G22
----- Summary Statistics
Sequencing vector: plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 131539 bases at least Q40
Consensus quality: 132013 bases at least Q30
Consensus quality: 132394 bases at least Q20
Insert size: 131000; agarose-fp
Insert size: 134477; sum-of-ctrls
Quality coverage: 12.00x in Q20 bases; agarose-fp
Quality coverage: 11.78x in Q20 bases; sum-of-ctrls
-----
* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
1
2274: contig of 2274 bp in length
*
2275
2374: gap of unknown length
*
2375
12667: contig of 10293 bp in length
*
12668
12767: gap of unknown length
*
12768
22060: contig of 9293 bp in length
*
22061
22160: gap of unknown length
*
22161
50759: contig of 28599 bp in length
*
50760
50859: gap of unknown length
*
50860
133877: contig of 83018 bp in length.
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/mol_type="genomic DNA"
/db_xref="taxon:9823"
/clone="RP44-332G22"
/clone_id="RP44"
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clone_end:"7
vector_side:left"
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2375..12667
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12768..22060
/note="assembly_fragment"
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50760..50859
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50860..133877
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ORIGIN

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Query Match 16.1%; Score 18; DB 14; Length 133877;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 60 TAAAGAGTCTTATAT 77  
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 Db 62360 TAAAGAGTCTTATAT 62343

RESULT 30  
 AC134236 148011 bp DNA linear PLN 06-JAN-2005  
 LOCUS Oryza sativa (japonica cultivar-group) chromosome 3 clone  
 DEFINITION OSUNBa0056G13, complete sequence.  
 AC134236  
 AC134236.4 GI:57164410  
 HTG.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Oryza sativa (japonica cultivar-group)  
 Oryza sativa (japonica cultivar-group)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Eriocaridaceae; Oryzaceae; Oryza.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 AUTHORS

Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J. and Collura, K.  
 Rice Genomic Sequence  
 Unpublished  
 2 (bases 1 to 148011)  
 Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Sasaki, C., Currie, J. and Collura, K.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 AUTHORS

Submitted (24-SEP-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA  
 3 (bases 1 to 148011)  
 Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Sasaki, C., Currie, J. and Collura, K.  
 Direct Submission  
 Submitted (23-OCT-2002) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA  
 4 (bases 1 to 148011)  
 Wing, R.A., Yu, Y., Soderlund, C., Kim, H.-R., Rambo, T., Currie, J. and Collura, K.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 AUTHORS

Submitted (06-JAN-2005) Arizona Genomics Institute, University of Arizona, 303 Forbes, Tucson, AZ 85721, USA  
 On Jan 6, 2005 this sequence version replaced gi:27356674.  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >=30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by more than one plasmid subclone; and the assembly was confirmed by restriction digest. There are three areas of single-subclones: 54466-54560, 57568-57653 and 115543-115568. From base 133735-133753 there are only PCR reads. The assembly overlaps from base 1-23123 with OSUNBa0090010 (accession # AC134237). The overlap is from 139009-162132 bases on OSUNBa0090010. The assembly overlaps from base 136321-149349 with OJ1263H11 (accession # AC118980). The overlap is from 1-13028 bases on OJ1263H11. The nucleotide sequence of this BAC clone was generated by combining Syngenta, Monsanto, and Arizona Genomics Institute sequencing data.

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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:39947"

ORIGIN  
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Query Match 16.1%; Score 18; DB 15; Length 148011;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 43406 GATATATTGGTTTACTGA 43423

RESULT 31  
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 LOCUS Mus musculus chromosome 14, clone RP24-180B18, complete sequence.  
 DEFINITION AC131986  
 AC131986.6 GI:45917422  
 HTG.

ACCESSION  
 VERSION  
 KEYWORDS  
 SOURCE  
 ORGANISM

Mus musculus (house mouse)  
 Mus musculus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
 Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 AUTHORS

Birren, B., Nusbaum, C. and Lander, E.  
 Mus musculus chromosome 14, clone RP24-180B18  
 Unpublished  
 2 (bases 1 to 160034)  
 Birren, B., Nusbaum, C., Lander, E., All, A., Allen, N., Anderson, S., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gird, S., Graham, L., Grand-Pierre, N., Hago, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., MacDonald, P., Major, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Minge, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Norman, C.H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmas, J., Telford, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission  
 Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 160034)  
 Birren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Madditt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matheue, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Minge, V., Murphy, T., Naylor, J., Nelson, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmas, J., Telford, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 AUTHORS

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
 3 (bases 1 to 160034)  
 Birren, B., Nusbaum, C., Lander, E., Abouelell, A., Allen, N., Anderson, M., Arachchi, H.M., Barna, N., Baetien, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hago, B., Hall, J., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, X., Lui, A., Madditt, R., Maclean, C., MacDonald, P., Major, J., Manning, J., Matheue, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Minge, V., Murphy, T., Naylor, J., Nelson, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunhkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupack, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talmas, J., Telford, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.  
 Direct Submission



JOURNAL  
Submitted (14-FEB-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
4 (bases 1 to 160034)  
REFERENCE  
AUTHORS  
Birken, B., Nusbbaum, C., Lander, B., Abouelleil, A., Allen, N.,  
Anderson, M., Anderson, S., Arachchi, H. M., Barna, N., Bastien, V.,  
Bloom, T., Boguslavsky, L., Boukhgalter, B., Camarata, J., Chang, J.,  
Chorepel, Y., Collymore, A., Cook, A., Cooke, P., Cornu, B.,  
DeRellano, K., Diaz, J. S., Dodge, S., Doolley, K., Dorris, L.,  
Erickson, J., Faro, S., Ferreira, P., Fitzgerald, M., Gage, D.,  
Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hafez, N.,  
Hagopian, D., Hagos, B., Hall, J., Horton, L., Hulme, M., Iliev, I.,  
Johnson, R., Jones, C., Kamat, A., Karakas, A., Kellis, C., Landers, T.,  
Levine, R., Lindblad-Toh, K., Liu, G., Liu, X., Lui, A., Mabbitt, R.,  
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O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K.,  
Phunhkhang, P., Pierre, N., Rachupka, A., Ramasamy, U., Raymond, C.,  
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Stojanovic, N., Stubbs, M., Talamas, J., Tesfaye, S., Theodore, J.,  
Topham, K., Travers, M., Vassiliev, H., Venkataraman, V. S., Viel, R.,  
Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L.,  
Zimmer, A. and Zody, M.  
Direct Submission  
Submitted (01-APR-2004) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Apr 1, 2004 this sequence version replaced gi:42557443.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/MIT Center for Genome Research  
Center code: W1BR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@road.mit.edu  
----- Project Information  
Center project name: L27106  
Center clone name: 180\_B\_18  
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Best Local Similarity 100.0%; Pred. No. 25;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



59 GTAAAGAGGCTCTAATA 76  
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 Db 29459 GTAAAGAGGCTCTAATA 29476  
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 LOCUS  
 DEFINITION  
 AC138788  
 Sae scrofa clone RP44-45613, WORKING DRAFT SEQUENCE, 5 ordered  
 pieces.  
 AC138788  
 AC138788.2 GI:28316609  
 HTG: HTGS\_PHASE2; HTGS\_DRAFT.  
 Sae scrofa (pig)  
 ORGANISM  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;  
 Sus.  
 1 (bases 1 to 183431)  
 Akhter,N., Antonellis,A., Ayele,K., Beckstrom-Sternberg,S.M.,  
 Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,  
 Carls,K., Coleman,B., Engle,J., Granite,S., Guan,X., Gupta,J.,  
 Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Idol,J.R., Karlins,E.,  
 Latic,P., Lee-Lin,S.-Q., Lesage,R., Maduro,Q.L., Maduro,V.B.,  
 Magallanes,E.H., Mastello,C., Maskeri,B., Mrowad,A.,  
 Paguirigan,C., Pearson,R., Portnoy,M.E., Prasad,A.,  
 Reddi-Dupue,N., Schandler,K., Schueler,M.G., Sison,C.,  
 Stenitrop,S., Thomas,J.W., Thomas,P.J., Touchman,J.W., Vogt,J.L.,  
 Weetherby,K.D., Wiggins,L., Young,A. and Green,E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 183431)  
 Green,E.D.  
 Direct Submission  
 Submitted (17-JAN-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 3 (bases 1 to 183431)  
 Green,E.D.  
 Direct Submission  
 Submitted (12-FEB-2003) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 On Feb 12, 2003 this sequence version replaced gi:27777587.  
 ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.zoo@nhgri.nih.gov  
 ----- Project Information  
 Center project name: dj3  
 Center project name: 456L03  
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 The sequence data in this record represents an 'enhanced'  
 version of a Phase 2 submission. Specifically, the indicated  
 order and orientation of each sequence contig has been  
 established using one or more of the following: read-pair  
 data from individual subclones, overlaps with neighboring  
 clones), alignment with available reference sequence (e.g.,  
 human), and/or confirmation by PCR testing. In addition,  
 the sequence assembly is based on at least 8X average  
 coverage in Q20 bases and has been reviewed to rule out  
 gross misassemblies, the low-quality ends of sequence  
 contigs have been trimmed away, and each base is associated  
 with a Phrap-derived quality score.  
 ----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 18237 bases at least Q40  
 Consensus quality: 182594 bases at least Q30  
 Consensus quality: 182875 bases at least Q20  
 Insert size: 172000; agarose-gel  
 Insert size: 183031; sum-of-contigs

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Quality coverage: 11.86x in Q20 bases; agarose-gel
Quality coverage: 11.15x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 5 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
*
* 1      26293: config of 26293 bp in length
* *
* 26294      26393: gap of unknown length
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* 26394      44648: config of 18255 bp in length
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* 44649      44748: gap of unknown length
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* 44749      98356: config of 53608 bp in length
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* 98357      98456: gap of unknown length
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* 98457      139176: config of 40720 bp in length
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* 139177     139276: gap of unknown length
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* 139277     183431: config of 44155 bp in length.
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vector_side:right"
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Query Match          16.1%; Score 18; DB 14; Length 183431;
Best Local Similarity 100.0%; Pred. No. 24;
Matches   18; Conservative   0; Mismatches       0; Indels   0; Gaps   0;
OY         60 TAAAGGAGGTCTAATAT 77
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|||||
|||||
|||||
RESULT 33
LOCUS      AC138784              190191 bp      DNA           11near HTG 12-FEB-2002
DEFINITION Sus scrofa clone RP44-297H9, WORKING DRAFT SEQUENCE, 9 ordered
pieces.
ACCESSION   AC138784
```



VERSION AC138784.2 GI:28316604  
 KEYWORDS HTG; HTGS PHASE2; HTGS\_DRAFT.  
 SOURCE Sus scrofa (pig)  
 ORGANISM Sus scrofa  
 Bufoyota, Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;  
 Sus.  
 1 (bases 1 to 190191)  
 Akhter, N., Antonellis, A., Ayele, K., Beckstrom-Sternberg, S.M.,  
 Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
 Carls, K., Coleman, B., Engle, J., Grant, S., Guan, X., Gupta, J.,  
 Haghighi, P., Han, J., Hansen, N., Ho, S.-L., Idol, J.R., Karlins, E.,  
 Latic, P., Lee-Lin, S.-Q., Lega, R., Maduro, O.L., Maduro, V.B.,  
 Margulies, E.H., Mastaglio, C., Maskeri, B., McDowell, J.,  
 Paquin, C., Pearson, R., Portnoy, M.E., Prasad, A.,  
 Reddi-Dugue, N., Schandler, K., Schueler, M.G., Sison, C.,  
 Stentrop, S., Thomas, J.W., Thomas, P.J., Touchman, J.W., Vogt, J.L.,  
 Wehber, K.D., Wiggins, L., Young, A., and Green, E.D.  
 NISC Comparative Sequencing Initiative  
 Unpublished  
 2 (bases 1 to 190191)  
 Green, E.D.  
 Direct Submission  
 Submitted (17-JAN-2003) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 3 (bases 1 to 190191)  
 Green, E.D.  
 Direct Submission  
 Submitted (12-FEB-2003) NIH Intramural Sequencing Center, 8717  
 Government Circle, Gaithersburg, MD 20877, USA  
 On Feb 12, 2003 this sequence version replaced gi:2777583.  
 ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: http://www.nisc.nih.gov  
 Contact: nisc.zoo@nigrl.nih.gov  
 ----- Project Information  
 Project name: dbu  
 Center project name: dbu  
 Center clone name: 297H09

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

----- Summary Statistics  
 Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 188791 bases at least Q40  
 Consensus quality: 189202 bases at least Q30  
 Consensus quality: 189356 bases at least Q20  
 Insert size: 185000; agarose-fp  
 Insert size: 189391; sum-of-contigs  
 Quality coverage: 12.43x in Q20 bases; agarose-fp  
 Quality coverage: 12.14x in Q20 bases; sum-of-contigs

----- NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. Gaps between the contigs are represented as runs of N. The order of the pieces is believed to be correct as given, however the sizes of the gaps between them are based on estimates that have been provided by the submitter.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.

FEATURES	SOURCE	1	1748	contig of 1748 bp in length
1749	1848	gap of unknown length		
1849	11075	contig of 9227 bp in length		
11076	11175	gap of unknown length		
11176	13319	contig of 2144 bp in length		
13320	13419	gap of unknown length		
13420	47969	contig of 34550 bp in length		
47970	48069	gap of unknown length		
48070	146877	contig of 98808 bp in length		
146878	146977	gap of unknown length		
146978	149802	contig of 2825 bp in length		
149803	149902	gap of unknown length		
149903	164961	contig of 15059 bp in length		
164962	165061	gap of unknown length		
165062	168068	contig of 3007 bp in length		
168069	168168	gap of unknown length		
168169	190191	contig of 22023 bp in length.		
190191	Location/Qualifiers			
1	190191			
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/mol_type="genomic DNA"				
/db_xref="taxon:9823"				
/clone="RP44-297H9"				
/clone_lib="RP44"				
1	1748			
/note="assembly_fragment"				
clone_end:SP6				
vector_side:left"				
1749	1848			
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1849	11075			
/note="assembly_fragment"				
11076	11175			
/estimated_length=unknown				
11176	13319			
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13320	13419			
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13420	47969			
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47970	48069			
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51740	190191			
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149803	149902			
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149903	164961			
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164962	165061			
/estimated_length=unknown				
165062	168068			
/note="assembly_fragment"				
168069	168168			
/estimated_length=unknown				
168169	190191			
/note="assembly_fragment"				
clone_end:T7				
vector_side:right"				

## ORIGIN

Query Match 16.1%; Score 18; DB 14; Length 190191;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 60 TAAAGAGGCTCTAATAT 77  
 |||







```

repeat_region      8967..10252
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                    /rpt_family="L1"
repeat_region      10301..10327
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repeat_region      complement(10328..10450)
                    /rpt_family="L1"
repeat_region      complement(10364..10368)
                    /note="<30 qual SNGL region"
unare
repeat_region      11986..12167
                    /rpt_family="B2_Mm2"
repeat_region      12181..12258
                    /rpt_family="L1MCL"
repeat_region      12420..12475
                    /rpt_family="GA-rich"
repeat_region      12868..12933
                    /rpt_family="L1_MM"
repeat_region      complement(13055..13176)
                    /rpt_family="Lx2"
repeat_region      14118..14159
                    /rpt_family="(CTATTA)n"
repeat_region      complement(14990..15172)
                    /rpt_family="LTR40b"
repeat_region      15175..15273
                    /rpt_family="BCL_MM"
repeat_region      complement(15496..15630)
                    /rpt_family="B3"
repeat_region      complement(15658..15762)
                    /rpt_family="Lx2B"
repeat_region      complement(15768..16023)
                    /rpt_family="Lx2"
repeat_region      complement(16025..16112)
                    /rpt_family="B2_MM2"
repeat_region      17099..17168
                    /rpt_family="AT-rich"
repeat_region      17526..17562
                    /rpt_family="AT-rich"
repeat_region      17591..17594
                    /rpt_family="(TA)n"
misc_feature
                    /note="clone boundary
                    clone.end:SP6
                    site:MbolI"
repeat_region      17617..17811
                    /rpt_family="B3A"
repeat_region      complement(18349..18713)
                    /rpt_family="Lx9"
repeat_region      18845..18907
                    /rpt_family="T-rich"
repeat_region      complement(18910..20528)
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repeat_region      complement(20530..20800)
                    /rpt_family="Lx2"
repeat_region      complement(20898..21124)
                    /rpt_family="Lx2B"
repeat_region      21472..21521
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repeat_region      21719..21838
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Query Match 16.1%; Score 18; DB 9; Length 235453;  
 Best Local Similarity 100.0%; Pred. No. 24;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 59 GTAAAGAGGTCTTATA 76  
 |||||  
 Db 168457 GTAAAGAGGTCTTATA 168474

RESULT 35  
 AC158076 236169 bp DNA linear HTG 01-JUL-2005  
 LOCUS  
 DEFINITION Bos taurus clone CH240-53D14, \*\*\* SEQUENCING IN PROGRESS \*\*\*, 34

unordered pieces.  
 AC158076  
 HTG; HTGS PHASE1; HTGS\_DRAFT; HTGS\_ENRICHED.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.

REFERENCE  
 AUTHORS  
 Muzny,D,Marle,M,Mezker,M,Lee,A,Abrahamson,S,Adams,C,Alder,J,  
 1 (bases 1 to 236169)

Allen,C,Allen,H,Ayragi,A,Ayodeji,M,Baca,E,Baden,H,  
 Anyalebechi,V,Aoyagi,A,Ayodeji,M,Baca,E,Baden,H,  
 Baldwin,D,Bandaranaike,D,Barber,M,Barnstead,M,Benahmed,F,  
 Blawalo,K,Blair,J,Blankenburg,K,Blyth,P,Brown,M,  
 Bryant,N,Buhay,C,Burch,P,Burrell,K,Calderson,E,  
 Cardenas,V,Carter,K,Cavazos,I,Ceasar,H,Center,A,  
 Chacko,J,Chavez,D,Chen,G,Chen,R,Chen,Y,Chen,Z,Chu,J,  
 Cleveland,C,Cockrell,R,Cox,C,Coyle,M,Cree,A,D'Souza,L,  
 Davila,M,L,Davis,C,Davy-Carroll,L,De Anda,C,Dederich,D,  
 Delgado,O,Denson,S,Derramo,C,Ding,Y,Dinh,H,Diva,K,  
 Draper,H,Dugan-Rocha,S,Dunn,A,Durbin,K,Duval,B,Eaves,K,  
 Egan,A,Escotto,M,Eugene,C,Evans,C,Falls,T,Fan,G,  
 Fernandez,S,Fanley,M,Flagg,N,Fortes,L,Foster,M,Foster,P,  
 Fraser,C,M,Gabis,A,Ganta,R,Garcia,A, Garner,T,Garra,M,  
 Gebregeorgis,E,Geier,K,Gill,R,Grady,M,Guerra,M,Guevara,W,  
 Gunaratne,P,Haaland,W,Hamil,C,Hamilton,C,Hamilton,K,  
 Harvey,Y,Havlak,P,Hawes,A,Henderson,N,Hernandez,J,  
 Hernandez,R,Hines,S,Hladun,S,L,Hodgson,A,Hogues,M,  
 Hollins,B,Howells,S,Huyl,K,S,Hume,J,Idlebird,D,Jackson,A,  
 Jackson,L,Jacob,L,Jiang,H,Johnson,B,Johnson,R,Jolivet,A,  
 Karpachy,S,Kelly,S,Kelly,S,Khan,Z,King,L,Kovar,C,  
 Kowis,C,Kraft,C,L,Lebow,H,Levan,J,Lewis,L,Li,Z,Liu,J,  
 Liu,J,Liu,W,Liu,Y,London,P,Longacre,S,Lopez,J,  
 Lorensuhewa,L,Louisege,H,Lozado,R,J,Lu,X, Ma,J,  
 Meshwari,M,Mahindartine,M,Mahmoud,M,Mallory,K,Mangum,A,  
 Mangum,B,Mapua,P,Martin,K,Martin,R,Martinez,E,  
 Mashiney,S,McLeod,M,P,McNeill,T,Z,Meenen,B,  
 Mlilosavljevic,A,Miner,G,Mitja,E,Montemayor,J,Moore,S,  
 Morgan,M,Morris,K,Morris,S,Munidsa,M,Murphy,M,Nair,L,  
 Nankervis,C,Neal,D,Newton,N,Nguyen,N,Norris,S,  
 Nwokeneme,O,Okunolu,G,Olanrunsoon,A,Pal,S,Parke,K,  
 Pasternak,S,Paul,H,Perez,A,Perez,L,Plamkoch,C,  
 Piopfer,F,Polindexter,A,Popovic,D,Primus,E,Pu,L,L,  
 Piazto,M,Quiroz,J,Rachlin,E,Reeves,K,Regier,M,A,Reigh,R,  
 Ralby,B,Ralby,M,Ren,Y,Reuter,M, Richards,S,Riggs,F,  
 Rives,C,Rodkey,T,Rojas,A,Rose,M,Rose,R,Ruiz,S,J,  
 Sanders,W,Savery,G,Scherer,S,Scott,G,Shatsman,S,Shen,H,  
 Shetty,J,Shvartsbeyn,A,Sison,I,Sitter,C,D,Smajls,D,  
 Sneed,A,Sodergren,E,Song,X,Z,Sorelle,R,Sosa,J,  
 Steinle,M,Strong,R,Sutton,A,Svatek,A,Tabor,P,Taylor,C,  
 Taylor,T,Thomas,N,Thomas,S,Tingey,A,Trejos,Z,Uemami,K,  
 Valas,R,Vera,V,Villalana,D,Waldron,L,Walker,B,Wang,J,  
 Wang,Q,Wang,S,Warren,J,Warren,R,Wel,X,White,F,  
 Williams,G,Willison,R,Wieczyk,R,Wooden,H,Worley,K,  
 Wright,D,Wright,R,Wu,J,Yakub,S,Yen,J,Yoon,L,Yoon,V,  
 Yu,F,Zhang,J,Zhou,J,Zhou,S,Zhou,S,Dunn,D,von  
 Niederhausen,A,Weles,R,Smith,D,R,Holt,R,A,Smith,H,O,  
 Weinstock,G, and Gibbs,R.A.  
 Direct Submission  
 Unpublished  
 2 (bases 1 to 236169)  
 Morley,K.C.  
 Direct Submission  
 Submitted (04-MAR-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA  
 3 (bases 1 to 236169)  
 Cow Genome Sequencing Consortium.  
 Direct Submission  
 Submitted (01-JUL-2005) Human Genome Sequencing Center, Department  
 of Molecular and Human Genetics, Baylor College of Medicine, One  
 Baylor Plaza, Houston, TX 77030, USA



## COMMENT

On Jun 28, 2005 this sequence version replaced gi:60498848.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

## ----- Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: <http://www.hgsc.bcm.tmc.edu/>

Contact: hgsc-help@bcm.tmc.edu

----- Project Information

Center project name: FDBM

Center clone name: CH240-53D14

----- Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 221843 bases at least Q40

Consensus quality: 224917 bases at least Q30

Consensus quality: 227783 bases at least Q20

Estimated insert size: 228810; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 34 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

```

1 13085: contig of 13085 bp in length
* 13086 13135: gap of 50 bp
* 13136 23111: contig of 9976 bp in length
* 23112 23161: gap of 50 bp
* 23162 28820: contig of 5659 bp in length
* 28821 28870: gap of 50 bp
* 28871 32283: contig of 3413 bp in length
* 32284 32333: gap of 50 bp
* 32334 45139: contig of 12806 bp in length
* 45140 45239: gap of unknown length
* 45240 65888: contig of 20599 bp in length
* 65889 65889: gap of 50 bp
* 65889 82920: contig of 17032 bp in length
* 82921 82970: gap of 50 bp
* 82971 89404: contig of 6434 bp in length
* 89405 89504: gap of unknown length
* 89505 92161: contig of 2657 bp in length
* 92162 92601: gap of 440 bp
* 92602 96968: contig of 4367 bp in length
* 96969 97018: gap of 50 bp
* 97019 100348: contig of 3330 bp in length
* 100349 100398: gap of 50 bp
* 100399 118336: contig of 17938 bp in length
* 118337 118386: gap of 50 bp
* 118387 122024: contig of 3638 bp in length
* 122025 122074: gap of 50 bp
* 122075 137540: contig of 15466 bp in length
* 137541 137590: gap of 50 bp
* 137591 140529: contig of 2939 bp in length
* 140530 141256: gap of 727 bp
* 141257 142493: contig of 1237 bp in length
* 142494 142593: gap of unknown length
* 142594 144775: contig of 2182 bp in length
* 144776 144825: gap of 50 bp

```

```

* 144826 160057: contig of 15232 bp in length
* 160058 160613: gap of 556 bp
* 160614 167391: contig of 6778 bp in length
* 167392 167441: gap of 50 bp
* 167442 180887: contig of 13446 bp in length
* 180888 180937: gap of 50 bp
* 180938 183751: contig of 2814 bp in length
* 183752 183851: gap of unknown length
* 183852 186450: contig of 2599 bp in length
* 186451 186500: gap of 50 bp
* 186501 192199: contig of 5699 bp in length
* 192200 193274: gap of 1075 bp in length
* 193275 194331: contig of 1056 bp in length
* 194332 194430: gap of unknown length
* 194431 200397: contig of 5967 bp in length
* 200398 200447: gap of 50 bp
* 200448 215923: contig of 15476 bp in length
* 215924 216023: gap of unknown length
* 216024 220873: contig of 4850 bp in length
* 220874 220923: gap of 50 bp
* 220924 225295: contig of 4372 bp in length
* 225296 225395: gap of unknown length
* 225396 226504: contig of 1109 bp in length
* 226505 226604: gap of unknown length
* 226605 227664: contig of 1060 bp in length
* 227665 227764: gap of unknown length
* 227765 229002: contig of 1238 bp in length
* 229003 229102: gap of unknown length
* 229103 231283: contig of 2181 bp in length
* 231284 231383: gap of unknown length
* 231384 234168: contig of 2785 bp in length
* 234169 234268: gap of unknown length
* 234269 236169: contig of 1901 bp in length.

```

## FEATURES

source Location/Qualifiers

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gap 1..236169
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      /mol_type="genomic DNA"
      /db_xref="taxon:9913"
      /clone="CH240-53D14"
gap 13086..13135
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gap 23112..23161
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gap 28821..28870
      /estimated_length=50
gap 32284..32333
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gap 45140..45239
      /estimated_length=unknown
gap 65839..65888
      /estimated_length=50
gap 82921..82970

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Query Match 16.1%; Score 18; DB 14; Length 236169;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 31 ACTGACGAGCAGCAACCG 48
Db 131914 ACTGACGAGCAGCAACCG 131897

```

```

RESULT 36
LOCUS ACT132997 245603 bp DNA linear HTG 09-MAY-2003
DEFINITION Rattus norvegicus clone CH230-4H8, *** SEQUENCING IN PROGRESS ***.
ACCESSION AC132997
VERSION AC132997.5 GI:30467825
KEYWORDS HTG, HTGS_PHASE2, HTGS_DRAFT, HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
          Chordata; Vertebrata; Euteleostomi;
          Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;

```



REFERENCE  
AUTHORS  
Sciurognathi; Muroidea; Muridae; Murinae; Rattus.  
1 (bases 1 to 245603)  
Murny D,Marie, Metzker M, Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Angiano, D., Anysedechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blawie, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D Souza, L., Davila, M. L., Davis, C., Davy-Carroll, L., De Anda, C., Dedeitch, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C. A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, T., Foster, P., Fraser, C. M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Gardy, M., Guerra, W., Guevara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howell, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Karpathy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowis, C., Kraft, C. L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshewa, L., Louised, H., Lozado, R. J., Lu, X., Ma, J., Maheshwari, M., Mahindartne, M., Mahmood, M., Malloy, K., Mangum, A., Mangun, B., Mapua, P., Martin, K., Martin, R., Martinez, B., Mawhiley, S., McLeod, M. P., McNeill, T. Z., Meenen, E., Mllosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L., Nankervis, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwaokemele, O., Okwunu, G., Olarnpusagoon, A., Pal, S., Parks, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkoch, C., Plopper, F., Poindexter, A., Popovic, D., Primus, E., Pu, L. L., Pizarro, M., Quiroz, J., Rachlin, B., Reeves, K., Regier, M. A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S. J., Sanders, W., Savery, G., Scheiner, S., Scott, G., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sisson, I., Sitter, C. D., Snajls, D., Sneed, A., Sodergren, E., Song, X. Z., Sorrell, R., Sosa, J., Steimle, M., Strong, R., Sutton, A., Swatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Woodey, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Dunn, D., von Niederhausein, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O., Weinstock, G. and Gibbs, R. A.

TITLE  
JOURNAL  
Direct Submission  
2 (bases 1 to 245603)  
REFERENCE  
AUTHORS  
Rat Genome Sequencing Consortium.  
TITLE  
JOURNAL  
Direct Submission  
Submitted (05-SEP-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 245603)  
REFERENCE  
AUTHORS  
Rat Genome Sequencing Consortium.  
TITLE  
JOURNAL  
Direct Submission  
Submitted (09-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
COMMENT  
On May 9, 2003 this sequence version replaced gi:24818196.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence

may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>  
Contact: hgsc-help@bcm.tmc.edu  
----- Project Information  
Center project name: GCGZ  
Center clone name: CH230-4H8  
----- Summary Statistics  
Assembly program: Atlas;  
Consensus quality: 220302 bases at least Q40  
Consensus quality: 221636 bases at least Q30  
Consensus quality: 222481 bases at least Q20  
Estimated insert size: 231760; sum-of-contigs estimation  
Quality coverage: 6x in Q20 bases; sum-of-contigs estimation  
-----  
\* NOTE: Estimated insert size may differ from sequence length  
\* (see [http://www.hgsc.bcm.tmc.edu/docs/genbank\\_draft\\_data.html](http://www.hgsc.bcm.tmc.edu/docs/genbank_draft_data.html)).  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 1 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submitter.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1 245603: contig of 245603 bp in length.  
Location/Qualifiers  
1. 245603  
/organism="Rattus norvegicus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10116"  
/clone="CH230-4H8"  
1. 1070  
/note="wgs end \_extension  
clone end: T7"  
misc\_feature  
238847..238940  
/note="clone\_boundary  
clone end: T7"  
site: Ecore1  
end sequence: BH306795"  
241107..241788  
/note="clone\_boundary  
clone end: Sp6  
site: Ecore1  
end sequence: BH306796"  
243980..245603  
/note="wgs end \_extension  
clone end: Sp6"  
ORIGIN  
Query Match 16.1%; Score 18; DB 14; Length 245603;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 70 CCTAATTCGCTGAGCAA 87  
Db 220020 CCTAATTCGCTGAGCAA 220037  
RESULT 37  
AC097881 276713 bp DNA linear HTG 10-MAY-2003  
LOCUS  
DEFINITION  
Rattus norvegicus clone CH230-78N20, \*\*\* SEQUENCING IN PROGRESS  
\*\*\*  
AC097881  
AC097881.7 GI:30520826



KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT; HTGS\_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM Rattus norvegicus

Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Rattus.

REFERENCE 1 (bases 1 to 276713)

AUTHORS

Munry, D., Marie, Metzger, M., Lee, A., Adams, S., Adams, C., Alder, J., Allen, C., Allen, H., Albrooks, S., Amin, A., Anguiano, D., Arnyelebechi, V., Ayagi, A., Ayodeji, M., Baca, E., Baden, H., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Blawie, K., Blair, J., Blankensbury, K., Blyth, P., Brown, M., Bryant, N., Buhay, C., Burck, P., Burrell, K., Calderon, E., Cardenas, V., Carter, K., Cavazos, I., Cesar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M., Davis, C., Davy-Carroll, L., De Anda, C., Dedrick, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Divya, K., Diaper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garra, M., Gebregorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guetara, W., Gunaratne, P., Haaland, W., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S. L., Hodgson, A., Hognes, M., Hollins, B., Howells, S., Hulik, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapachy, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Lorensheva, L., Louised, H., Lozada, R.J., Lu, X., Ma, J., Maheshwari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martinez, E., Mawney, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Milosavljevic, A., Miner, G., Minja, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munday, M., Murphy, N., Natir, L., Naneris, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwankweli, O., Okmonu, G., Olarunmugbon, A., Pal, S., Parks, K., Pasernak, S., Paul, H., Perez, A., Perez, L., Pfankoch, C., Ploper, F., Poindexter, A., Popovic, D., Primis, E., Pu, L., Puzo, M., Quito, J., Rachlin, E., Reeves, K., Register, M.A., Reigh, R., Reilly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rivers, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savary, G., Scherer, S., Scott, S., Shatman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Sison, I., Sitter, C.D., Smaj, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Taber, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingey, A., Trejos, Z., Umami, K., Valas, R., Vera, V., Villasana, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczek, R., Wooden, H., Wolley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, F., Zhang, J., Zhou, J., Zhou, X., Zhao, X., Zhou, D., Von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

TITLE Direct Submission

JOURNAL Unpublished

REFERENCE 2 (bases 1 to 276713)

AUTHORS Worley, K.C.

TITLE Direct Submission

JOURNAL Submitted (23-OCT-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

REFERENCE 3 (bases 1 to 276713)

AUTHORS Rat Genome Sequencing Consortium.

TITLE Direct Submission

JOURNAL Submitted (10-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA

COMMENT

On May 10, 2003 this sequence version replaced gi:25009621. The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas

(http://www.hgsc.bcm.tmc.edu/projects/rat/). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

#### Genome Center

Center: Baylor College of Medicine

Center code: BCM

Web site: http://www.hgsc.bcm.tmc.edu/

Contact: hgsc-help@bcm.tmc.edu

Project Information

Center project name: GFMO

Center clone name: CH230-78N20

Summary Statistics

Assembly program: Atlas 3.0;

Consensus quality: 226137 bases at least Q40

Consensus quality: 230697 bases at least Q30

Consensus quality: 233673 bases at least Q20

Estimated insert size: 240772; sum-of-contigs estimation

Quality coverage: 6x in Q20 bases; sum-of-contigs estimation

\* NOTE: Estimated insert size may differ from sequence length

(see http://www.hgsc.bcm.tmc.edu/docs/genbankdraft\_date.html).

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 1 contigs. Gaps between the contigs

\* are represented as runs of N. The order of the pieces

\* is believed to be correct as given, however the sizes

\* of the gaps between them are based on estimates that have

\* provided by the submitter.

\* This sequence will be replaced

\* by the finished sequence as soon as it is available and

\* the accession number will be preserved.

1 276713: contig of 276713 bp in length.

Location/Qualifiers

1..276713

/organism="Rattus norvegicus"

/mol\_type="genomic DNA"

/db\_xref="taxon:10116"

/clone="CH230-78N20"

6880..9572

/note="wgs\_contig"

172469..174101

/note="wgs\_contig"

209259..211474

/note="wgs\_contig"

259231..261963

/note="wgs\_contig"

#### ORIGIN

Query Match 16.1%; Score 18; DB 14; Length 276713;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OR 70 CCTAATATCGGTGACCAA 87

DB 63866 CCTAATATCGGTGACCAA 63883

AC131978/C

LOCUS

DEFINITION

AC131978

AC131978.3

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978

AC131978



Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Muridae; Murinae; Mus.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS

1 (bases 1 to 344458)  
Mus musculus, clone RP24-151D24  
Unpublished  
2 (bases 1 to 344458)  
Birten, B., Nusbaum, C., Lander, E., Ali, A., Allen, N., Anderson, S., Barina, N., Basclet, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Chazaro, B., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J.S., Dodge, S., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Gord, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Maclean, C., Macdonald, P., Major, J., Matthews, V., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., Notman, C.H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Roy, A., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Submitted (28-AUG-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
3 (bases 1 to 344458)  
Birten, B., Nusbaum, C., Lander, E., Abouellell, A., Allen, N., Anderson, S., Arachchi, H.M., Barina, N., Basclet, V., Bloom, T., Boguslavsky, L., Boukhalter, B., Camarata, J., Chang, J., Choepel, Y., Collamore, A., Cook, A., Cooke, P., Corum, B., Dearellano, K., Diaz, J.S., Dodge, S., Dooley, K., Dorris, L., Erickson, J., Fero, S., Ferreira, P., Fitzgerald, M., Gage, D., Galagan, J., Gardyna, S., Graham, L., Grand-Pierre, N., Hagos, B., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Landers, T., Levine, R., Lindblad-Toh, K., Liu, G., Liu, A., Mabbitt, R., Maclean, C., Macdonald, P., Major, J., Manning, J., Matthews, C., McCarthy, M., Meldrum, J., Meneus, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Nicol, R., Norbu, C., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Radhuk, A., Ramasamy, V., Raymond, C., Retta, R., Rise, C., Rogov, P., Roman, J., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Smith, C., Spencer, B., Stange-Thomann, N., Stojanovic, N., Stubbs, M., Talamas, J., Teefaye, S., Theodore, J., Topham, K., Travers, M., Vassiliev, H., Venkataraman, V.S., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (27-MAR-2003) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Mar 27, 2003 this sequence version replaced gi:27552601.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html

Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIPR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu

Project Information  
Center project name: L27096  
Center clone name: 151\_D\_24

Summary Statistics  
Sequencing vector: Plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye, 100% of reads  
Assembly program: Phrap; version 0.960731  
Consensus quality: 335174 bases at least Q40  
Consensus quality: 339094 bases at least Q30  
Consensus quality: 34059 bases at least Q20  
Insert size: 341958; sum-of-configs

Quality coverage: 4.8 in Q20 bases; sum-of-configs

NOTE: This is a 'working draft' sequence. It currently consists of 26 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

1 2513: contig of 2513 bp in length  
2514: gap of 100 bp  
2613: contig of 1129 bp in length  
3743: gap of 100 bp in length  
3842: gap of 983 bp in length  
4825: contig of 1463 bp in length  
4926: gap of 100 bp in length  
6388: contig of 1637 bp in length  
6489: gap of 100 bp in length  
8125: contig of 2226 bp in length  
8226: gap of 100 bp in length  
10451: contig of 1619 bp in length  
10552: gap of 100 bp in length  
12171: contig of 60971 bp in length  
12270: gap of 100 bp in length  
73242: gap of 100 bp in length  
73341: gap of 1205 bp in length  
74546: contig of 1205 bp in length  
74547: gap of 100 bp in length  
79238: contig of 4592 bp in length  
79338: gap of 100 bp in length  
83678: contig of 4340 bp in length  
83779: gap of 100 bp in length  
88810: contig of 5032 bp in length  
88910: gap of 100 bp in length  
95083: contig of 6173 bp in length  
95183: gap of 100 bp in length  
100922: contig of 5739 bp in length  
101022: gap of 100 bp in length  
101023: contig of 6670 bp in length  
107693: gap of 100 bp in length  
112594: contig of 4802 bp in length  
112595: gap of 100 bp in length  
124543: contig of 11849 bp in length  
124544: gap of 100 bp in length  
124644: contig of 11754 bp in length  
136397: gap of 100 bp in length  
136398: gap of 100 bp in length  
148905: contig of 12408 bp in length  
148906: gap of 100 bp in length  
149005: gap of 100 bp in length  
149842: contig of 20837 bp in length  
169843: gap of 100 bp in length  
169844: contig of 18906 bp in length  
188848: gap of 100 bp in length  
188949: contig of 23842 bp in length  
212790: gap of 100 bp in length  
212791: contig of 43222 bp in length  
256112: gap of 100 bp in length  
256113: contig of 39914 bp in length  
296127: gap of 100 bp in length  
296227: contig of 46945 bp in length  
343171: gap of 100 bp in length  
343271: contig of 1187 bp in length  
343272: gap of 100 bp in length  
344458: contig of 1187 bp in length.

Location/Qualifiers  
1. 344458  
/organism="Mus musculus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:10090"  
/clone="RP24-151D24"  
/clone\_1ib="RPCT-24 Male Mouse BAC"  
1. 2513  
/note="assembly\_fragment  
clone\_end:SP6  
vector\_side:left"  
2514. 2613

misc\_feature  
gap



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misc_feature      /estimated_length=100
                  /note="assembly_fragment"
gap              3743..3842
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gap              8126..8225
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misc_feature      8226..10451
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misc_feature      10552..12170
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gap              12171..12270
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misc_feature      12271..73241
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misc_feature      74647..79238
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Query Match      16.1%; Score 18; DB 14; Length 344458;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              59 GTAAAGAGTCTTAATA 76
Db              238161 GTAAAGAGTCTTAATA 238144

RESULT 39
LOCUS          AY157815              475 bp      DNA      linear      PLN 27-OCT-2003
DEFINITION     Arachis stenosperma clone S3S4_A_19 resistance protein gene,
partial cds.
ACCESSION      AY157815
VERSION        AY157815.1 GI:37221906
KEYWORDS
SOURCE         Arachis stenosperma
ORGANISM       Arachis stenosperma
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae;
Aeschynomeneae; Arachis.
1 (bases 1 to 475)
Bertoli,D.J., Leal-Bertoli,S.C.M., Lion,M.B., Santos,V.L.,
Papais,G. Jr., Cannon,S.B. and Guimaraes,P.M.

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TITLE          A large scale analysis of resistance gene homologues in Arachis
JOURNAL        Mol. Genet. Genomics 270 (1), 34-45 (2003)
PUBMED         12928866
REFERENCE      2 (bases 1 to 475)
AUTHORS        Bertoli,D.J., Leal-Bertoli,S.C.M., Lion,M.B., Santos,V.L. and
Guimaraes,P.M.
TITLE          Direct Submission
JOURNAL        Submitted (02-OCT-2002) Biotechnology, EMBRAPA Recursos Geneticos e
Biociencia, Parque Estacao Ecologica Norte, Final W5 Norte,
Brasilia, DF 70.770-900, Brazil
FEATURES
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ORIGIN
Query Match      15.2%; Score 17; DB 15; Length 475;
Best Local Similarity 100.0%; Pred. No. 14e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy              23 ATTGGTTACTGACGAG 39
Db              273 ATTGGTTACTGACGAG 269

RESULT 40
LOCUS          BV387409              573 bp      DNA      linear      STS 29-JAN-2005
DEFINITION     S244P630FC10.T0 AlaskaGraywolf Canis lupus STS genomic, sequence
tagged site.
ACCESSION      BV387409.1 GI:57761061
VERSION        BV387409.1
KEYWORDS       Canis lupus (gray wolf)
SOURCE         Canis lupus
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
Canis.
1 (bases 1 to 573)
Lindblad-Toh,K.
The genome sequence of Canis familiaris
Unpublished (2004)

REFERENCE      Contact: Kerstin Lindblad-Toh
AUTHORS        Whitehead Institute for Biomedical Research, Center for Genome
JOURNAL        Research
320 Charles Street, Cambridge, MA 02141, USA
Tel.: 6172521477
Fax: 6172580903
Email: kersti@genome.wi.mit.edu
Primer A: No sequence submitted
Primer B: No sequence submitted
STS size: 573
Protocol:
WGS-discovery (WGS):
Paired-end low-coverage whole genome shotgun reads were generated
from 9 breeds
(German Shepherd, Rottweiler, Bedlington Terrier, Beagle, Labrador

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Retriever, English Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese Water Dog -100,000 each) and five other canids (Chinese, Alaskan, Indian and Spanish Gray Wolf as well as the Californian Coyote).

The WGS reads were placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were annotated with alleles from the boxer and the breed or canid from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.

WGA-discovery (WGA) of Boxer/Poodle SNPs: A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this sequence lacked base quality scores, arbitrary quality scores of phred 40 were assigned before the poodle sequence was placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSAHA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.

Internal-WGA-discovery (I-WGA): A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were defined as mismatch positions that had a base quality of  $\geq 30$  on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.

# FEATURES

## Source

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## STS

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Best Local Similarity 100.0%; Pred. No. 1.4e+02; Mismatches 0; Indels 0; Gaps 0;

QY	14	GAATGATATATGTTT	30
Db	114	GAATGATATATGTTT	98

Search completed: April 11, 2006, 18:03:37  
Job time : 759.017 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:17 ; Search time 156.046 Seconds  
(without alignments)  
4783.489 Million cell updates/sec

Title: US-10-712-654-25

Perfect score: 112  
Sequence: 1 ggtacatctgcgcgaatgat.....ggtagcttaagaagctctgt 112

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size : 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

N Geneseq 21: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004as: \*  
13: geneseqn2004bs: \*  
14: geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	112	100.0	112	13	ADR48527
2	112	100.0	560	13	ADR48536
3	32	28.6	32	8	ACC71903
4	30	26.8	30	8	ACC71904
5	29	25.9	29	13	ADR48512
6	29	25.9	29	13	ADR48513
7	27	24.1	27	13	ADR48514
8	27	24.1	27	13	ADR48511
9	26	23.2	26	8	ACC71914
10	25	22.3	25	8	ACC71913
11	18	16.1	1042	12	ADJ42339
12	17	15.2	855	13	ADJ42339
13	17	15.2	973	13	ADJ42339
14	17	15.2	973	13	ADJ42339
15	16	14.3	225	2	AAK10983
16	16	14.3	434	6	ABZ08502
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19	16	14.3	564	13	ADU12685

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24	16	14.3	825	2	ADR01833
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26	16	14.3	829	10	ADF74833
27	16	14.3	1392	10	ADF74831
28	16	14.3	1392	10	ADF74839
29	16	14.3	1399	10	ADF74835
30	16	14.3	1399	10	ADF74845
31	16	14.3	1476	10	ADF74827
32	16	14.3	1665	5	ADL45295
33	16	14.3	2000	11	ACI37062
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38	16	14.3	2995	3	AAF16046
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40	16	14.3	4021	4	AAK51866
41	16	14.3	4525	14	ADZ49430
42	16	14.3	8354	6	ABS52100
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44	16	14.3	8395	6	ABL32175
45	16	14.3	8645	6	ABS78652
46	16	14.3	11365	6	ABK87505
47	16	14.3	12044	4	ABL10238
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49	16	14.3	89972	14	AEBS5711
50	16	14.3	110000	14	AEBS9175_07
51	16	14.3	110000	14	AEBS9175_08
52	16	14.3	110000	14	AEBS42401_07
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75	15	13.4	321	10	ADG91703
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89	15	13.4	431	5	ABS27540
90	15	13.4	431	5	AAI02442
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92	15	13.4	444	13	ADV39815



93	15	13.4	467	9	ACH38314	Human end	166	15	13.4	1635	4	AAH62728	Abh22728 Shrimp wh	
94	15	13.4	468	9	ACH38029	Human end	C 167	15	13.4	1648	4	ABL26823	AbL26823 Drosophill	
C	95	15	13.4	469	5	AA590062	DNA encod	C 168	15	13.4	1655	4	ABL05415	AbL05415 Drosophill
	96	15	13.4	528	4	AA551303	Enterococ	C 169	15	13.4	1659	8	ADA70976	Ada70976 Rice gene
	97	15	13.4	531	4	ABA60555	Human foe	C 170	15	13.4	1674	6	ABN68480	ABN68480 Streptoco
98	15	13.4	531	4	AA140444	Probe #91	C 171	15	13.4	1677	13	ADV83901	ADV83901 Streptoco	
99	15	13.4	531	4	AAK34725	Human bon	C 172	15	13.4	1801	12	AA729602	AA729602 Human EHO	
100	15	13.4	531	4	AAK08837	Human bra	C 173	15	13.4	1847	13	ADRO6545	ADr06545 Full leng	
101	15	13.4	531	4	AB634495	Human liv	174	15	13.4	1928	5	AA686188	AA686188 DNA encod	
102	15	13.4	534	6	ABN69215	Streptoco	175	15	13.4	1964	12	ADU74986	ADU74986 Marter ge	
103	15	13.4	534	8	ACA46483	Prokaryot	C 176	15	13.4	1968	3	AA635408	AA635408 Cat flea	
104	15	13.4	534	8	ACA48160	Prokaryot	C 177	15	13.4	1982	3	AA635407	AA635407 Cat flea	
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108	15	13.4	534	10	ABX05845	S. pneumo	C 181	15	13.4	2001	3	AAAF2276	AAf22276 M. caprau	
C	109	15	13.4	535	6	ABQ92777	Triticum	C 182	15	13.4	2010	6	AAH50505	Ahh50505 S. epider
	110	15	13.4	537	4	AA554485	Staphyloc	C 183	15	13.4	2112	4	AAH50505	AAH50505 S. epider
	111	15	13.4	537	4	AA555836	Staphyloc	C 184	15	13.4	2117	11	ADM03565	AdM03565 Human CDN
112	15	13.4	537	4	AA555095	Staphyloc	C 185	15	13.4	2131	3	AA635406	AA635406 Cat flea	
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114	15	13.4	537	4	AAH53853	S. epider	C 187	15	13.4	2370	6	ABO69215	ABO69215 Listeria	
115	15	13.4	537	8	ACA20145	Prokaryot	C 188	15	13.4	2453	3	ABL12184	ABL12184 Drosophill	
116	15	13.4	537	8	ACA36779	Prokaryot	C 189	15	13.4	2553	3	AA635413	AA635413 Cat flea	
117	15	13.4	537	10	ADC93286	E. faeciu	C 190	15	13.4	2553	3	AA635414	AA635414 Cat flea	
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119	15	13.4	537	13	ADV84111	Streptoco	C 192	15	13.4	2567	6	ABQ70911	ABQ70911 Listeria	
120	15	13.4	537	14	ADM94535	Prolifera	C 193	15	13.4	2696	4	ABL05332	ABL05332 Drosophill	
121	15	13.4	552	8	ABZ42377	Streptoco	C 194	15	13.4	2724	4	ABL02637	ABL02637 Drosophill	
122	15	13.4	552	13	ADR93563	Novel S.	C 195	15	13.4	2853	5	AA590071	AA590071 DNA encod	
123	15	13.4	552	14	AEA57433	Streptoco	C 196	15	13.4	2872	3	AAZ57437	AAZ57437 Heat-rest	
124	15	13.4	558	6	ABN90993	Staphyloc	C 197	15	13.4	2872	3	AAZ46834	AAZ46834 Heat-rest	
125	15	13.4	558	13	ADS03364	Staphyloc	C 198	15	13.4	2917	4	ABL05604	ABL05604 Drosophill	
126	15	13.4	570	9	ADB06451	Alloiococ	C 199	15	13.4	2939	4	ABL02737	ABL02737 Drosophill	
127	15	13.4	637	4	ABR05333	Drosophill	C 200	15	13.4	3016	4	ABL05328	ABL05328 Drosophill	
128	15	13.4	649	12	ADO63763	Transcrip	C 201	15	13.4	3050	4	ABL10236	ABL10236 Drosophill	
129	15	13.4	649	14	AEA26252	Stress to	C 202	15	13.4	3061	8	ABX05390	ABx05390 Human nov	
130	15	13.4	654	11	ACL13612	Rice abio	C 203	15	13.4	3126	3	AA635412	AA635412 Cat flea	
131	15	13.4	655	11	AD130772	Human CDN	C 204	15	13.4	3126	3	AA635411	AA635411 Cat flea	
132	15	13.4	655	13	ADS82839	Human lym	C 205	15	13.4	3126	4	AAH55007	Ahh55007 S. epider	
133	15	13.4	759	8	ACA47297	Prokaryot	C 206	15	13.4	3302	4	AAH54652	AAH54652 S. epider	
134	15	13.4	795	13	ADT91210	Single ch	C 207	15	13.4	3409	4	ABL05530	ABL05530 Drosophill	
135	15	13.4	799	8	ABX05374	Human nov	C 208	15	13.4	3581	12	ADB06386	ADB06386 Novel hum	
136	15	13.4	883	6	ABN98749	Arabidops	C 209	15	13.4	3723	4	ABL20000	ABL20000 Drosophill	
137	15	13.4	926	4	AA121728	Probe #11	C 210	15	13.4	3723	4	ABL05414	ABL05414 Drosophill	
138	15	13.4	926	4	ABA66807	Human foe	C 211	15	13.4	3834	4	ABL05420	ABL05420 Drosophill	
139	15	13.4	926	4	AA147014	Probe #15	C 212	15	13.4	3906	4	ABL08138	ABL08138 Drosophill	
140	15	13.4	926	4	ABA48885	Human bre	C 213	15	13.4	4116	4	ABL20280	ABL20280 Drosophill	
141	15	13.4	926	4	ABA33868	Probe #12	C 214	15	13.4	4173	2	AA772214	AA772214 Grapevine	
142	15	13.4	926	4	AAK40959	Human bon	C 215	15	13.4	4212	4	ABL12981	ABL12981 Drosophill	
143	15	13.4	926	4	AAK15235	Human bra	C 216	15	13.4	5205	4	ABL26822	ABL26822 Drosophill	
144	15	13.4	926	4	AB640541	Human liv	C 217	15	13.4	5645	14	ADZ62402	ADz62402 Murine My	
145	15	13.4	926	5	AA107413	Probe #74	C 218	15	13.4	5818	6	ABO71014	ABq71014 Listeria	
146	15	13.4	926	6	AB814926	Human gen	C 219	15	13.4	6661	6	ABL61920	ABL61920 Colon ade	
147	15	13.4	975	3	AA650239	Arabidops	C 220	15	13.4	6968	4	ABL15278	ABL15278 Drosophill	
148	15	13.4	990	12	ADN36383	Escherich	C 221	15	13.4	6968	4	AA630357	AA630357 Human dia	
149	15	13.4	1047	2	AAO45678	PM4 PCR	C 222	15	13.4	7554	4	ABL08502	ABL08502 Drosophill	
150	15	13.4	1159	2	AA798563	AAq798563 DNA encod	C 223	15	13.4	8355	13	ADRR8435	ADr84435 Aspergill	
151	15	13.4	1162	13	ADK49254	Plant ful	C 224	15	13.4	9106	4	ABL12980	ABL12980 Drosophill	
152	15	13.4	1210	2	AAZ63332	S. pneumo	C 225	15	13.4	9613	4	ABL02636	ABL02636 Drosophill	
153	15	13.4	1281	3	AAZ57438	Heat-rest	C 226	15	13.4	10596	10	ACF72203	ACf72203 Photorhab	
154	15	13.4	1281	3	AAZ46835	Heat-rest	C 227	15	13.4	11831	2	AAV52198	AAV52198 Streptoco	
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156	15	13.4	1284	8	AAZ46836	Heat-rest	C 229	15	13.4	12676	4	ABL20502	ABL20502 Drosophill	
157	15	13.4	1320	8	ABX05239	Human nov	C 230	15	13.4	13916	14	ADW44204	ADw44204 Staphyloc	
158	15	13.4	1350	13	AD558762	Bacterial	C 231	15	13.4	14141	4	ABL06822	ABL06822 Drosophill	
159	15	13.4	1431	10	ACP68004	Photorhab	C 232	15	13.4	14557	6	AAK13304	AAK13304 Enterococ	
160	15	13.4	1431	13	AAZ44074	L. delbru	C 233	15	13.4	14557	6	AB599099	ABe99099 Enterococ	
161	15	13.4	1468	4	AAH78885	Human exc	C 234	15	13.4	16397	2	AAV74516	AAV74516 Staphyloc	
162	15	13.4	1462	4	AAH78885	Human exc	C 235	15	13.4	21500	4	AA559633	AA559633 Propionib	
163	15	13.4	1460	2	AAV35659	Heat-rest	C 236	15	13.4	21500	8	ACF64562	ACf64562 Propionib	
164	15	13.4	1524	10	ADK64311	Disease t	C 237	15	13.4	22281	11	ACN44616	ACn44616 Mouse gen	
165	15	13.4	1608	13	AD596607	Drosophill	C 238	15	13.4	24227	4	ABL02736	ABL02736 Drosophill	



C 239	15	13.4	27324	4	ABA89226	Escherich	C 312	14	12.5	378	6	ABL87372	AD187372 Human ova
240	15	13.4	39678	4	AAK84996	AaK84996 Human imm	C 313	14	12.5	388	9	ACC26358	ACC26358 Human sec
C 241	15	13.4	40766	4	ABL28686	ABL28686 Drosophil	C 314	14	12.5	396	9	ACH17483	ACH17483 Human adu
C 242	15	13.4	42429	4	ABL17910	ABL17910 Drosophil	C 315	14	12.5	400	13	ACR87802	ACR87802 Human SIR
243	15	13.4	44145	13	ADV87730	Adv87730 Streptoco	316	14	12.5	406	4	AAS35190	AAS35190 Human car
244	15	13.4	44145	13	ADV78983	Adv78983 Streptoco	317	14	12.5	406	10	ADE45269	AdE45269 Human car
245	15	13.4	54668	13	ADV87738	Adv87738 Streptoco	318	14	12.5	406	6	ADJ06687	AdJ06687 Human car
246	15	13.4	54668	13	ADV78991	Adv78991 Streptoco	319	14	12.5	408	6	ABS69624	ABs69624 Novel mur
C 247	15	13.4	65011	6	ABS79015	AbE79015 E. coli C	320	14	12.5	411	3	AAF09545	Aaf09545 Fusarium
C 248	15	13.4	68611	10	ADH80582	Adh80582 Escherich	321	14	12.5	411	13	ADUS3586	ADUS3586 Human
C 249	15	13.4	86431	6	AEQ74964_7	Continuation (8 of	322	14	12.5	411	14	ADZ91589	AdZ91589 Fusarium
C 250	15	13.4	106664	13	ADV35021	Adv35021 Murine cd	323	14	12.5	417	4	AAS35898	Aas35898 Human car
251	15	13.4	110000	3	AAF22305_01	Continuation (2 of	324	14	12.5	417	4	AAK78702	AAK78702 Human imm
252	15	13.4	110000	4	AAI99682_10	Continuation (11 o	325	14	12.5	417	10	ADRA6592	AdE46592 Human car
253	15	13.4	110000	4	AAI99682_11	Continuation (12 o	326	14	12.5	417	11	ACH94667	ACH94667 Klebsiell
254	15	13.4	110000	4	AAI99683_10	Continuation (11 o	327	14	12.5	417	13	ADJ08010	AdJ08010 Human car
255	15	13.4	110000	4	AAI99683_11	Continuation (12 o	C 328	14	12.5	418	12	ADL10143	AdL10143 Cat flea
256	15	13.4	110000	6	ABN71527_00	Abn71527 Streptoco	329	14	12.5	438	10	ADA19315	Ada19315 Human ins
257	15	13.4	110000	6	ABN71527_15	Continuation (16 o	330	14	12.5	443	6	AAS21059	Aas21059 Isolated
258	15	13.4	110000	6	ABN71527_16	Continuation (17 o	331	14	12.5	443	6	AAS20998	Aas20998 DNA sequ
259	15	13.4	110000	6	ABQ67196_4	Continuation (5 of	C 332	14	12.5	444	8	ACRA8516	ACRA8516 Prokaryot
260	15	13.4	110000	6	ABQ69245_11	Continuation (12 o	333	14	12.5	450	11	ADT96600	ADT96600 Colton can
261	15	13.4	110000	6	ABQ69245_16	Continuation (17 o	334	14	12.5	450	11	ADK43082	AdK43082 Human cdn
C 262	15	13.4	110000	6	ABQ69245_27	Continuation (28 o	C 335	14	12.5	453	4	AAK64561	AAK64561 Human imm
263	15	13.4	110000	6	ABQ67197_10	Continuation (11 o	C 336	14	12.5	459	3	AAZ51881	Aaz51881 N. tabacu
C 264	15	13.4	110000	6	ABO67195_0	Abq67195 Listeria	C 337	14	12.5	460	9	ACH22476	ACH22476 Human adu
C 265	15	13.4	110000	6	ABR03041_26	Continuation (27 o	338	14	12.5	461	4	AAK83326	AAK83326 Human imm
C 266	15	13.4	110000	6	ABA03041_27	Continuation (28 o	339	14	12.5	467	4	AAL35695	AAL35695 Human mus
C 267	15	13.4	110000	9	ADB12064_00	AdB12064 Altiolococ	340	14	12.5	467	4	AAL35694	AAL35694 Human mus
268	15	13.4	110000	10	ADF77343_04	Continuation (5 of	341	14	12.5	467	8	ABX58682	ABX58682 CDNA enco
269	15	13.4	110000	10	ABS56454_00	AbS56454 Streptoco	342	14	12.5	467	8	ABX58683	ABX58683 CDNA enco
270	15	13.4	110000	10	ACF67367_06	Continuation (7 of	343	14	12.5	467	12	ADJ29432	AdJ29432 Human mus
C 271	15	13.4	110000	10	ACF67367_52	Continuation (53 o	344	14	12.5	467	12	ADJ29433	AdJ29433 Human mus
C 272	15	13.4	110000	10	ACF65387_3	Continuation (4 of	345	14	12.5	476	4	AAK62750	AAK62750 Human imm
273	15	13.4	110000	10	ACF65384_0	AcF65384 Phototrab	346	14	12.5	485	8	ABZ53523	ABZ53523 Aspergill
274	15	13.4	110000	12	ADQ34435_2	Continuation (3 of	347	14	12.5	493	13	ACN47876	ACn47876 Colton pr
275	15	13.4	110000	13	ABD32921_2	Continuation (3 of	C 348	14	12.5	498	2	AAK13446	AAK13446 Enterococ
276	15	13.4	110000	13	ABD32921_2	Continuation (3 of	C 349	14	12.5	498	6	ABS99241	ABS99241 Enterococ
C 277	15	13.4	110000	13	ADS99457_0	AdS99457 Human kin	C 350	14	12.5	500	3	AAC93904	AAC93904 Cat flea
278	15	13.4	110000	13	ADV81204_00	Adv81204 Streptoco	C 351	14	12.5	500	9	ACCT2972	ACCT2972 Cat flea
279	15	13.4	110000	13	ADN451204_17	AdN451204 Human gen	C 352	14	12.5	500	12	ADL09614	AdL09614 Cat flea
C 280	15	13.4	133955	11	ACNV45170	Acn45170 Human gen	C 353	14	12.5	504	3	AAZ51883	Aaz51883 N. tabacu
281	15	13.4	134442	13	ABD32824	Abd32824 Mouse can	C 354	14	12.5	505	3	AACT4868	AACT4868 Human ORF
282	15	13.4	160271	4	AAF85116	Aaf85116 Nucleotid	C 355	14	12.5	506	5	AAH28262	AAH28262 Phoa prom
283	15	13.4	160271	4	AAF85756	Aaf85756 Human chr	C 356	14	12.5	506	10	ACA61197	ACA61197 DNA encod
284	15	13.4	160271	4	AAF85750	Aaf85750 Bipolar a	C 357	14	12.5	508	3	AAZ51877	Aaz51877 N. tabacu
285	15	13.4	160271	4	AA506667	Aa506667 Human chr	358	14	12.5	509	3	AAZ51878	Aaz51878 N. tabacu
286	15	13.4	160271	4	AA504864	Aa504864 Human chr	C 359	14	12.5	520	10	ADH29050	ADH29050 Human chr
287	15	13.4	160271	5	AAH23764	Aah23764 Human chr	C 360	14	12.5	522	1	AAH30057	Aah30057 E. coli a
288	15	13.4	160271	5	AAH40997	Aah40997 160kb fra	C 361	14	12.5	522	1	AAH60041	Aah60041 Sequence
289	15	13.4	160271	5	AA504858	Aa504858 Human chr	C 362	14	12.5	522	1	AAH60041	Aah60041 Sequence
290	15	13.4	207542	14	ABE32385	Aeb32385 Human gen	C 363	14	12.5	522	2	AAH60474	AaH60474 DNA firegm
291	15	13.4	207557	14	ABE32371	Aeb32371 Human gen	C 364	14	12.5	528	1	AAH60474	AaH60474 DNA firegm
C 292	15	13.4	264965	12	ADN16203	Adn16203 Human sul	C 365	14	12.5	532	6	ABO47941	ABO47941 Oligonuc
C 293	15	13.4	268685	6	ABS56563	AbS56563 Human STL	366	14	12.5	532	6	ABO47940	ABO47940 Oligonuc
294	15	13.4	305107	4	AAH62689	Aah62689 Shrimp wh	367	14	12.5	532	14	ABCO3713	ABCO3713 Zebrafish
C 295	15	13.4	339234	12	ADQ59437	Adq59437 Human can	368	14	12.5	540	12	ADU41863	AdJ41863 Plant cdn
C 296	15	13.4	339234	14	ADZ13744	Adz13744 Murine ca	C 369	14	12.5	541	13	ADU12046	AdU12046 Solid tum
C 297	14	12.5	60	6	ABN35217	Abn35217 Murine spl	C 370	14	12.5	555	13	ACN62112	ACN62112 Colton gy
298	14	12.5	121	10	ADH92451	Adh92451 Human gen	371	14	12.5	571	4	ABAS9515	ABAS9515 Human foe
299	14	12.5	160	3	AACT0111	Aact0111 Human sec	372	14	12.5	571	4	AAI39377	AAI39377 Probe #80
C 300	14	12.5	180	6	ADH31687	Adh31687 Yeast sma	373	14	12.5	571	4	AAK33654	AAK33654 Human bon
301	14	12.5	244	12	ADP63312	Adp63312 Maize car	374	14	12.5	571	4	AAK07788	AAK07788 Human bry
302	14	12.5	251	11	ADMA4708	Adma4708 Insect re	375	14	12.5	571	4	ABSS3469	ABSS3469 Human liv
C 303	14	12.5	265	12	ADP92724	Adp92724 Cotton ex	376	14	12.5	588	4	AAI17491	AAI17491 Probe #74
C 304	14	12.5	288	2	AAV12676	Aav12676 Vh251/gam	377	14	12.5	588	4	ABA62422	ABA62422 Human foe
C 305	14	12.5	288	2	AAV66036	Aav66036 Vh251/gam	378	14	12.5	588	4	AAI42398	AAI42398 Probe #11
306	14	12.5	294	10	ABX87658	Abx87658 Corn ear-	379	14	12.5	588	4	ABA29755	ABA29755 Probe #82
307	14	12.5	306	10	ABX86201	Abx86201 Corn ear-	380	14	12.5	588	4	AAK36636	AAK36636 Human bon
308	14	12.5	308	6	ADP63313	Adp63313 Maize car	381	14	12.5	588	4	AAK10760	AAK10760 Human bry
C 309	14	12.5	318	6	ADH31688	Adh31688 Yeast sma	382	14	12.5	588	4	ABSS36292	ABSS36292 Human liv
310	14	12.5	327	13	ADU02060	Adu02060 Novel hum	383	14	12.5	588	6	ABSI0632	ABSI0632 Human gen
C 311	14	12.5	336	14	ACL72672	ACL72672 M. xanthu	C 384	14	12.5	589	2	AAH64524	AAH64524 hpgT1.SSI



C 385	14	12.5	593	2	AAQ76310	Aag76310	Plaemid p	C 458	14	12.5	1113	1	AAAE0164	AAAE0164	Bacterial
C 386	14	12.5	594	13	ADQ79112	Adq79112	Novel can	C 459	14	12.5	1114	13	ADX10976	ADX10976	Plant ful
C 387	14	12.5	618	5	ABV50319	Abv50319	Human pro	C 460	14	12.5	1115	3	AAE07954	AAE07954	Fusarium
C 388	14	12.5	629	6	ABO50342	AbO50342	Oligonuc1	C 461	14	12.5	1115	13	ADU51995	ADU51995	Fusarium
C 389	14	12.5	629	6	ABO50343	AbO50343	Oligonuc1	C 462	14	12.5	1115	14	ADZ89998	ADZ89998	Fusarium
C 390	14	12.5	639	3	AAFI13016	Aaf113016	Aspergill1	C 463	14	12.5	1164	6	ABN91998	ABN91998	Staphyloc
C 391	14	12.5	639	13	ADU57057	Adu57057	Aspergill1	C 464	14	12.5	1167	13	ADSO1519	ADSO1519	Staphyloc
C 392	14	12.5	639	13	ADZ95060	Adz95060	Aspergill1	C 465	14	12.5	1174	22	AAQ79522	AAQ79522	Pha prom
C 393	14	12.5	650	4	AAH04477	Aah04477	Human cDN	C 466	14	12.5	1182	11	ABD01596	ABD01596	Pseudomon
C 394	14	12.5	654	4	ABL27405	AbL27405	Drosophil	C 467	14	12.5	1212	9	ADA32378	ADA32378	DNA encod
C 395	14	12.5	663	13	ACN62520	Acn62520	Cotton de	C 468	14	12.5	1227	8	ACNA7800	ACNA7800	Prokaryot
C 396	14	12.5	667	11	ADM45703	Adm45703	Insect re	C 469	14	12.5	1242	3	AAE25163	AAE25163	Construct
C 397	14	12.5	669	5	AAE63150	Aae63150	Human pur	C 470	14	12.5	1319	3	AAE68100	AAE68100	Human sec
C 398	14	12.5	671	6	ABQ44437	Abq44437	Oligonuc1	C 471	14	12.5	1338	10	ACCG6287	ACCG6287	Gene sequ
C 399	14	12.5	671	6	ABQ44436	Abq44436	Oligonuc1	C 472	14	12.5	1338	10	ADK63671	ADK63671	Disease t
C 400	14	12.5	681	5	AAE68700	Aae68700	DNA encod	C 473	14	12.5	1353	13	ADSE6342	ADSE6342	Bacterial
C 401	14	12.5	681	5	AAE82137	Aae82137	DNA encod	C 474	14	12.5	1353	13	ADSE63001	ADSE63001	Bacterial
C 402	14	12.5	700	4	AAH93048	Aah93048	Human inf	C 475	14	12.5	1377	13	ADSS5955	ADSS5955	Bacterial
C 403	14	12.5	711	10	ADP02727	Adp02727	Bacterial	C 476	14	12.5	1378	13	ADK62480	ADK62480	Plant ful
C 404	14	12.5	726	10	ACC60826	Acc60826	Gene sequ	C 477	14	12.5	1380	9	ADA32682	ADA32682	DNA encod
C 405	14	12.5	726	10	ADK62145	Adk62145	Disease t	C 478	14	12.5	1392	6	AAE94443	AAE94443	Human hyd
C 406	14	12.5	726	14	ACL68651	Act68651	M. xanthu	C 479	14	12.5	1425	6	ABO99020	ABO99020	Human ORF
C 407	14	12.5	732	14	ABE03388	Aeb03388	Mycobacte	C 480	14	12.5	1428	8	ACA37366	ACA37366	Prokaryot
C 408	14	12.5	732	14	AEA79291	Aea79291	Novel M.	C 481	14	12.5	1431	8	ACA48346	ACA48346	Prokaryot
C 409	14	12.5	750	2	AAZ17451	Aaz17451	Human gen	C 482	14	12.5	1431	9	ADA29614	ADA29614	DNA encod
C 410	14	12.5	753	6	ABN66635	Abn66635	Streptoco	C 483	14	12.5	1456	10	ADC32169	ADC32169	Human nov
C 411	14	12.5	756	13	ADV84719	Adv84719	Streptoco	C 484	14	12.5	1461	8	ACA23706	ACA23706	Prokaryot
C 412	14	12.5	757	2	AAQ43199	Aaq43199	Sequence	C 485	14	12.5	1471	10	ADE78313	ADE78313	Endometr
C 413	14	12.5	757	2	AAQ66268	Aaq66268	IGF-1 fus	C 486	14	12.5	1500	2	AAQ76311	AAQ76311	Plaemid p
C 414	14	12.5	757	2	AAQ62171	Aaq62171	Iamb sign	C 487	14	12.5	1510	6	ABK35647	ABK35647	CDNA sequ
C 415	14	12.5	759	10	ADE99787	Ade99787	Bacterial	C 488	14	12.5	1512	8	ACA37904	ACA37904	Prokaryot
C 416	14	12.5	770	8	ADA69009	Ada69009	Arabidops	C 489	14	12.5	1516	4	AAK91327	AAK91327	Human d1g
C 417	14	12.5	790	8	ABT96152	Abt96152	Human neu	C 490	14	12.5	1516	5	AAK32154	AAK32154	Human l1v
C 418	14	12.5	790	8	ABT932210	Abt932210	Human neu	C 491	14	12.5	1516	6	ABN90509	ABN90509	Human l1v
C 419	14	12.5	794	6	ABQ88762	Abq88762	Human pro	C 492	14	12.5	1516	11	ADJ15422	ADJ15422	Human l1v
C 420	14	12.5	794	9	ADB811706	Adb811706	Human cDN	C 493	14	12.5	1525	13	ADR89901	ADR89901	Human FRE
C 421	14	12.5	794	14	ACL63506	Act63506	Human col	C 494	14	12.5	1590	13	ADT43077	ADT43077	Bacterial
C 422	14	12.5	795	8	ADA70626	Ada70626	Rice gene	C 495	14	12.5	1596	13	ADR85580	ADR85580	Aspergill1
C 423	14	12.5	798	8	ACA30716	Act30716	Prokaryot	C 496	14	12.5	1602	2	ACA39747	ACA39747	Prokaryot
C 424	14	12.5	801	13	ADS54443	AdS54443	Bacterial	C 497	14	12.5	1604	2	AAK80609	AAK80609	cmph gene
C 425	14	12.5	804	3	ACG76254	Act76254	Human ORF	C 498	14	12.5	1604	6	ABL42149	ABL42149	Nucleotid
C 426	14	12.5	804	3	ACA20579	Acta20579	Prokaryot	C 499	14	12.5	1668	4	AAI61285	AAI61285	Human pol
C 427	14	12.5	808	13	ADR60227	Adr60227	Cotton cD	C 500	14	12.5	1674	4	ABL08609	ABL08609	Human pol
C 428	14	12.5	816	9	ADA29156	Ada29156	DNA encod	C 501	14	12.5	1674	6	ABO69285	ABO69285	Drosophil
C 429	14	12.5	822	13	ADR93046	Adr93046	Novel S.	C 502	14	12.5	1674	6	ABO67833	ABO67833	Listeria
C 430	14	12.5	822	14	AEA56816	Aea56816	Streptoco	C 503	14	12.5	1674	14	AEA40178	AEA40178	Rice ORBT
C 431	14	12.5	825	10	ABX07621	Abx07621	S. pneumo	C 504	14	12.5	1698	11	ABD01589	ABD01589	Pseudomon
C 432	14	12.5	828	13	ADR43830	Adr43830	Streptoco	C 505	14	12.5	1701	11	ABD01615	ABD01615	Pseudomon
C 433	14	12.5	834	5	AAH66181	Aah66181	C glutam1	C 506	14	12.5	1738	4	ABJ06169	ABJ06169	M. tuberc
C 434	14	12.5	840	6	ABO88763	AbO88763	Human pro	C 507	14	12.5	1742	2	AAK01146	AAK01146	M. tuberc
C 435	14	12.5	840	6	ADB811707	AdB811707	Human cDN	C 508	14	12.5	1742	2	AAK01180	AAK01180	M. tuberc
C 436	14	12.5	858	6	ABZ22199	Abz22199	Candida a	C 509	14	12.5	1742	5	AAK012458	AAK012458	Mycobacte
C 437	14	12.5	879	8	AAQ79523	Aaq79523	Phoa prom	C 510	14	12.5	1742	5	AAK03783	AAK03783	M. tuberc
C 438	14	12.5	879	8	ACA33235	Acta33235	Prokaryot	C 511	14	12.5	1742	6	AAK47089	AAK47089	Mycobacte
C 439	14	12.5	882	4	AAAS52896	Aaas52896	Enterococ	C 512	14	12.5	1742	6	ABE63313	ABE63313	M. tuberc
C 440	14	12.5	886	3	AAFI15074	Aafi15074	Trichoder	C 513	14	12.5	1742	6	AAAD28347	AAAD28347	Mycobacte
C 441	14	12.5	886	13	ADU59115	Adu59115	Trichoder	C 514	14	12.5	1811	13	ADS60717	ADS60717	Bacterial
C 442	14	12.5	886	14	ADZ97118	Adz97118	Trichoder	C 515	14	12.5	1811	12	ADOS9780	ADOS9780	E. coli m
C 443	14	12.5	915	6	ABK97628	Abk97628	Human pro	C 516	14	12.5	1835	4	AAI93012	AAI93012	Human pol
C 444	14	12.5	927	8	ACA53152	Acta53152	Prokaryot	C 517	14	12.5	1838	13	ADK33852	ADK33852	Plant ful
C 445	14	12.5	942	5	AAAT77329	Aaat77329	DNA encod	C 518	14	12.5	1845	9	ADA29091	ADA29091	DNA encod
C 446	14	12.5	950	2	AAAT83973	Aaat83973	DNA encod	C 519	14	12.5	1854	9	ADB10879	ADB10879	Allotococ
C 447	14	12.5	957	4	AAAT71175	Aaat71175	Corynebac	C 520	14	12.5	1854	9	ADB10877	ADB10877	Allotococ
C 448	14	12.5	963	5	AAH65669	Aah65669	C glutam1	C 521	14	12.5	1854	12	ADJ27118	ADJ27118	Allotococ
C 449	14	12.5	964	10	ADD13634	Add13634	C. glutam	C 522	14	12.5	1857	5	AAE90304	AAE90304	DNA encod
C 450	14	12.5	965	12	ACH87012	Ach87012	Human gen	C 523	14	12.5	1859	4	AAI66002	AAI66002	Human per
C 451	14	12.5	993	6	ABK74452	Abk74452	Bacillius	C 524	14	12.5	1868	13	ADR84993	ADR84993	Human sec
C 452	14	12.5	1017	8	ACA46349	Acta46349	Prokaryot	C 525	14	12.5	1907	3	AACT9848	AACT9848	Aspergill1
C 453	14	12.5	1046	1	AAAE0165	Aae0165	Sequence	C 526	14	12.5	1938	11	ABD01624	ABD01624	Pseudomon
C 454	14	12.5	1052	8	ABZ25874	Abz25874	Human sec	C 527	14	12.5	1951	6	ABQ73919	ABQ73919	Plaemid p
C 455	14	12.5	1080	5	AAAS92678	Aaas92678	DNA encod	C 528	14	12.5	1957	4	AAH21511	AAH21511	Human GRP
C 456	14	12.5	1105	6	ABK97629	Abk97629	Human pro	C 529	14	12.5	1962	6	ABQ90184	ABQ90184	M. capsul
C 457	14	12.5	1109	4	AAAF72760	Aaf72760	Human pro	C 530	14	12.5	1974	14	AEA40177	AEA40177	Rice ORBT



C 531	14	12.5	1983	14	ACL6910	604	14	12.5	2932	8	ADA41546	Ada41546 Human sec
C 532	14	12.5	1992	11	ACL28955	605	14	12.5	2932	10	ADA57677	Ada57677 BAC fragm
C 533	14	12.5	1994	7	ADS31265	606	14	12.5	2966	13	ADT14879	Adt14879 Plant cDN
C 534	14	12.5	1994	7	ADY36653	607	14	12.5	2988	8	ADAD05252	Adad05252 Human sec
C 535	14	12.5	2000	6	ABZ17312	608	14	12.5	2988	8	ADA40317	Ada40317 Human sec
C 536	14	12.5	2000	6	ABZ15272	609	14	12.5	2988	10	ADAA56479	Adaa56479 Gene enco
C 537	14	12.5	2000	8	ADA73342	610	14	12.5	2996	14	ADZ49615	Adz49615 Insulin p
C 538	14	12.5	2000	10	ACC61883	611	14	12.5	3000	12	ADDA14135	Addda14135 Plasmid p
C 539	14	12.5	2000	11	ADK64963	612	14	12.5	3000	12	ADDA14138	Addda14138 Plasmid p
C 540	14	12.5	2000	11	ACL35539	613	14	12.5	3003	13	ADQ84953	Adq84953 Human tum
C 541	14	12.5	2000	12	ADU41228	614	14	12.5	3004	13	ADQ22282	Adq22282 Human sof
C 542	14	12.5	2016	13	ACN39077	615	14	12.5	3100	10	ABZ82072	Abz82072 Dual-prom
C 543	14	12.5	2019	8	ACA30891	616	14	12.5	3106	4	AAH34342	Aah34342 Human col
C 544	14	12.5	2021	14	AEA51351	617	14	12.5	3119	4	ABL27408	AbL27408 Drosophill
C 545	14	12.5	2052	14	ADAD05253	618	14	12.5	3224	8	AAFP4625	Aaf4625 Novel pro
C 546	14	12.5	2052	8	ADA40318	619	14	12.5	3224	10	ADBE38374	Adbe38374 Human pro
C 547	14	12.5	2052	10	ADAA56480	620	14	12.5	3224	10	ADDA19317	Addda19317 Human ins
C 548	14	12.5	2070	4	ADAD05225	621	14	12.5	3224	10	ACG72764	Accg72764 Human can
C 549	14	12.5	2070	8	ADA39764	622	14	12.5	3224	12	ADP07325	Adp07325 Human MAR
C 550	14	12.5	2070	10	ADAA55955	623	14	12.5	3224	12	ADP07325	Adp07325 Human HSA
C 551	14	12.5	2074	3	ABA98644	624	14	12.5	3224	12	ADQ17597	Adq17597 Human sof
C 552	14	12.5	2143	2	AAHX03840	625	14	12.5	3224	13	ADR25921	Adr25921 Breast ca
C 553	14	12.5	2143	2	AAAS33339	626	14	12.5	3224	14	ADY61874	Ady61874 Human gen
C 554	14	12.5	2143	5	AAAF31463	627	14	12.5	3240	8	AAH54379	Aah54379 S. epider
C 555	14	12.5	2143	5	ABEB27975	628	14	12.5	3242	12	ADDA14124	Addda14124 Plasmid p
C 556	14	12.5	2152	14	AAH17335	629	14	12.5	3244	4	AAAF46210	Aaf46210 Human DNA
C 557	14	12.5	2187	14	ADY85276	630	14	12.5	3244	8	ACA89660	Acca89660 CDNA enco
C 558	14	12.5	2208	8	ADH70522	631	14	12.5	3244	8	ACA73670	Acca73670 Human sec
C 559	14	12.5	2208	11	ACML26500	632	14	12.5	3244	8	ACA05985	Acca05985 Human sec
C 560	14	12.5	2224	11	ADCM03427	633	14	12.5	3244	8	ACA66819	Acca66819 CDNA enco
C 561	14	12.5	2234	14	ACL63817	634	14	12.5	3244	8	ACF20394	Accf20394 Human sec
C 562	14	12.5	2234	14	AAAF16129	635	14	12.5	3244	8	ACF19780	Accf19780 Human sec
C 563	14	12.5	2239	4	AAAF2785	636	14	12.5	3244	8	ACD22068	Accd22068 Human sec
C 564	14	12.5	2329	10	ADG32012	637	14	12.5	3244	8	ACF13233	Accf13233 Human sec
C 565	14	12.5	2329	13	ADRE6490	638	14	12.5	3244	8	ACD25336	Accd25336 Human sec
C 566	14	12.5	2329	13	ADRE65806	639	14	12.5	3244	8	ACF00385	Accf00385 Human sec
C 567	14	12.5	2329	13	ADU06179	640	14	12.5	3244	8	ACA72442	Acca72442 Novel hum
C 568	14	12.5	2339	14	ADZ61883	641	14	12.5	3244	8	ACD04966	Accd04966 Novel hum
C 569	14	12.5	2423	4	ABLI17858	642	14	12.5	3244	8	ACD18427	Accd18427 Human sec
C 570	14	12.5	2439	4	AAI160568	643	14	12.5	3244	8	ACD08434	Accd08434 Human sec
C 571	14	12.5	2515	10	ADBE78312	644	14	12.5	3244	8	ACA88868	Acca88868 Novel hum
C 572	14	12.5	2604	4	ABLI13475	645	14	12.5	3244	8	ACA70310	Acca70310 Human sec
C 573	14	12.5	2622	8	ACA21131	646	14	12.5	3244	8	ACD12532	Accd12532 Novel hum
C 574	14	12.5	2634	9	ADA32749	647	14	12.5	3244	8	ACCT74447	Accct74447 Human sec
C 575	14	12.5	2643	8	ABET20520	648	14	12.5	3244	8	ACD16075	Accd16075 Human sec
C 576	14	12.5	2668	12	ADOS7288	649	14	12.5	3244	8	ACD25643	Accd25643 Novel hum
C 577	14	12.5	2688	12	ADQ84801	650	14	12.5	3244	8	ACD18120	Accd18120 Human sec
C 578	14	12.5	2688	13	ACN37843	651	14	12.5	3244	8	ACCB8407	Accb8407 Human sec
C 579	14	12.5	2690	10	ADD29862	652	14	12.5	3244	8	ACD21761	Accd21761 Human sec
C 580	14	12.5	2700	10	ABZ82071	653	14	12.5	3244	8	ACD18828	Accd18828 Human sec
C 581	14	12.5	2702	2	AAQ04681	654	14	12.5	3244	8	ABX98438	Abx98438 Human sec
C 582	14	12.5	2702	10	ADDI18789	655	14	12.5	3244	8	ACD14189	Accd14189 Human CDN
C 583	14	12.5	2702	13	ADRE67213	656	14	12.5	3244	8	ACD09969	Accd09969 Human sec
C 584	14	12.5	2703	5	AAAS80855	657	14	12.5	3244	8	ACCB8714	Accb8714 Human sec
C 585	14	12.5	2728	4	AAH16332	658	14	12.5	3244	8	ACD21454	Accd21454 Human sec
C 586	14	12.5	2755	13	ADXS5147	659	14	12.5	3244	8	ABX75826	Abx75826 Human CDN
C 587	14	12.5	2758	4	ABLI15175	660	14	12.5	3244	8	ABX98029	Abx98029 Human PRO
C 588	14	12.5	2779	12	ADQ96437	661	14	12.5	3244	8	ACA97505	Acca97505 Novel hum
C 589	14	12.5	2835	6	ABZ11729	662	14	12.5	3244	8	ACA57968	Acca57968 Human PRO
C 590	14	12.5	2835	12	ADMA44247	663	14	12.5	3244	8	ACD14496	Accd14496 Human PRO
C 591	14	12.5	2835	2	AAHX01147	664	14	12.5	3244	8	ACC91279	Accc91279 Human sec
C 592	14	12.5	2836	2	AAHX01181	665	14	12.5	3244	8	ACC89021	Accc89021 Human sec
C 593	14	12.5	2836	4	AAAS12459	666	14	12.5	3244	8	ACD07218	Accd07218 Human PRO
C 594	14	12.5	2836	4	AAAS03813	667	14	12.5	3244	8	ACA67669	Acca67669 Human PRO
C 595	14	12.5	2836	6	AAAD47090	668	14	12.5	3244	8	ACC81724	Accc81724 Human sec
C 596	14	12.5	2836	6	ABBS63314	669	14	12.5	3244	8	ACC89328	Accc89328 Human sec
C 597	14	12.5	2836	6	AAAD28348	670	14	12.5	3244	8	ACC86684	Accc86684 Human sec
C 598	14	12.5	2837	10	ADCC30501	671	14	12.5	3244	8	ACC89942	Accc89942 Human sec
C 599	14	12.5	2853	12	ADN05001	672	14	12.5	3244	8	ACC93121	Accc93121 Human sec
C 600	14	12.5	2853	13	ADU06088	673	14	12.5	3244	8	ACA72749	Acca72749 Human PRO
C 601	14	12.5	2855	4	ABLI27404	674	14	12.5	3244	8	ACA89267	Acca89267 Human sec
C 602	14	12.5	2881	12	ADJ48283	675	14	12.5	3244	8	ACA70003	Acca70003 Human sec
C 603	14	12.5	2901	10	ADA19316	676	14	12.5	3244	8	ACA97146	Acca97146 Novel hum



C 677	14	12.5	3244	8	ACA91142	Novel	hum	C 750	14	12.5	3244	9	ACD32130	Adc32130	Human	sec
C 678	14	12.5	3244	8	ACA70924	Human	sec	C 751	14	12.5	3244	9	ACF18938	Acf18938	Human	sec
C 679	14	12.5	3244	8	ACA95434	Novel	hum	C 752	14	12.5	3244	9	ACF09385	Acf09385	Human	sec
C 680	14	12.5	3244	8	ACC86377	Human	sec	C 753	14	12.5	3244	9	ACF78506	Acf78506	Human	sec
C 681	14	12.5	3244	8	ACC90249	Human	sec	C 754	14	12.5	3244	9	ACF52105	Acf52105	Human	sec
C 682	14	12.5	3244	8	ACD12857	Human	sec	C 755	14	12.5	3244	9	ACF26592	Acf26592	Human	sec
C 683	14	12.5	3244	8	ACF20087	Human	sec	C 756	14	12.5	3244	9	ACF24385	Acf24385	Human	sec
C 684	14	12.5	3244	8	ABX77031	Human	PRO	C 757	14	12.5	3244	9	ACF63696	Acf63696	Human	sec
C 685	14	12.5	3244	8	ACA73363	Novel	hum	C 758	14	12.5	3244	9	ACF50570	Acf50570	Human	sec
C 686	14	12.5	3244	8	ACA68906	Novel	hum	C 759	14	12.5	3244	9	ACH08041	ACH08041	Human	sec
C 687	14	12.5	3244	8	ACA74750	CDNA	encc	C 760	14	12.5	3244	9	ACF13847	Acf13847	Human	sec
C 688	14	12.5	3244	8	ACA70617	Human	sec	C 761	14	12.5	3244	9	ACD41773	ACD41773	Human	sec
C 689	14	12.5	3244	8	ACD14803	Human	PRO	C 762	14	12.5	3244	9	ACF32186	Acf32186	Human	sec
C 690	14	12.5	3244	8	ACA68475	Novel	hum	C 763	14	12.5	3244	9	ACF23464	Acf23464	Human	sec
C 691	14	12.5	3244	8	ABX98940	Novel	hum	C 764	14	12.5	3244	9	ACF40154	Acf40154	Human	sec
C 692	14	12.5	3244	8	ABX98940	Novel	hum	C 765	14	12.5	3244	9	ACD45676	ACD45676	Human	sec
C 693	14	12.5	3244	8	ACA95741	Novel	hum	C 766	14	12.5	3244	9	ACF53333	ACF53333	Human	sec
C 694	14	12.5	3244	8	ACD04659	Novel	hum	C 767	14	12.5	3244	9	ACF27513	Acf27513	Human	sec
C 695	14	12.5	3244	8	ACC88100	Human	sec	C 768	14	12.5	3244	9	ACF45351	Acf45351	Human	sec
C 696	14	12.5	3244	8	ACF12762	Human	sec	C 769	14	12.5	3244	9	ACF29969	Acf29969	Human	sec
C 697	14	12.5	3244	8	ACA96477	Human	PRO	C 770	14	12.5	3244	9	ACD90045	ACD90045	Human	sec
C 698	14	12.5	3244	8	ACA65251	Human	PRO	C 771	14	12.5	3244	9	ACD84826	ACD84826	Human	PRO
C 699	14	12.5	3244	8	ACA73977	Human	sec	C 772	14	12.5	3244	9	ACD99986	ACD99986	Human	sec
C 700	14	12.5	3244	8	ACA74389	Novel	hum	C 773	14	12.5	3244	9	ACF77278	Acf77278	Human	sec
C 701	14	12.5	3244	8	ACA96784	Human	PRO	C 774	14	12.5	3244	9	ACF76971	Acf76971	Human	sec
C 702	14	12.5	3244	8	ACD10890	CDNA	encc	C 775	14	12.5	3244	9	ACF49956	Acf49956	Human	sec
C 703	14	12.5	3244	8	ACD91586	Human	sec	C 776	14	12.5	3244	9	ACF50263	Acf50263	Human	sec
C 704	14	12.5	3244	8	ACD02921	CDNA	encc	C 777	14	12.5	3244	9	ACD09662	ACD09662	Human	sec
C 705	14	12.5	3244	8	ACC87486	Human	sec	C 778	14	12.5	3244	9	ACD08741	ACD08741	Human	sec
C 706	14	12.5	3244	8	ACC86070	Human	sec	C 779	14	12.5	3244	9	ACF12455	ACF12455	Human	sec
C 707	14	12.5	3244	8	ACA65558	Human	PRO	C 780	14	12.5	3244	9	ACC94963	ACC94963	Human	sec
C 708	14	12.5	3244	8	ACA94375	Human	sec	C 781	14	12.5	3244	9	ACD22682	ACD22682	Human	sec
C 709	14	12.5	3244	8	ACA98119	Human	PRO	C 782	14	12.5	3244	9	ACF15382	Acf15382	Human	sec
C 710	14	12.5	3244	8	ACA91621	Novel	hum	C 783	14	12.5	3244	9	ACC97477	ACC97477	Human	sec
C 711	14	12.5	3244	8	ACA90835	Novel	hum	C 784	14	12.5	3244	9	ACC92507	ACC92507	Human	sec
C 712	14	12.5	3244	8	ACD16382	Human	sec	C 785	14	12.5	3244	9	ACF14154	Acf14154	Human	sec
C 713	14	12.5	3244	8	ACD17543	Human	sec	C 786	14	12.5	3244	9	ACF14461	Acf14461	Human	sec
C 714	14	12.5	3244	8	ACC92200	Human	sec	C 787	14	12.5	3244	9	ACF09692	Acf09692	Human	sec
C 715	14	12.5	3244	8	ACA75057	CDNA	encc	C 788	14	12.5	3244	9	ACD45983	ACD45983	Human	sec
C 716	14	12.5	3244	8	ACA91928	Human	PRO	C 789	14	12.5	3244	9	ACD48132	ACD48132	Human	sec
C 717	14	12.5	3244	8	ACA91572	Human	sec	C 790	14	12.5	3244	9	ACD67863	ACD67863	Human	sec
C 718	14	12.5	3244	8	ACC90972	Human	sec	C 791	14	12.5	3244	9	ACF29355	ACF29355	Human	sec
C 719	14	12.5	3244	8	ACA65982	CDNA	encc	C 792	14	12.5	3244	9	ACD85133	ACD85133	Human	sec
C 720	14	12.5	3244	8	ACA95127	CDNA	encc	C 793	14	12.5	3244	9	ACD84212	ACD84212	Human	PRO
C 721	14	12.5	3244	8	ACD16689	Human	sec	C 794	14	12.5	3244	9	ACD88203	ACD88203	Human	sec
C 722	14	12.5	3244	8	ACD15768	Human	sec	C 795	14	12.5	3244	9	ACF30890	ACF30890	Human	sec
C 723	14	12.5	3244	8	ABX16871	Human	CDN	C 796	14	12.5	3244	9	ACF32493	ACF32493	Human	sec
C 724	14	12.5	3244	8	ACA97812	Human	PRO	C 797	14	12.5	3244	9	ACH12153	ACH12153	CDNA	encc
C 725	14	12.5	3244	9	ACA99261	Novel	hum	C 798	14	12.5	3244	9	ACH12460	ACH12460	Human	sec
C 726	14	12.5	3244	9	ACC91893	Human	sec	C 799	14	12.5	3244	9	ACD40852	ACD40852	Human	sec
C 727	14	12.5	3244	9	ACD11394	Novel	hum	C 800	14	12.5	3244	9	ACF18324	ACF18324	Human	sec
C 728	14	12.5	3244	9	ACD15154	Human	sec	C 801	14	12.5	3244	9	ACF088771	Acf088771	Human	sec
C 729	14	12.5	3244	9	ACD11918	Human	sec	C 802	14	12.5	3244	9	ACF31572	ACF31572	Human	sec
C 730	14	12.5	3244	9	ACC96047	Human	sec	C 803	14	12.5	3244	9	ACF52412	ACF52412	Human	sec
C 731	14	12.5	3244	9	ACF16610	Human	sec	C 804	14	12.5	3244	9	ACF50281	ACF50281	Human	sec
C 732	14	12.5	3244	9	ACF02728	Human	sec	C 805	14	12.5	3244	9	ACD50281	ACD50281	Human	sec
C 733	14	12.5	3244	9	ACF03035	Human	sec	C 806	14	12.5	3244	9	ACF38984	ACF38984	Human	sec
C 734	14	12.5	3244	9	ACF03622	Human	sec	C 807	14	12.5	3244	9	ACF26899	ACF26899	Human	sec
C 735	14	12.5	3244	9	ACF10306	Human	sec	C 808	14	12.5	3244	9	ACF24999	ACF24999	Human	sec
C 736	14	12.5	3244	9	ACF18199	Human	sec	C 809	14	12.5	3244	9	ACF46579	ACF46579	Human	sec
C 737	14	12.5	3244	9	ACD46904	Human	sec	C 810	14	12.5	3244	9	ACF28127	ACF28127	Human	sec
C 738	14	12.5	3244	9	ACD49667	Human	sec	C 811	14	12.5	3244	9	ACD89431	ACD89431	Human	sec
C 739	14	12.5	3244	9	ACF28484	Human	sec	C 812	14	12.5	3244	9	ACF64003	ACF64003	Human	sec
C 740	14	12.5	3244	9	ACD89124	Human	sec	C 813	14	12.5	3244	9	ACF60643	ACF60643	Human	sec
C 741	14	12.5	3244	9	ACD84519	Human	PRO	C 814	14	12.5	3244	9	ACH12767	ACH12767	CDNA	encc
C 742	14	12.5	3244	9	ACD99293	CDNA	encc	C 815	14	12.5	3244	9	ACH10190	ACH10190	Human	sec
C 743	14	12.5	3244	9	ADA78323	Human	sec	C 816	14	12.5	3244	9	ACD04045	ACD04045	Human	sec
C 744	14	12.5	3244	9	ACF49035	Human	sec	C 817	14	12.5	3244	9	ACD10583	ACD10583	Human	sec
C 745	14	12.5	3244	9	ACD09355	Human	sec	C 818	14	12.5	3244	9	ACF42610	ACF42610	Human	sec
C 746	14	12.5	3244	9	ACF12148	Human	sec	C 819	14	12.5	3244	9	ACF18631	ACF18631	Human	sec
C 747	14	12.5	3244	9	ACF41382	Human	sec	C 820	14	12.5	3244	9	ACF02421	ACF02421	Human	sec
C 748	14	12.5	3244	9	ACF15996	Human	sec	C 821	14	12.5	3244	9	ACF21929	ACF21929	Human	sec
C 749	14	12.5	3244	9	ACF16303	Human	sec	C 822	14	12.5	3244	9	ACF10613	ACF10613	Human	sec



C 823	14	12.5	3244	9	ACF34065	C 896	14	12.5	3244	9	ACF48421	ACf48421	Human	sec
C 824	14	12.5	3244	9	ACF45027	C 897	14	12.5	3244	9	ACF38370	ACf38370	Human	sec
C 825	14	12.5	3244	9	ACD90659	C 898	14	12.5	3244	9	ACF25306	ACf25306	Human	sec
C 826	14	12.5	3244	9	ACD91772	C 899	14	12.5	3244	9	ACF27206	ACf27206	Human	sec
C 827	14	12.5	3244	9	ACF30583	C 900	14	12.5	3244	9	ACF29662	ACf29662	Human	sec
C 828	14	12.5	3244	9	ACD87282	C 901	14	12.5	3244	9	ACD87896	ACd87896	Human	sec
C 829	14	12.5	3244	9	ACF60336	C 902	14	12.5	3244	9	ACF76357	ACf76357	Human	sec
C 830	14	12.5	3244	9	ACF46886	C 903	14	12.5	3244	9	ACF9649	ACf9649	Human	sec
C 831	14	12.5	3244	9	ACF75743	C 904	14	12.5	3244	9	ACF44106	ACf44106	Human	sec
C 832	14	12.5	3244	9	ADH80115	C 905	14	12.5	3244	9	ACH06451	ACH06451	Human	sec
C 833	14	12.5	3244	9	ACF17403	C 906	14	12.5	3244	9	ACH06758	ACH06758	Human	sec
C 834	14	12.5	3244	9	ACF23157	C 907	14	12.5	3244	9	ADA83640	ADa83640	CDNA	enco
C 835	14	12.5	3244	9	ACF08157	C 908	14	12.5	3244	9	ACG92814	ACg92814	Human	sec
C 836	14	12.5	3244	9	ACF08464	C 909	14	12.5	3244	9	ACG93428	ACg93428	Human	sec
C 837	14	12.5	3244	9	ACR40768	C 910	14	12.5	3244	9	ACF19473	ACf19473	Human	sec
C 838	14	12.5	3244	9	ACF53947	C 911	14	12.5	3244	9	ACD13164	ACd13164	Human	sec
C 839	14	12.5	3244	9	ACD47211	C 912	14	12.5	3244	9	ACF06622	ACf06622	Human	sec
C 840	14	12.5	3244	9	ACF48114	C 913	14	12.5	3244	9	ACG94656	ACG94656	Human	sec
C 841	14	12.5	3244	9	ACF47500	C 914	14	12.5	3244	9	ACG98084	ACg98084	Human	sec
C 842	14	12.5	3244	9	ACF46272	C 915	14	12.5	3244	9	ACC94349	ACC94349	Human	sec
C 843	14	12.5	3244	9	ACD86661	C 916	14	12.5	3244	9	ACF42303	ACf42303	Human	sec
C 844	14	12.5	3244	9	ACF52719	C 917	14	12.5	3244	9	ACD31209	ACd31209	Human	sec
C 845	14	12.5	3244	9	ACF53026	C 918	14	12.5	3244	9	ACD43238	ACd43238	Human	sec
C 846	14	12.5	3244	9	ACF65019	C 919	14	12.5	3244	9	ACD43545	ACd43545	CDNA	enco
C 847	14	12.5	3244	9	ACF76664	C 920	14	12.5	3244	9	ACF15075	ACf15075	Human	sec
C 848	14	12.5	3244	9	ACF61564	C 921	14	12.5	3244	9	ACF01807	ACf01807	Human	sec
C 849	14	12.5	3244	9	ACF61871	C 922	14	12.5	3244	9	ACF31879	ACf31879	Human	sec
C 850	14	12.5	3244	9	ACD30902	C 923	14	12.5	3244	9	ACD67556	ACd67556	Human	sec
C 851	14	12.5	3244	9	ACD31823	C 924	14	12.5	3244	9	ACD48746	ACd48746	Human	sec
C 852	14	12.5	3244	9	ACD32744	C 925	14	12.5	3244	9	ACD49053	ACd49053	Human	sec
C 853	14	12.5	3244	9	ACF17710	C 926	14	12.5	3244	9	ACF51491	ACf51491	Human	sec
C 854	14	12.5	3244	9	ACF07543	C 927	14	12.5	3244	9	ACF54254	ACf54254	Human	sec
C 855	14	12.5	3244	9	ACF20701	C 928	14	12.5	3244	9	ACF25978	ACf25978	Human	sec
C 856	14	12.5	3244	9	ACF21315	C 929	14	12.5	3244	9	ACF39291	ACf39291	Human	sec
C 857	14	12.5	3244	9	ACF21008	C 930	14	12.5	3244	9	ACF29048	ACf29048	Human	sec
C 858	14	12.5	3244	9	ACD47825	C 931	14	12.5	3244	9	ACD90965	ACd90965	Human	sec
C 859	14	12.5	3244	9	ACF47807	C 932	14	12.5	3244	9	ACD86668	ACd86668	Human	sec
C 860	14	12.5	3244	9	ACF53640	C 933	14	12.5	3244	9	ACH05530	ACH05530	CDNA	enco
C 861	14	12.5	3244	9	ACD86975	C 934	14	12.5	3244	9	ACF65326	ACf65326	Human	sec
C 862	14	12.5	3244	9	ACH05223	C 935	14	12.5	3244	9	ADB20683	ADb20683	Human	sec
C 863	14	12.5	3244	9	ACF44720	C 936	14	12.5	3244	9	ACF43799	ACf43799	Human	sec
C 864	14	12.5	3244	9	ADA81842	C 937	14	12.5	3244	9	ACH09269	ACH09269	Human	sec
C 865	14	12.5	3244	9	ACD23375	C 938	14	12.5	3244	9	ACH09576	ACH09576	Human	sec
C 866	14	12.5	3244	9	ACD24722	C 939	14	12.5	3244	9	ADA78935	ADa78935	Human	sec
C 867	14	12.5	3244	9	ACD39925	C 940	14	12.5	3244	9	ACF09999	ACf09999	Human	sec
C 868	14	12.5	3244	9	ACD40232	C 941	14	12.5	3244	9	ACF51184	ACf51184	Human	sec
C 869	14	12.5	3244	9	ACF13540	C 942	14	12.5	3244	9	ACF24078	ACf24078	Human	sec
C 870	14	12.5	3244	9	ACF03342	C 943	14	12.5	3244	9	ACD88510	ACd88510	Human	sec
C 871	14	12.5	3244	9	ACF78813	C 944	14	12.5	3244	9	ACH09883	ACH09883	Human	sec
C 872	14	12.5	3244	9	ACF11534	C 945	14	12.5	3244	9	ACH10804	ACH10804	Human	sec
C 873	14	12.5	3244	9	ACF50877	C 946	14	12.5	3244	9	ACD11611	ACd11611	Human	sec
C 874	14	12.5	3244	9	ACF34372	C 947	14	12.5	3244	9	ACC96661	ACC96661	Human	sec
C 875	14	12.5	3244	9	ACD46597	C 948	14	12.5	3244	9	ACC98691	ACC98691	Human	sec
C 876	14	12.5	3244	9	ACD48439	C 949	14	12.5	3244	9	ACF41996	ACf41996	Human	sec
C 877	14	12.5	3244	9	ACF27820	C 950	14	12.5	3244	9	ACF16917	ACf16917	Human	sec
C 878	14	12.5	3244	9	ACF24692	C 951	14	12.5	3244	9	ACD32437	ACd32437	Human	sec
C 879	14	12.5	3244	9	ACD85747	C 952	14	12.5	3244	9	ACD30595	ACd30595	Human	sec
C 880	14	12.5	3244	9	ACD90352	C 953	14	12.5	3244	9	ACD41466	ACd41466	Human	sec
C 881	14	12.5	3244	9	ACD83905	C 954	14	12.5	3244	9	ACF07850	ACf07850	Human	sec
C 882	14	12.5	3244	9	ACF49342	C 955	14	12.5	3244	9	ACF31265	ACf31265	Human	sec
C 883	14	12.5	3244	9	ACH07427	C 956	14	12.5	3244	9	ACF77585	ACf77585	Human	sec
C 884	14	12.5	3244	9	ACH07734	C 957	14	12.5	3244	9	ACF11227	ACf11227	Human	sec
C 885	14	12.5	3244	9	ACH08348	C 958	14	12.5	3244	9	ACF33107	ACf33107	Human	sec
C 886	14	12.5	3244	9	ACH11539	C 959	14	12.5	3244	9	ACF26285	ACf26285	Human	sec
C 887	14	12.5	3244	9	ACH11846	C 960	14	12.5	3244	9	ACD83598	ACd83598	Human	sec
C 888	14	12.5	3244	9	ACH10497	C 961	14	12.5	3244	9	ACF23771	ACf23771	Human	sec
C 889	14	12.5	3244	9	ACF01500	C 962	14	12.5	3244	9	ACF43195	ACf43195	Human	sec
C 890	14	12.5	3244	9	ACF41075	C 963	14	12.5	3244	9	ACF43492	ACf43492	Human	sec
C 891	14	12.5	3244	9	ACD24415	C 964	14	12.5	3244	9	ACH06144	ACH06144	CDNA	enco
C 892	14	12.5	3244	9	ACD31516	C 965	14	12.5	3244	9	ACH08962	ACH08962	Human	sec
C 893	14	12.5	3244	9	ACF18017	C 966	14	12.5	3244	9	ACC90556	ACC90556	Human	sec
C 894	14	12.5	3244	9	ACF32800	C 967	14	12.5	3244	9	ACF10920	ACf10920	Human	sec
C 895	14	12.5	3244	9	ACF40461	C 968	14	12.5	3244	9	ACC93735	ACC93735	Human	sec



c 969	14	12.5	3244	9	ACC6354	Human sec
c 970	14	12.5	3244	9	ACD25629	Human sec
c 971	14	12.5	3244	9	ACF02114	Human sec
c 972	14	12.5	3244	9	ACF22236	Human sec
c 973	14	12.5	3244	9	ACF22236	Human sec
c 974	14	12.5	3244	9	ACF09078	Human sec
c 975	14	12.5	3244	9	ACF33414	Human sec
c 976	14	12.5	3244	9	ACF54868	Human sec
c 977	14	12.5	3244	9	ACD48728	Human sec
c 978	14	12.5	3244	9	ACD47518	Human sec
c 979	14	12.5	3244	9	ACD49360	Human sec
c 980	14	12.5	3244	9	ACF38063	Human sec
c 981	14	12.5	3244	9	ACF30276	Human sec
c 982	14	12.5	3244	9	ACD87589	Human sec
c 983	14	12.5	3244	9	ACF62178	Human sec
c 984	14	12.5	3244	9	ACH11111	Human sec
c 985	14	12.5	3244	9	ACD10276	Human sec
c 986	14	12.5	3244	9	ACD17001	CDNA enco
c 987	14	12.5	3244	9	ACC99298	Human sec
c 988	14	12.5	3244	9	ACF00692	Human sec
c 989	14	12.5	3244	9	ACD41159	Human sec
c 990	14	12.5	3244	9	ACF14768	Human sec
c 991	14	12.5	3244	9	ACF22543	Human sec
c 992	14	12.5	3244	9	ACF79120	Human sec
c 993	14	12.5	3244	9	ACF11841	Human sec
c 994	14	12.5	3244	9	ACF51798	Human sec
c 995	14	12.5	3244	9	ACF33721	Human sec
c 996	14	12.5	3244	9	ACD49974	Human sec
c 997	14	12.5	3244	9	ACF37756	Human sec
c 998	14	12.5	3244	9	ACF28741	Human sec
c 999	14	12.5	3244	9	ACD88817	Human sec
c1000	14	12.5	3244	9	ACF75436	Human sec

## ALIGNMENTS

```

RESULT 1
ADR48527
ID   ADR48527 standard; DNA; 112 BP.
XX
XX   ADR48527;
AC
XX
DT   04-NOV-2004 (first entry)
XX
XX   capB target sequence #1.
DE
XX   Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM   pXOI; pXO2; target sequence; ds.
XX
XX   Bacillus anthracis.
OS
XX   WO2004070001-A2.
PN
XX   19-AUG-2004.
PD
XX   12-NOV-2003; 2003WO-US036240.
PF
XX   15-NOV-2002; 2002US-0426552P.
PR   16-MAY-2003; 2003US-0471082P.
XX
XX   (GENP-) GEN-PROBE INC.
PA
XX   Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
PI
XX   WPI; 2004-604428/58.
DR
XX   New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT   sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
XX   infections.
PS   Claim 1; SEQ ID NO 25; 61bp; English.
XX

```

```

CC   The present invention relates to an oligonucleotide of 20-40 nucleotides
CC   that specifically hybridizes to a sequence contained in a Bacillus
CC   anthracis target sequence. The methods and compositions of the present
CC   invention are useful for detecting the presence of Bacillus anthracis
CC   nucleic acid in a sample, in particular for detecting cutaneous and
CC   respiratory anthrax infections. Two synthetic genetic target sequences,
CC   derived from pagA and capB gene sequences, were synthesized to provide
CC   known standards for testing oligonucleotides for detection of the genes
CC   carried by the plasmids pXOI and pXO2, without requiring handling of
CC   virulent Bacillus anthracis. The present sequence represents a capB
CC   target sequence.
CC
SQ   Sequence 112 BP; 33 A; 20 C; 34 G; 25 T; 0 U; 0 Other;
XX
XX   Query Match      100.0%; Score 112; DB 13; Length 112;
XX   Best Local Similarity 100.0%; Pred. No. 2.4e-53;
XX   Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY   1 GGTACATCTGCGCAATGATATATTGGTTTACTGACGAGAGCAACCGATTACGCCGT 60
DB   1 GGTACATCTGCGCAATGATATATTGGTTTACTGACGAGAGCAACCGATTACGCCGT 60
OY   61 AAAGAGGTCTTAATATCGTGACGACGCGGTAGTTAAAGGCTGCTG 112
DB   61 AAAGAGGTCTTAATATCGTGACGACGCGGTAGTTAAAGGCTGCTG 112
RESULT 2
ADR48536
ID   ADR48536 standard; DNA; 560 BP.
XX
XX   ADR48536;
AC
XX
DT   04-NOV-2004 (first entry)
XX
XX   capB target sequence #3.
DE
XX   Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM   pXOI; pXO2; target sequence; ds.
XX
XX   Bacillus anthracis.
OS
XX   WO2004070001-A2.
PN
XX   19-AUG-2004.
PD
XX   12-NOV-2003; 2003WO-US036240.
PF
XX   15-NOV-2002; 2002US-0426552P.
PR   16-MAY-2003; 2003US-0471082P.
XX
XX   (GENP-) GEN-PROBE INC.
PA
XX   Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
PI
XX   WPI; 2004-604428/58.
DR
XX   New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT   sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
XX   infections.
PS   Claim 1; SEQ ID NO 34; 61bp; English.
XX
XX   The present invention relates to an oligonucleotide of 20-40 nucleotides
XX   that specifically hybridizes to a sequence contained in a Bacillus
XX   anthracis target sequence. The methods and compositions of the present
XX   invention are useful for detecting the presence of Bacillus anthracis
XX   nucleic acid in a sample, in particular for detecting cutaneous and
XX   respiratory anthrax infections. Two synthetic genetic target sequences,
XX   derived from pagA and capB gene sequences, were synthesized to provide
XX   known standards for testing oligonucleotides for detection of the genes
XX   carried by the plasmids pXOI and pXO2, without requiring handling of
XX   virulent Bacillus anthracis. The present sequence represents a capB
CC

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CC target sequence.

Sequence 560 BP; 181 A; 89 C; 131 G; 159 T; 0 U; 0 Other;

Query Match	100.0%	Score 112; DB 13;	Length 560;
Best Local Similarity	100.0%	Pred. No. 2.4e-53;	
Matches 112; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;

Dy  
1 GGTACACTCTGCGCCGAATGATATAATTGGTTTACTGCAGAGCAACCGATTAAAGCCCGT 60

Dd  
7 GGTAACAATCTGCGCAGCATGATATATTGGTTTACTGCAGAGCAACCGATTAAAGCCCGT 66

[illegible]

RESULT 3  
ACC71903  
ID ACC71903 standard; DNA; 32 BP.

AC ACC71903;

DT 04-AUG-2003 (first entry)

DE B. anthracis caps specific probe 1.

KM Encapsulation protein B; cagB; protective antigen; pagA; lethal factor,  
KM 1ef; fluorescence resonance energy transfer; FRET; probe; ss.

**Bacillus anthracis.**

PN EP1304387-A1.

PD 23-APR-2003.

PF 10-OCT-2002; 2002EP-00022398.

PR 15-OCT-2001; 2001US-0329826P.

XX

PA (MAYO-) MAYO FOUND MEDICAL EDUCATION &amp; RES.

PI Bell CA, Uh1 JR, Cockerill FR;

DR WPI; 2003-450920/43.

PT Detecting *Bacillus anthracis* in a sample by amplifying *B. anthracis* caps.  
PT pA<sub>1</sub> and left nucleic acids followed by hybridization with labelled caps.  
PT pA<sub>2</sub> and left probes, and detection by fluorescence resonance energy  
PT transfer.

PS Disclosure; Page 3; 31pp; English.

CC The invention relates to detecting *Bacillus anthracis* in a biological or  
CC non-biological sample. The method involves (a) amplifying a portion of *B.*  
CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA),  
CC and/or lethal factor (lef) nucleic acids using specific primers; (b)  
CC contacting the sample with a pair of capB and/or pagA and/or lef probes  
CC labelled with fluorescent moieties; and (c) detecting the presence or  
CC absence of fluorescence resonance energy transfer (FRET) between the  
CC probes. The method is useful for identifying *B. anthracis* DNA from  
CC specimens for diagnosis of *B. anthracis* infection and to identifying hoax  
CC cases of *B. anthracis*. The methods can also used for *B. anthracis*  
CC efficacy studies or epidemiology studies. The method is rapid, and allows  
CC real-time detection of *B. anthracis* in a biological sample or in a non-  
CC biological sample. The method is more sensitive and specific than  
CC existing assays. Sequences ACC11903-904 represent *B. anthracis* capB  
CC specific probes

SQ Sequence 32 BP; 11 A; 7 C; 7 G; 7 T; 0 U; 0 Other;

Query Match 28.6%; Score 32; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 7.3e-08;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy		47 CGATTAGCGCCGTAAGAAGGTCTAATATC	78
Db		1 CGATTAGCGCCGTAAGAAGGTCTAATATC	32

RESULT 4	
ACC71904	
ID	ACC71904 standard; DNA; 30 BP.

AC ACC71904;

DT 04-AUG-2003 (first entry)

DE B. anthracis capB specific probe 2.

KW Encapsulation protein B; capB; protective antigen; pagA; lethal factor;;

XX

XX

XX

XX

XX XX

PR 05-FEB-2002; 2002US-00068238.

PA (HOFF ) ROCHE DIAGNOSTICS GMBH.

XX

XX

PT Detecting *Bacillus anthracis* in a sample by amplifying *B. anthracis* caps  
PT pgs and left nucleic acids followed by hybridization with labelled caps  
PT pgs and left probes, and detection by fluorescence resonance energy  
PT transfer.

PS Disclosure; Page 3; 31pp; English

The invention relates to detecting *Bacillus anthracis* in a biological or non-biological sample. The method involves (a) amplifying a portion of *B. anthracis* encapsulation protein B (capB) and/or protective antigen (pagA) and/or lethal factor (lef) nucleic acids using specific primers; (b) contacting the sample with a pair of capB and/or pagA and/or lef probes labelled with fluorescent moieties; and (c) detecting the presence or absence of fluorescence resonance energy transfer (FRET) between the probes. The method is useful for identifying *B. anthracis* DNA from specimens for diagnosis of *B. anthracis* infection and to identifying hoax cases of *B. anthracis*. The methods can also be used for *B. anthracis* efficacy studies or epidemiology studies. The method is rapid, and allows real-time detection of *B. anthracis* in a biological sample or in a non-biological sample. The method is more sensitive and specific than existing assays. Sequences ACCT1903-904 represent *B. anthracis* capB specific probes

**SQ** Sequence 30 BP; 9 A; 4 C; 12 G; 5 T; 0 U; 0 Other;

Query Match	26.84;	Score 30;	DB 8;	length 30;
Best Local Similarity	100.04;	Pred. No. 1e-06;		
Matches 30;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```
QY      80 GTGACCAACGCAGCGTAGTTAAAGAGGCTG 109
      |||||
Dbb     1 GTGACCAACGCAGCGTAGTTAAAGAGGCTG 30
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RESULT 5
ADR48512/c
ID ADR48512 standard; DNA; 29 BP.
XX
AC ADR48512;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #2.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM pXO1; pXO2; probe; ss.
XX
OS Unidentified.
XX
PN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX
PR 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX
DR WPI; 2004-604428/58.
XX
XX WPI; 2004-604428/58.
XX
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
PS Claim 8; SEQ ID NO 10; 61bp; English.
XX
CC The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXO1 and pXO2, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pXO1 and pXO2 detection kits.
XX
SQ Sequence 29 BP; 6 A; 8 C; 6 G; 9 T; 0 U; 0 Other;
XX
Query Match 25.9%; Score 29; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 28 TTTACTGACGAGGACGACCGATTAGCG 56
DB 29 TTTACTGACGAGGACGACCGATTAGCG 1
XX
RESULT 6
ADR48513/c
ID ADR48513 standard; DNA; 29 BP.
XX
AC ADR48513;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #3.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM pXO1; pXO2; probe; ss.
XX

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OS Unidentified.
XX
PN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX
PR 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX
DR WPI; 2004-604428/58.
XX
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
PS Claim 8; SEQ ID NO 11; 61bp; English.
XX
CC The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXO1 and pXO2, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pXO1 and pXO2 detection kits.
XX
SQ Sequence 29 BP; 6 A; 8 C; 6 G; 9 T; 0 U; 0 Other;
XX
Query Match 25.9%; Score 29; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.7e-06;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 57 CCGTAAGAGAGGCTCTATATCGGTGAGC 85
DB 29 CCGTAAGAGAGGCTCTATATCGGTGAGC 1
XX
RESULT 7
ADR48514/c
ID ADR48514 standard; DNA; 27 BP.
XX
AC ADR48514;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #4.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM pXO1; pXO2; probe; ss.
XX
OS Unidentified.
XX
PN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX
PR 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX

```



```
XX WPI; 2004-604428/58.
DR
XX
XX New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
XX Claim 8; SEQ ID NO 12; 61bp; English.
XX
XX The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pX01 and pX02, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pX01 and pX02 detection kits.
XX
SQ Sequence 27 BP; 5 A; 10 C; 4 G; 8 T; 0 U; 0 Other;
Query Match 24.1%; Score 27; DB 13; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy 86 AACGACGGGTGTTAAAGAGCGCTGCTG 112
Db 27 AACGACGGGTGTTAAAGAGCGCTGCTG 1
RESULT 8
ID ADR48511/c
XX ADR48511;
XX
XX 04-NOV-2004 (first entry)
DT
XX capB probe #1.
DE
XX
XX Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM pX01; pX02; probe; ss.
XX
XX Unidentified.
OS
XX
XX WO2004070001-A2.
PN
XX
XX 19-AUG-2004.
PD
XX
XX 12-NOV-2003; 2003WO-US036240.
PF
XX
XX 15-NOV-2002; 2002US-0426552P.
PR
XX 16-MAY-2003; 2003US-0471082P.
PX
XX
XX (GENP-) GEN-PROBE INC.
PA
XX Norman SA, Bungo JU, Hogan JJ, Weisburg WG;
PI
XX WPI; 2004-604428/58.
DR
XX
XX New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
XX Claim 8; SEQ ID NO 9; 61bp; English.
XX
XX The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
```

```
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pX01 and pX02, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pX01 and pX02 detection kits.
XX
SQ Sequence 27 BP; 8 A; 8 C; 4 G; 7 T; 0 U; 0 Other;
Query Match 24.1%; Score 27; DB 13; Length 27;
Best Local Similarity 100.0%; Pred. No. 5.1e-05;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Dy 1 GGTACATCTGGCGAATGATATATTGG 27
Db 27 GGTACATCTGGCGAATGATATATTGG 1
RESULT 9
ID ACC71914
XX ACC71914;
XX
XX 04-AUG-2003 (first entry)
DT
XX
XX B. anthracis capB specific probe 4.
DE
XX
XX Encapsulation protein B; capB; protective antigen; pagA; lethal factor;
KM lef; fluorescence resonance energy transfer; FRET; probe; ss.
XX
XX Bacillus anthracis.
OS
XX
XX BP1304387-A1.
PN
XX
XX 23-APR-2003.
PD
XX
XX 10-OCT-2002; 2002EP-00022398.
PF
XX
XX 15-OCT-2001; 2001US-0329826P.
PR
XX 05-FEB-2002; 2002US-00068238.
PX
XX
XX (HOFF ) ROCHER DIAGNOSTICS GMBH.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Bell CA, Uhl JR, Cockerill FR;
PI
XX
XX WPI; 2003-450920/43.
DR
XX
XX Detecting Bacillus anthracis in a sample by amplifying B. anthracis capB,
PT pagA and lef nucleic acids followed by hybridization with labelled capB,
PT pagA and lef probes, and detection by fluorescence resonance energy
PT transfer.
XX
XX Disclosure; Page 3; 31bp; English.
PS
XX
XX The invention relates to detecting Bacillus anthracis in a biological or
CC non-biological sample. The method involves (a) amplifying a portion of B.
CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA)
CC and/or lethal factor (lef) nucleic acids using specific primers; (b)
CC contacting the sample with a pair of capB and/or pagA and/or lef probes
CC labelled with fluorescent moieties; and (c) detecting the presence or
CC absence of fluorescence resonance energy transfer (FRET) between the
CC probes. The method is useful for identifying B. anthracis DNA from
CC specimens for diagnosis of B. anthracis infection and to identifying hoax
CC cases of B. anthracis. The methods can also be used for B. anthracis
CC efficacy studies or epidemiology studies. The method is rapid, and allows
CC real-time detection of B. anthracis in a biological sample or in a non-
CC biological sample. The method is more sensitive and specific than
CC existing assays. Sequences ACC71913-914 represent B. anthracis capB
CC specific probes
XX
SQ Sequence 26 BP; 9 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
```



Query Match 23.2%; Score 26; DB 8; Length 26;  
 Best Local Similarity 100.0%; Pred. No. 0.00019;  
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 81 TGAGCAACGACGAGGTAAAGAG 106  
 DB 1 TGAGCAACGACGAGGTAAAGAG 26

RESULT 10  
 ACC71913  
 ID ACC71913 standard; DNA; 25 BP.  
 XX  
 AC ACC71913;  
 XX  
 DT 04-AUG-2003 (first entry)  
 XX  
 DE B. anthracis capB specific probe 3.  
 XX  
 KM Encapsulation protein B; capB; protective antigen; pagA; lethal factor;  
 KM left; fluorescence resonance energy transfer; FRET; probe; ss.  
 XX  
 OS Bacillus anthracis.  
 XX  
 PN BP1304387-A1.  
 XX  
 PD 23-APR-2003.  
 XX  
 PF 10-OCT-2002; 2002BP-00022398.  
 XX  
 PR 15-OCT-2001; 2001US-0329826P.  
 XX  
 PR 05-FEB-2002; 2002US-00068238.  
 XX  
 PA (HOPE) ROCHE DIAGNOSTICS GMBH.  
 PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
 XX  
 PI Bell CA, Uhl JR, Cockerill FR;  
 XX  
 DR WPI; 2003-450920/43.  
 XX  
 PT Detecting Bacillus anthracis in a sample by amplifying B. anthracis capB,  
 PT pagA and left nucleic acids followed by hybridization with labelled capB,  
 PT pagA and left probes, and detection by fluorescence resonance energy  
 PT transfer.  
 XX  
 PS Disclosure; Page 3; 31pp; English.  
 XX  
 CC The invention relates to detecting Bacillus anthracis in a biological or  
 CC non-biological sample. The method involves (a) amplifying a portion of B.  
 CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA)  
 CC and/or lethal factor (left) nucleic acids using specific primers; (b)  
 CC contacting the sample with a pair of capB and/or pagA and/or left probes  
 CC labelled with fluorescent moieties; and (c) detecting the presence or  
 CC absence of fluorescence resonance energy transfer (FRET) between the  
 CC probes. The method is useful for identifying B. anthracis DNA from  
 CC specimens for diagnosis of B. anthracis infection and to identifying hoax  
 CC cases of B. anthracis. The methods can also be used for B. anthracis  
 CC efficacy studies or epidemiology studies. The method is rapid, and allows  
 CC real-time detection of B. anthracis in a biological sample or in a non-  
 CC biological sample. The method is more sensitive and specific than  
 CC existing assays. Sequences ACC71913-914 represent B. anthracis capB  
 CC specific probes  
 CC  
 CC Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;

Query Match 22.3%; Score 25; DB 8; Length 25;  
 Best Local Similarity 100.0%; Pred. No. 0.00069;  
 Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 55 CGCCGTAAGAGTCTAATATCG 79  
 DB 1 CGCCGTAAGAGTCTAATATCG 25

RESULT 11  
 ADJ42339  
 ID ADJ42339 standard; cDNA; 1042 BP.  
 XX  
 AC ADJ42339;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 DE Plant cDNA #3339.  
 XX  
 KM Plant; gene; ss; transcription; plant genome augmentation; cereal;  
 KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;  
 KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;  
 KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;  
 KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;  
 KM antifungal.  
 XX  
 OS Eukaryota.  
 XX  
 PN US2004016025-A1.  
 XX  
 PD 22-JAN-2004.  
 XX  
 PF 26-SEP-2002; 2002US-00260238.  
 XX  
 PR 26-SEP-2001; 2001US-0325277P.  
 XX  
 PR 26-SEP-2001; 2001US-0325448P.  
 XX  
 PR 04-APR-2002; 2002US-0370620P.  
 XX  
 PA (BUDW) BUDWORTH P.  
 PA (MOUG) MOUGHAMER T.  
 PA (BRIG) BRIGGS S P.  
 PA (COOP) COOPER B.  
 PA (GLAZ) GLAZEBROOK J.  
 PA (GOFF) GOFF S A.  
 PA (KATA) KATAGIRI F.  
 PA (KREP) KREPS J.  
 PA (PROV) PROVART N.  
 PA (RICK) RICHE D.  
 PA (ZHUT) ZHU T.  
 XX  
 PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;  
 PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;  
 XX  
 DR WPI; 2004-190374/18.  
 XX  
 CC New rice promoter, useful for manipulating crop plants to alter or  
 CC improve phenotypic characteristics, e.g. produce large quantities of oil  
 CC or proteins, resistance to insecticides, virus or fungi, stress tolerance  
 CC or high nutritional value.  
 XX  
 PS Example 13; SEQ ID NO 3339; 230pp; English.  
 XX  
 CC The invention relates to plant nucleotide sequences that direct seed-  
 CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential  
 CC or constitutive transcription of an operatively linked nucleic acid  
 CC segment. The invention also relates to a method for augmenting a plant  
 CC genome and a method of identifying a gene, where its expression is  
 CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
 CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
 CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
 CC sorghum, rice or wheat. The polynucleotides and the polypeptides they  
 CC encode are useful for manipulating crop plants to alter or improve  
 CC phenotypic characteristics, to produce large quantities of oil or  
 CC proteins, to incur resistance to insecticides, viruses or fungi, and to  
 CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
 CC have a high nutritional value with reduced apical dominance or dwarfism,  
 CC early flowering or altered metabolic pathways. This sequence represents a  
 CC plant nucleic acid of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification but was obtained in  
 CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.



XX SQ Sequence 1042 BP; 261 A; 270 C; 269 G; 242 T; 0 U; 0 Other;  
Query Match 16.1%; Score 18; DB 12; Length 1042;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 78 CGGTGACGACGACGGT 95  
DB 586 CGGTGACGACGACGGT 603  
RESULT 12  
ADX09767  
ID ADX09767 standard; cDNA; 855 BP.  
AC ADX09767;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 4342.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
FN US200403488-A1.  
XX  
PD 19-FEB-2004.  
XX  
PE 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 4342; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake

CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.  
XX  
SQ Sequence 855 BP; 205 A; 256 C; 218 G; 176 T; 0 U; 0 Other;  
Query Match 15.2%; Score 17; DB 13; Length 855;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 32 CTGACGAGACGACCG 48  
DB 613 CTGACGAGACGACCG 629  
RESULT 13  
ADX30084  
ID ADX30084 standard; cDNA; 973 BP.  
AC ADX30084;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 12904.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
FN US200403488-A1.  
XX  
PD 19-FEB-2004.  
XX  
PE 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITUJ/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAOY/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 12904; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?DocID:200403488. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in



CC	ftp.segdata.uspcio.gov/sequence.html?DocID=200403488. The polynucleotide
CC	of the invention are also useful in physical arrays of molecules and as
CC	plant breeding markers. The recombinant DNA construct is useful for
CC	improving plant tolerance to cold, heat, drought, herbicides, extreme
CC	osmotic conditions, pathogens or pests, for manipulating growth rate in
CC	plant cells by modification of the cell cycle pathway, for conferring
CC	increased resistance to plant disease, for producing galactomanan,
CC	lignin or plant growth regulators, for increasing the rate of homologous
CC	recombination in plants, for improving yield by modification of
CC	photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake
CC	or by providing improved plant growth and development under at least one
CC	stress condition or for modifying seed oil or protein yield and/or
CC	content. This sequence represents a plant full length insert
CC	polynucleotide that can be used in the recombinant DNA construct of the
CC	invention.
SQ	Sequence 974 BP; 241 A; 285 C; 241 G; 207 T; 0 U; 0 Other;
Query Match	15.2%; Score 17; DB 13; Length 974;
Best Local Similarity	100.0%; Pred. NO. 25;
Matches 17; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
Oy	32 CTGACGAGCAGCAACC 48       610 CTGACGAGCAGCAACC 626
Dd	
RESULT 15	
ID	AAAX10983 standard; DNA; 225 BP.
XX	AAAX10983;
XX	30-MAR-1999 (first entry)
DE	Human biallelic polymorphic DNA fragment WI-7461.
KW	Polymorphism; biallelic; human; forensic; paternity testing; disease;
KM	detection; phenotypic typing; characteristic; infection; hereditary;
KW	autoimmune disease; cancer; inflammation; drug; therapy; medicament;
KM	treatment; marker; ss.
OS	Homo sapiens.
PN	WO9820165-A2.
PD	14-MAY-1998.
PF	05-NOV-1997; 97MO-USO20313.
PR	06-NOV-1996; 96US-0030455P.
PA	(MHED ) WHITEHEAD INST BIOMEDICAL RES.
PI	Lander ES, Wang D, Hudson T;
Pt	WPI; 1998-286974/25.
PT	New isolated nucleic acid segments from the human genome - used for
PT	determining polymorphic forms for use in e.g. forensics, paternity
PT	testing or phenotypic typing for disease.
PS	Claim 1, Page 103; 310pp; English.
XX	
CC	AAAX10269-XI2937 are human DNA fragments which contain biallelic
CC	polymorphic markers which have been isolated using the primers
CC	represented in AAAX09121-XI0268. The base occupying the polymorphic site
CC	is indicated by the appropriate IUPAC-IUB ambiguity code. These fragments
CC	can be used in methods for determining polymorphic forms in an individual
CC	for use in e.g. forensics, paternity testing or for phenotypic typing for
CC	diseases such as agammaglobulinemia, diabetes insipidus, Lesch-Nyman
CC	syndrom, muscular dystrophy, Wiskott-Aldrich syndrome, Fabry's disease,
CC	familial hypercholesterolemia, polycystic kidney disease, hereditary



CC spherocytosis, von Willebrand's disease, tuberous sclerosis, hereditary  
CC haemorrhagic telangiectasia, familial colonic polyposis, Ehlers-Danlos  
CC syndrome, osteogenesis imperfecta, acute intermittent porphyria,  
CC autoimmune diseases, inflammation, cancer, diseases of the nervous  
CC system, infection by pathogenic microorganisms, and characteristics such  
CC as longevity, appearance (e.g. baldness, obesity), strength, speed,  
CC endurance, fertility, and susceptibility or receptivity to particular  
CC drugs or therapeutic treatments. The isolated polymorphic nucleic acid  
CC segments can also be used to produce medicaments for the treatment or  
CC prophylaxis of such diseases  
XX  
SQ Sequence 225 BP; 51 A; 61 C; 58 G; 54 T; 0 U; 1 Other;  
XX  
Query Match 14.3%; Score 16; DB 2; Length 225;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 95 TAGTTAAAGAGGCTGC 110  
|||  
46 TAGTTAAAGAGGCTGC 61  
Db  
RESULT 16  
ABZ08502  
ID ABZ08502 standard; cDNA; 434 BP.  
XX  
AC ABZ08502;  
XX  
DT 09-JAN-2003 (first entry)  
XX  
DE Human leukocyte derived cDNA SEQ ID NO 8493.  
XX  
KW Human; leukocyte; gene expression profiling; allograft rejection;  
KW atherosclerosis; congestive heart failure; systemic lupus erythematosus;  
KW rheumatoid arthritis; osteoarthritis; cytomegalovirus; infection; gene;  
KW ss.  
XX  
OS Homo sapiens.  
XX  
FN WO200257414-A2.  
XX  
PD 25-JUL-2002.  
XX  
PE 22-OCT-2001; 2001WO-US047856.  
XX  
PR 20-OCT-2000; 2000US-0241994P.  
PR 08-JUN-2001; 2001US-0296764P.  
XX  
PA (BIOC-) BIOCARDIA INC.  
PI Wohlgemuth J, Fry K, Matcuk G, Altman P, Prentice J, Phillips J;  
PI Ly N, Woodward R, Quertemous T, Johnson F;  
XX  
DR WPI; 2002-636525/68.  
XX  
PT New system for leukocyte expression profiling, diagnosing a disease, or  
PT monitoring (the rate of) progression of a disease, e.g. atherosclerosis  
PT or congestive heart failure, comprises diagnostic oligonucleotides.  
XX  
PS Claim 26; Page 1927-1928; 0pp; English.  
XX  
CC The invention relates to a system for detecting gene expression, which  
CC comprises one or two isolated DNA molecules that detect expression of a  
CC gene, where the gene corresponds to any of 8143 oligonucleotides  
CC (ABZ00010-ABZ08152) each having 50 base pairs (bp). The system is useful  
CC for leukocyte expression profiling. It is particularly useful for  
CC diagnosing a disease, monitoring (rate of) progression of a disease,  
CC predicting therapeutic outcome, determining prognosis for a patient,  
CC predicting disease complications in an individual or monitoring response  
CC to treatment in an individual. The diseases include cardiac allograft  
CC rejection, kidney allograft rejection, liver allograft rejection,  
CC atherosclerosis, congestive heart failure, systemic lupus erythematosus,  
CC rheumatoid arthritis, osteoarthritis or cytomegalovirus infection. The

CC present sequence is that of a human leukocyte expressed cDNA of the  
CC invention  
XX  
SQ Sequence 434 BP; 107 A; 85 C; 74 G; 168 T; 0 U; 0 Other;  
XX  
Query Match 14.3%; Score 16; DB 6; Length 434;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 16 ATGATATATTGGTTTA 31  
|||  
Db 378 ATGATATATTGGTTTA 393  
XX  
RESULT 17  
ACN88034/c  
ID ACN88034 standard; DNA; 526 BP.  
XX  
AC ACN88034;  
XX  
DT 02-DEC-2004 (first entry)  
XX  
DE Breast cancer related marker, seq id 9184.  
XX  
KW Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
XX  
OS Homo sapiens.  
XX  
FN US2003099974-A1.  
XX  
PD 29-MAY-2003.  
XX  
PE 18-JUN-2002; 2002US-00198846.  
XX  
PR 18-JUN-2001; 2001US-0306220P.  
XX  
PA (MILL-) MILLENNIUM PHARM INC.  
PI Lillie J, Xu Y, Wang Y, Steinmann K;  
XX  
DR WPI; 2003-787014/74.  
XX  
PT Novel isolated polypeptide associated with breast cancer, useful for  
PT detecting presence of polypeptide in sample, as a marker for breast  
PT cancer.  
XX  
PS Disclosure; SEQ ID NO 9184; 36pp; English.  
XX  
CC The invention relates to an isolated polypeptide (I) associated with  
CC breast cancer which is encoded by a nucleic acid molecule comprising a  
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to  
CC the polypeptide of the invention. The activity of the polypeptide of the  
CC invention may be described as cytostatic. The antibody is useful for  
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
CC invention are useful in the detection of breast tumours. (I) is useful as  
CC a marker for breast cancer and in breast cancer therapy. Sequences given  
CC in records ACN78851-ACN92934 represent nucleic acid markers associated  
CC with breast cancer. Note: The sequence listing does not form part of the  
CC specification but may be obtained in electronic format from the USPTO web  
CC site at [seqdata.uspto.gov/sequence.html?DocID=2003099974](http://seqdata.uspto.gov/sequence.html?DocID=2003099974)  
XX  
SQ Sequence 526 BP; 160 A; 102 C; 112 G; 143 T; 0 U; 9 Other;  
XX  
Query Match 14.3%; Score 16; DB 11; Length 526;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 15 AATGATATATTGGTTT 30  
|||  
Db 520 AATGATATATTGGTTT 505  
XX  
RESULT 18



ADT90536/C  
 ID ADT90536 standard; DNA; 543 BP.  
 XX  
 AC ADT90536;  
 XX  
 DT 13-JAN-2005 (first entry)  
 XX  
 DE Human gene over-expressed in a cancerous cell, SEQ ID 649.  
 XX  
 KW cancer; detection; pre-cancerous; antineoplastic; cancer therapy;  
 KM cytosolic; gene therapy; gene; da.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2004091548-A2.  
 XX  
 PD 28-OCT-2004.  
 XX  
 PF 15-APR-2004; 2004WO-US009289.  
 XX  
 PR 15-APR-2003; 2003US-0462895P.  
 XX  
 PA (AVAL-) AVALON PHARM INC.  
 XX  
 PI Stovel JW, Cain CB, Horrigan SK, Augustus M;  
 DR WPI; 2004-784489/77.  
 XX  
 PT Diagnosing cancer in a mammal comprises determining amplification of  
 PT specific genes, e.g., serine/threonine kinase 6, in the genome of a  
 PT mammal.  
 XX  
 PS Claim 3; SEQ ID NO 649; 92bp; English.  
 XX  
 CC The invention relates to a novel method for diagnosing cancer in a  
 CC mammal. The method comprises determining amplification of specific genes,  
 CC given in the specification, in the genome of a mammal. The invention  
 CC further comprises methods for: diagnosing cancer or a pre-cancerous  
 CC condition in a mammal; inhibiting cancer or a pre-cancerous condition in  
 CC a mammalian cell; identifying an agent having therapeutic activity in a  
 CC human patient; identifying an anti-neoplastic agent; determining the  
 CC cancerous status of a cell; identifying a compound as an anti-neoplastic  
 CC agent; treating cancer; monitoring the progress of cancer therapy in a  
 CC patient; determining the likelihood of success of cancer therapy in a  
 CC patient; producing test data with respect to the anti-neoplastic activity  
 CC of a compound; and determining the progress of a treatment for cancer in  
 CC a patient following commencement of a cancer treatment on the patient.  
 CC The methods and compositions of the invention have cytostatic activity  
 CC and may be used in gene therapy. The method is useful in diagnosing or  
 CC treating cancer in a mammal. This polynucleotide sequence represents a  
 CC gene over-expressed in a cancerous cell, used in the novel cancer  
 CC diagnosis method of the invention.  
 CC  
 XX  
 SQ Sequence 543 BP; 207 A; 99 C; 73 G; 164 T; 0 U; 0 Other;  
 QY  
 Query Match 14.3%; Score 16; DB 13; Length 543;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 15 AATGATATATGTTT 30  
 125 AATGATATATGTTT 110  
 RESULT 19  
 ADU12685  
 ID ADU12685 standard; DNA; 564 BP.  
 XX  
 AC ADU12685;  
 XX  
 DT 27-JAN-2005 (first entry)  
 XX  
 DE Solid tumour prognosis gene seqid 3124.

XX  
 KW cytosolic; gene therapy; expression profile; solid tumour;  
 KM peripheral blood mononuclear cell; PBMC; prognosis; da.  
 XX  
 OS unidentified.  
 XX  
 FN WO2004097052-A2.  
 XX  
 PD 11-NOV-2004.  
 XX  
 PF 29-APR-2004; 2004WO-US013587.  
 XX  
 PR 29-APR-2003; 2003US-0466067P.  
 XX  
 PR 23-JAN-2004; 2004US-0538246P.  
 XX  
 PA (AMHP) WYETH.  
 PA (STRA) STRAHS A.  
 XX  
 PI Strahs A, Trepicchio WL, Burczynski ME, Twine NC, Slonim DK;  
 PI Immerman F, Dörner AJ;  
 DR WPI; 2004-804779/79.  
 XX  
 PT A method, useful for prognosing and treating solid tumor, comprises  
 PT comparing an expression profile of a gene expressed in peripheral blood  
 PT mononuclear cells to a reference expression profile of a gene.  
 XX  
 PS Disclosure; Page; 11pp; English.  
 XX  
 CC The invention describes a method comprising comparing an expression  
 CC profile of at least one gene in a peripheral blood sample of a patient to  
 CC at least one reference expression profile of the at least one gene, where  
 CC the patient has a solid tumour, and each of the gene is differentially  
 CC expressed in peripheral blood mononuclear cells (PBMCs) of a first class  
 CC of patients as compared to PBMCs of a second class of patients, where  
 CC both the first and second classes of patients have the solid tumour, and  
 CC each of the first and second classes is a subcluster formed by an  
 CC unsupervised clustering analysis of gene expression profiles in PBMCs of  
 CC a population of patients who have the solid tumour, and where the  
 CC majority of the first class of patients has a first clinical outcome, and  
 CC the majority of the second class of patients has a second clinical  
 CC outcome. Also described are: a system comprising (i) a memory of a  
 CC storage medium including data that represent an expression profile of at  
 CC least one gene in a peripheral blood sample of a patient who has a solid  
 CC tumour, (ii) at least another storage medium including data that  
 CC represent at least one reference expression profile of the gene, (iii) a  
 CC program capable of comparing the expression profile to the reference  
 CC expression profile, and (iv) a processor capable of executing the  
 CC program, where expression levels of the gene in peripheral blood  
 CC mononuclear cells of patients who have the solid tumour correlate with  
 CC clinical outcomes of the patients; and a nucleic acid or protein array  
 CC comprising concentrated probes for solid tumour prognosis genes, where  
 CC PBMCs of a first class of patients as compared to PBMCs of a second class  
 CC of patients, where both the first and second classes of patients have a  
 CC solid tumour, and where the first class of patients has a first clinical  
 CC outcome, and the second class of patients has a second clinical outcome.  
 CC The method, system, and array are useful for prognosing and treating  
 CC solid tumours. This sequence represents a solid tumour prognosis gene of  
 CC the invention. Note: The sequence data for this patent did not form part  
 CC of the printed specification, but was obtained in electronic format  
 CC directly from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
 CC  
 XX  
 SQ Sequence 564 BP; 148 A; 63 C; 93 G; 195 T; 0 U; 65 Other;  
 QY  
 Query Match 14.3%; Score 16; DB 13; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 DB 15 AATGATATATGTTT 30  
 450 AATGATATATGTTT 465



RESULT 20  
 ADX16743  
 ID ADX16743 standard; DNA; 564 BP.  
 AC ADX16743;  
 XX  
 XX  
 DT 05-MAY-2005 (first entry)  
 XX  
 XX  
 DE Human cancer marker gene Seq 99.  
 KM  
 KM cancer; diagnosis; colorectal tumor; gene expression; cytostatic;  
 KM tumor marker; ds.  
 XX  
 XX Homo sapiens.  
 OS  
 OS  
 PN WO2005015236-A2.  
 PD  
 PD 17-FEB-2005.  
 PF  
 PF 16-JUL-2004; 2004WO-EP007936.  
 PR  
 PR 18-JUL-2003; 2003EP-00015667.  
 PR 22-SEP-2003; 2003EP-00021130.  
 XX  
 PA (HOFF ) ROCHE DIAGNOSTICS GMBH.  
 PA (HOFF ) HOFFMANN LA ROCHE & CO AG F.  
 PI  
 PI Rueger R, Auer J, Portsmann B, Werner M, Wiese A;  
 DR WPI; 2005-163311/17.  
 XX  
 PT Evaluating the progression of cancer of a patient who is afflicted with  
 PT an adenocarcinoma comprises comparing the levels of expression of one or  
 PT several marker genes in both patient and control samples.  
 PS  
 PS Claim 1; SEQ ID NO 99; 334bp; English.  
 XX  
 XX This invention relates to a novel method for evaluating the progression  
 CC of cancer in a patient afflicted with an adenocarcinoma. Specifically, it  
 CC refers to a method that compares the levels of expression of one or  
 CC several marker genes given in the specification in both a patient sample  
 CC and a sample from a control subject afflicted with an adenocarcinoma  
 CC which did not recur within 5 years following surgical removal of the  
 CC tumor. The present invention describes that a significant difference  
 CC between the expression levels of the marker genes in both samples is an  
 CC indication that the patient carries the risk of cancer progression.  
 CC Accordingly, it further provides methods useful in the preparation of  
 CC drug compositions used for the inhibition of adenocarcinomas and in  
 CC particular for the treatment of colorectal cancer. As such, these  
 CC compositions exhibit cytostatic activity. This polynucleotide sequence is  
 CC a human marker gene used to evaluate cancer progression, given in an  
 CC exemplification of the invention.  
 XX  
 SO Sequence 564 BP; 148 A; 63 C; 93 G; 195 T; 0 U; 65 Other;  
 Query Match 14.3%; Score 16; DB 14; Length 564;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 15 AATGATATATTGGTTT 30  
 Db 450 AATGATATATTGGTTT 465

RESULT 21  
 ACH80230  
 ID ACH80230 standard; DNA; 569 BP.  
 AC ACH80230;  
 XX  
 XX  
 DT 29-JUL-2004 (first entry)  
 XX

DE Human genome derived single exon probe #13425.  
 XX  
 KM Human; probe; ss; gene expression; single exon probe; microarray;  
 KM alternative splicing event; genomic alteration.  
 XX  
 XX Homo sapiens.  
 OS  
 OS  
 PN US2003194704-A1.  
 PD  
 PD 16-OCT-2003.  
 PF  
 PF 03-APR-2002; 2002US-00029386.  
 PR  
 PR 03-APR-2002; 2002US-00029386.  
 XX  
 XX  
 PA (PENN/) PENN S G.  
 PA (RANK/) RANK D R.  
 PA (HANZ/) HANZEL D K.  
 XX  
 XX  
 PI Penn SG, Rank DR, Hanzel DK;  
 DR WPI; 2004-119264/12.  
 XX  
 XX  
 PT New human genome-derived single exon nucleic acid probes useful for human  
 PT gene expression analysis, for identifying or characterizing alternative  
 PT splicing events, for assessing genomic alterations or as tools for  
 PT surveying tissues.  
 PS  
 PS Claim 15; SEQ ID NO 13425; 80bp; English.  
 XX  
 XX The invention relates to a nucleic acid probe for measuring human gene  
 CC expression, comprising any of the 27,400 fully defined nucleotide  
 CC sequences in the specification, or their complements or fragments, and  
 CC encoding at least 8 amino acids of any of the 688 amino acid sequences  
 CC fully defined in the specification. The probe is a single exon probe that  
 CC hybridises under high stringency conditions to a nucleic acid molecule  
 CC expressed in human cells or tissues. Also included are a spatially-  
 CC addressable set of single exon nucleic acid probes for measuring human  
 CC gene expression (comprising a plurality of single exon nucleic acid  
 CC probes cited above, where each of the plurality of probes is separately  
 CC and addressably isolatable or amplifiable from the plurality), a single  
 CC exon microarray for measuring human gene expression, a method of  
 CC measuring human gene expression, a vector comprising the single exon  
 CC probe cited above, an ORF-encoded peptide comprising at least 8  
 CC contiguous amino acids of any of the above-mentioned amino acid  
 CC sequences (optionally with conservative amino acid substitutions), an  
 CC isolated antibody that binds specifically to a peptide cited above,  
 CC methods of selling and/or licensing single exon probes or microarrays to  
 CC a customer desiring to measure gene expression, a method of providing  
 CC human gene expression data by subcription, and a computer-readable  
 CC storage medium which contains a database having a plurality of records  
 CC (each record including data on the expression of a single exon probe  
 CC cited above. The probe, methods and apparatus are useful in gene  
 CC expression analysis. The probes may be used as tools for surveying  
 CC tissues to detect the presence of expressed messages that contain their  
 CC specific exon, or in constructing genome-derived single exon microarrays.  
 CC In addition, the probes are used in identifying and characterising  
 CC alternative splicing events, in detecting and characterising gross  
 CC alterations in the genomic locus that includes their exon, in assessing  
 CC smaller genomic alterations, in priming the synthesis of nucleic acids,  
 CC or in expressing the ORF-encoded peptide. The present sequence is a human  
 CC single exon probe of the invention. Note: The sequence data for this  
 CC patent did not form part of the printed specification, but was obtained  
 CC in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?docID=20030194704  
 XX  
 SO Sequence 569 BP; 185 A; 112 C; 84 G; 188 T; 0 U; 0 Other;  
 Query Match 14.3%; Score 16; DB 12; Length 569;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 93 GGTAGTTAAAGAGGCT 108



Db 95 GGTAGTTAAAGAGCT 110  
|||||  
RESULT 22  
ACN60627  
ID ACN60627 standard; cDNA; 608 BP.  
XX  
AC ACN60627;  
DT 02-DEC-2004 (first entry)  
XX  
DE Cotton gymnocium tissue EST Clone ID: LIB3829-025-Q6-K6-H10, SEQ:15408.  
XX  
KM Cotton; plant; EST; expressed sequence tag; transgenic plant; gymnocium;  
KM variety Nucleon33B; library LIB3829; molecular tag; molecular marker;  
KM genetic mapping; molecular mapping; seed germination; plant growth;  
KM plant quality; plant yield; plant breeding; tissue printing; ss.  
XX  
OS Gossypium hirsutum.  
XX  
PN US2004123340-A1.  
XX  
PD 24-JUN-2004.  
XX  
PF 12-DEC-2001; 2001US-00021323.  
XX  
PR 14-DEC-2000; 2000US-0255619P.  
XX  
PA (DEIK/) DEIKMAN J.  
PA (FENG/) FENG P C C.  
PA (FINC/) FINCHER K L.  
PA (ZIEG/) ZIEGLER T E.  
XX  
PI Delkman J, Feng PCC, Fincher KL, Ziegler TE;  
XX  
DR WPI; 2004-479808/45.  
XX  
PT New isolated nucleic acid molecule that encodes a plant protein or its  
PT fragment, useful for isolating a variety of agronomically significant  
PT genes associated with plant growth, quality or yield, and as molecular  
PT tags to map genes.  
XX  
PS Claim 1; SEQ ID NO 15408; 34pp; English.  
XX  
CC The invention relates to 17880 cotton expressed sequence tags (ESTs;  
CC ACN45220-ACN63099). The ESTs were isolated from cDNA libraries generated  
CC from primed or non-primed seeds from variety DP50B, mature seeds from  
CC variety Coker 312 Boswell 96 Field, and androecium tissue, gymnocium  
CC tissue, developing fibres, carpel walls and sepra from variety  
CC Nucleon33B. The invention also relates to substantially purified  
CC proteins or their fragments encoded by nucleic acid molecules of the  
CC invention, and to transformed plants having a nucleic acid construct  
CC comprising a nucleic acid of the invention. The cotton ESTs are useful as  
CC molecular tags to isolate genetic regions, to isolate genes, to map  
CC genes, to determine gene function and to determining whether genes are  
CC members of a particular gene family. The nucleic acid molecules may be  
CC used for isolating a variety of agronomically significant genes  
CC associated with plant growth, quality, yield, and could also serve as  
CC links in metabolic and catabolic pathways. The nucleic acid molecules are  
CC also useful for identifying genes important in initiating and maintaining  
CC seed germination or that may be used to mitigate stresses encountered  
CC during seed germination. The ESTs additionally enable the acquisition of  
CC promoters and cis-regulatory elements which will be useful to express  
CC agronomically significant genes in these tissues and/or other tissues,  
CC and also permits the acquisition of molecular markers useful in breeding  
CC schemes, genetic and molecular mapping, and in cloning of agronomically  
CC significant genes. The nucleic acid molecules are further useful for  
CC detecting the expression level or pattern of a protein or mRNA and for  
CC detecting the presence or quantity of a protein by tissue printing. The  
CC present sequence represents a specifically claimed EST isolated from a  
CC cotton variety Nucleon33B gymnocium tissue cDNA library (LIB3829). The  
CC sequence data for this patent did not form part of the printed

CC specification, but was obtained in electronic format directly from the US  
CC patent office at [seqdata.uspto.gov/sequence.html?docID=US20040123340](http://seqdata.uspto.gov/sequence.html?docID=US20040123340)  
XX  
SQ Sequence 608 BP; 184 A; 93 C; 167 G; 164 T; 0 U; 0 Other;  
Query Match 14.3%; Score 16; DB 13; Length 608;  
Best local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 95 AGTTAAAGAGCTGCT 111  
Db 206 AGTTAAAGAGCTGCT 221  
|||||  
RESULT 23  
ADG32998  
ID ADG32998 standard; DNA; 814 BP.  
XX  
AC ADG32998;  
XX  
DT 26-FEB-2004 (first entry)  
XX  
DE Human DNA differentially expressed in patients with SLE SeqID322.  
XX  
KM human; ds; autoimmune; chronic inflammatory disease; SLE;  
XX systemic lupus erythematosus; rheumatoid arthritis; cholecystitis;  
KM Sjogren's disease; CREST syndrome; scleroderma; ankylosing spondylitis;  
KM ulcerative colitis; primary biliary sclerosing cholangitis; appendicitis;  
KM diverticulitis; primary biliary sclerosis.  
XX  
OS Homo sapiens.  
XX  
PN WO2003090694-A2.  
XX  
PD 06-NOV-2003.  
XX  
PF 24-APR-2003; 2003WO-US013015.  
XX  
PR 24-APR-2002; 2002US-00131827.  
XX  
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.  
XX  
PI Wohlgemuth J, Fry K, Woodward R, Ly N;  
XX  
DR WPI; 2003-877243/81.  
XX  
PT Diagnosing or monitoring autoimmune and chronic inflammatory diseases,  
PT such as rheumatoid arthritis, systemic lupus erythematosus, ulcerative  
PT colitis, psoriasis and asthma by detecting the expression level of one or  
PT more genes.  
XX  
PS Claim 18; SEQ ID NO 322; 877pp; English.  
XX  
CC This invention relates to novel methods for diagnosing and monitoring  
CC autoimmune and chronic inflammatory diseases. Specifically, it refers to  
CC the identification of genes that have a clinical utility as diagnostic  
CC tools for the management of, in particular, patients with systemic lupus  
CC erythematosus (SLE) or rheumatoid arthritis (RA). Accordingly, the  
CC present invention describes a method for determining the levels of  
CC multiple differentially expressed genes of a patient, in a concerted  
CC manner, in order to achieve an improved diagnostic assay with sensitivity  
CC and specificity for the disease in question. As such, these genes are  
CC useful for the diagnosis of various other inflammatory disorders  
CC including cholecystitis, Sjogren's disease, CREST syndrome, scleroderma,  
CC ankylosing spondylitis, ulcerative colitis, primary biliary sclerosing  
CC cholangitis, appendicitis, diverticulitis, and primary biliary sclerosing  
CC This polynucleotide is a DNA sequence representing human mRNA that is  
CC differentially expressed in patients with SLE, used in an exemplification  
CC of the invention.  
XX  
SQ Sequence 814 BP; 246 A; 141 C; 141 G; 286 T; 0 U; 0 Other;  
Query Match 14.3%; Score 16; DB 10; Length 814;



Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATTGTTT 30  
Db 170 AATGATATATTGTTT 185

## RESULT 24

ADRO1833  
ID ADRO1833 standard; DNA; 825 BP.

XX  
AC ADRO1833;

DT 23-SEP-2004 (first entry)

DE A. gossypii genomic DNA PAC1368RP.

XX  
KW Filamentous fungi; ds; forensic identification; gene characterisation;

XX  
KW intergenomic comparison; chromosome mapping.

OS Bremothecium gossypii.

PN US6239264-B1.

PD 29-MAY-2001.

PF 24-DEC-1997; 97US-00998416.

PR 31-DEC-1996; 97CH-000000016.

PA (SYNG-) SYNGENTA PARTICIPATIONS AG.

PI Philippsen P, Poehlmann R, Steiner-Lange S, Mohr C, Wendland J;  
PI Knechtle P, Reibischung C;

DR WPI; 1998-388120/33.

PT New gene for adenylate cyclase from *Ashbya gossypii* - useful for  
PT generating recombinant microorganisms with alteration in gene of cAMP-  
PT dependent signalling pathway for increasing production of fine chemicals.

PS Example 3; SEQ ID NO 525; 632pp; English.

XX The invention relates to isolated DNA molecules comprising isolated  
CC genomic DNA sequences from the filamentous fungi *Ashbya gossypii*, the  
CC sequences comprising ADRO1309, ADRO1366, ADRO1367, ADRO1388, ADRO1428,  
CC ADRO1466, ADRO1629, ADRO1637, ADRO2057, ADRO2345 and ADRO2369, chosen  
CC from 1047 disclosed genomic sequences. Also included is a cloning vector  
CC comprising a nucleotide sequence chosen from the above sequences. The  
CC novel *Ashbya gossypii* genomic sequences are useful for forensic  
CC identification, gene characterisation, for studying gene organisation by  
CC intergenomic comparison (with *Saccharomyces cerevisiae*), identifying  
CC biosynthetic genes for selectable markers, to isolate  
CC promoters/terminators/centromeres, chromosome mapping, and in identifying  
CC sequences unique to *Ashbya gossypii* for species identification. The  
CC present sequence is an *A. gossypii* novel genomic sequence of the  
CC invention.

SQ Sequence 825 BP; 211 A; 203 C; 179 G; 208 T; 0 U; 24 Other;

Query March 14.3%; Score 16; DB 2; Length 825;

Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 79 GGTGAGCAACGACGAGG 94  
Db 83 GGTGAGCAACGACGAGG 98

## RESULT 25

ADP74847  
ID ADP74847 standard; cDNA; 829 BP.

XX  
AC ADP74847;

DT 26-FEB-2004 (first entry)

DE Murine NOVX cDNA to treat human pathological conditions (SeqID 61).

XX  
KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;  
KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
KW haematopoietic disease; dyslipidaemia; anorectic; vitruide; nootropic;  
KW antiinflammatory; neuroprotective; antilipemic; anabolic; cardiac;  
KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
KW tissue typing; preventive medicine; pharmacogenomic.

OS Mus musculus.

PN WO2003076578-A2.

PD 18-SEP-2003.

PF 06-MAR-2003; 2003WO-US006794.

PR 06-MAR-2002; 2002US-0361974P.

PR 08-MAR-2002; 2002US-00093463.

PR 08-MAR-2002; 2002WO-US007288.

PR 15-MAR-2002; 2002US-0365034P.

PR 19-MAR-2002; 2002US-0365477P.

PR 20-MAR-2002; 2002US-0365884P.

PR 20-MAR-2002; 2002US-0365985P.

PR 22-MAR-2002; 2002US-0366982P.

PR 12-APR-2002; 2002US-0372018P.

PR 12-APR-2002; 2002US-0372022P.

PR 23-APR-2002; 2002US-0374682P.

PR 12-JUN-2002; 2002US-0388096P.

PR 14-JUN-2002; 2002US-0389143P.

PR 26-JUN-2002; 2002US-0391779P.

PR 15-AUG-2002; 2002US-0403743P.

PR 13-SEP-2002; 2002US-0410755P.

PR 23-SEP-2002; 2002US-0412957P.

PR 22-OCT-2002; 2002US-0420382P.

PR 05-MAR-2003; 2003US-00420382.

PA (CURA-) CURAGEN CORP.

PI Alsobrook JP, Anderson DW, Boldog FL, Burgess CE, Chaudhuri A;  
PI Colman SD, Edinger SR, Eitenberg S, Gangoli ER, Gerlach VL;  
PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malynkar UM;  
PI Mezes PS, Miller CE, Millet I, Padigaru M, Patturajan M, Peyman J;  
PI Qian X, Raetelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
PI Sukumaran S, Vernet CM, Voss EZ, Zhong M;

DR WPI; 2003-697890/66.

DR P-PSDB; ADP74848.

PT New isolated NOVX polypeptides and polynucleotides, useful for  
PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
PT asthma, or infections.

PS Claim 20; SEQ ID NO 61; 282pp; English.  
XX This invention relates to a novel nucleic acid, and encoded polypeptides  
XX thereof, which have properties related to the stimulation of biochemical  
XX or physiological responses in a cell, tissue, organ or organism.  
XX Specifically, it refers to the use of biologically active fragments for  
XX diagnostic and prognostic assays and furthermore in the treatment of  
XX diverse pathological conditions. The present invention describes novel  
XX human and murine NOVX proteins, as well as methods to modulate their  
XX expression using antisense oligos, ribozymes and peptide nucleic acids.  
XX The polypeptides, nucleic acid molecules and antibodies are useful in the  
XX manufacture of a medicament for treating metabolic disorders, diabetes,  
XX anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune



CC and haematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,  
 CC vincidine, nootropic, antiinflammatory, neuroprotective, antilipase,  
 CC anabolic and cardiant. Furthermore, they are useful in screening assays  
 CC to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the  
 CC invention.

XX Sequence 829 BP, 157 A, 236 C, 277 G, 159 T, 0 U, 0 Other;  
 SQ

Query Match 14.3%; Score 16; DB 10; Length 829;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 AGGTAAGTTAAAGAGG 106  
 Db 710 AGGTAAGTTAAAGAGG 725

RESULT 26  
 ADF74833  
 ID ADF74833 standard; cDNA; 829 BP.  
 XX  
 AC ADF74833;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Murine NOVX cDNA to treat human pathological conditions (SeqID 47).  
 XX  
 KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; vincidine; nootropic;  
 KW antiinflammatory; neuroprotective; antilipase; anabolic; cardiant;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003076578-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 06-MAR-2003; 2003WO-US006794.  
 XX  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR 08-MAR-2002; 2002US-00093463.  
 PR 15-MAR-2002; 2002WO-US007288.  
 PR 19-MAR-2002; 2002US-0365034P.  
 PR 20-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 20-MAR-2002; 2002US-0365985P.  
 PR 22-MAR-2002; 2002US-0366928P.  
 PR 12-APR-2002; 2002US-0372018P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-0388096P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Aldebrock JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VL,  
 PI Gorman L, Guo X, Kekuda R, Li U, MacLachlan T, Malyskar UM,  
 PI Mezes PS, Miller CE, Millet I, Padigaru M, Paturajan M, Peyman J;

PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
 PI Sukumaran S, Verneet CM, Voss EZ, Zhong M;  
 XX WPI: 2003-697890/66.  
 DR P-PDSB; ADF74834.  
 XX  
 XX New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 XX  
 XX Claim 20; SEQ ID NO 47; 282pp; English.  
 XX  
 XX This invention relates to a novel nucleic acid, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOVX proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and haematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,  
 CC vincidine, nootropic, antiinflammatory, neuroprotective, antilipase,  
 CC anabolic and cardiant. Furthermore, they are useful in screening assays  
 CC to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the  
 CC invention.

XX  
 SQ Sequence 829 BP, 157 A, 236 C, 277 G, 159 T, 0 U, 0 Other;  
 XX

Query Match 14.3%; Score 16; DB 10; Length 829;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 AGGTAAGTTAAAGAGG 106  
 Db 710 AGGTAAGTTAAAGAGG 725

RESULT 27  
 ADF74831  
 ID ADF74831 standard; cDNA; 1392 BP.  
 XX  
 AC ADF74831;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Murine NOVX cDNA to treat human pathological conditions (SeqID 45).  
 XX  
 KW gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; vincidine; nootropic;  
 KW antiinflammatory; neuroprotective; antilipase; anabolic; cardiant;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 XX  
 OS Mus musculus.  
 XX  
 PN WO2003076578-A2.  
 XX  
 PD 18-SEP-2003.  
 XX  
 PF 06-MAR-2003; 2003WO-US006794.  
 XX  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR 08-MAR-2002; 2002US-00093463.  
 PR 15-MAR-2002; 2002WO-US007288.



PR 15-MAR-2002; 2002US-0365034P.  
 PR 19-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 20-MAR-2002; 2002US-0365985P.  
 PR 22-MAR-2002; 2002US-0365985P.  
 PR 12-APR-2002; 2002US-0372021P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-0386096P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alsbrook JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VM;  
 PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyanar UM;  
 PI Mezes PS, Miller CE, Millet I, Padigaru M, Patturajan M, Peyman J;  
 PI Qian X, Raselli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
 PI Sukumaran S, Vernet CM, Voos EZ, Zhong M;  
 PI  
 XX WPI; 2003-697890/66.  
 DR P-PSDB; ADF74832.  
 XX  
 PT New isolated NOXV polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOXV-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 PT  
 XX  
 PS Claim 20; SEQ ID NO 45; 282pp; English.  
 PS  
 XX  
 CC This invention relates to a novel nucleic acid, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOXV proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and hematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,  
 CC virucide, neurotropic, antiinflammatory, neuroprotective, antiipaeamic,  
 CC anabolic and cardiatic. Furthermore, they are useful in screening assays  
 CC to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polynucleotide is a murine NOXV cDNA of the  
 CC invention.  
 CC  
 XX  
 SQ Sequence 1392 BP; 294 A; 380 C; 432 G; 286 T; 0 U; 0 Other;  
 SQ  
 Query Match 14.3%; Score 16; DB 10; Length 1392;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 91 AGGCTAGTTAAAGAGC 106  
 |||||  
 |||||  
 Db 1276 AGCGTAGTTAAAGAGC 1291  
 RESULT 28  
 ADF74839 standard; cDNA; 1392 BP.  
 XX

AC ADF74839;  
 XX  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX  
 DE Murine NOXV cDNA to treat human pathological conditions (SeqID 53).  
 DE  
 XX gene; ss; mouse; murine; NOXV; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW hematopoietic disease; dyslipidaemia; anorectic; virucide; neurotropic;  
 KW antiinflammatory; neuroprotective; antiipaeamic; anabolic; cardiatic;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 KW  
 XX Mus musculus.  
 OS  
 XX WO2003076578-A2.  
 EN  
 XX  
 PD 18-SEP-2003.  
 PD  
 XX  
 XX 06-MAR-2003; 2003WO-US006794.  
 PE  
 XX 06-MAR-2002; 2002US-0361974P.  
 XX 08-MAR-2002; 2002US-00093463.  
 PR 08-MAR-2002; 2002WO-US007288.  
 PR 15-MAR-2002; 2002US-0365034P.  
 PR 19-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 20-MAR-2002; 2002US-0365985P.  
 PR 22-MAR-2002; 2002US-0372021P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-0386096P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 PR  
 XX  
 PA (CURA-) CURAGEN CORP.  
 PA  
 PI Alsbrook JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VM;  
 PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyanar UM;  
 PI Mezes PS, Miller CE, Millet I, Padigaru M, Patturajan M, Peyman J;  
 PI Qian X, Raselli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
 PI Sukumaran S, Vernet CM, Voos EZ, Zhong M;  
 PI  
 XX WPI; 2003-697890/66.  
 DR P-PSDB; ADF74840.  
 DR  
 XX  
 PT New isolated NOXV polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOXV-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 PT  
 XX  
 PS Claim 20; SEQ ID NO 53; 282pp; English.  
 PS  
 XX This invention relates to a novel nucleic acid, and encoded polypeptides  
 XX thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOXV proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and hematopoietic diseases as well as various dyslipidaemias.  
 CC



CC Accordingly, these molecules have many activities including anorectic, vitamin D, nootropic, antiinflammatory, neuroprotective, antilipemic, antidiabetic, and cardiac. Furthermore, they are useful in screening assays to identify small molecules that modulate or inhibit, for example, neurogenesis, wound healing and angiogenesis. The nucleic acids are also used as in chromosome mapping, tissue typing, preventive medicine and pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the invention.

XX Sequence 1392 BP; 294 A; 380 C; 432 G; 286 T; 0 U; 0 Other;

Query Match 14.3%; Score 16; DB 10; Length 1392;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 AGCGTACTTAAAGAG 106  
 |||||  
 Db 1276 AGCGTACTTAAAGAG 1291

RESULT 29  
 ID ADF74835 standard; cDNA; 1399 BP.  
 AC ADF74835;  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX Murine NOVX cDNA to treat human pathological conditions (SeqID 49).  
 DE  
 XX gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; vitamin D; nootropic;  
 KW antiinflammatory; neuroprotective; antilipemic; anabolic; cardiac;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 KM  
 XX Mus musculus.  
 OS  
 PN WO2003076578-A2.  
 XX 18-SEP-2003.  
 PD  
 XX 06-MAR-2003; 2003WO-US006794.  
 PF  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR 08-MAR-2002; 2002US-00093463.  
 PR 08-MAR-2002; 2002WO-US007288.  
 PR 15-MAR-2002; 2002US-0365034P.  
 PR 19-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 20-MAR-2002; 2002US-0365985P.  
 PR 22-MAR-2002; 2002US-0366928P.  
 PR 12-APR-2002; 2002US-0372018P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-038096P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 XX  
 XX (CURA-) CURAGEN CORP.  
 PA  
 XX Aljabrook JP, Anderson DM, Boldog FI, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettemberg S, Gangolli EA, Gerlach VL;  
 PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malyankar DM,  
 PI Mezes PS, Miller CE, Millet I, Padigaru M, Patumraj M, Peyman J;  
 PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;

PI Sukumaran S, Vernet CM, Voss EZ, Zhong M;  
 XX WPI: 2003-697890/66.  
 DR P-PSDB; ADF74836.  
 XX  
 XX New isolated NOVX polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOVX-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 XX  
 XX Claim 20; SEQ ID NO 49; 282pp; English.  
 PS  
 XX This invention relates to a novel nucleic acid, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOVX proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and haematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,  
 CC vitamin D, nootropic, antiinflammatory, neuroprotective, antilipemic,  
 CC anabolic and cardiac. Furthermore, they are useful in screening assays  
 CC to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the  
 CC invention.  
 XX  
 XX Sequence 1399 BP; 289 A; 401 C; 420 G; 289 T; 0 U; 0 Other;

Query Match 14.3%; Score 16; DB 10; Length 1399;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 91 AGCGTACTTAAAGAG 106  
 |||||  
 Db 710 AGCGTACTTAAAGAG 725

RESULT 30  
 ADF74845  
 ID ADF74845 standard; cDNA; 1399 BP.  
 AC ADF74845;  
 XX 26-FEB-2004 (first entry)  
 DT  
 XX Murine NOVX cDNA to treat human pathological conditions (SeqID 59).  
 DE  
 XX gene; ss; mouse; murine; NOVX; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; vitamin D; nootropic;  
 KW antiinflammatory; neuroprotective; antilipemic; anabolic; cardiac;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 KM  
 XX Mus musculus.  
 OS  
 PN WO2003076578-A2.  
 XX 18-SEP-2003.  
 PD  
 XX 06-MAR-2003; 2003WO-US006794.  
 PF  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR 08-MAR-2002; 2002US-00093463.  
 PR 08-MAR-2002; 2002WO-US007288.  
 PR 15-MAR-2002; 2002US-0365034P.



PR 19-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 22-MAR-2002; 2002US-0365985P.  
 PR 12-APR-2002; 2002US-0372018P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-0388095P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 (CURA-) CURAGEN CORP.  
 XX  
 PA Alabrook JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VL;  
 PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malayanar UM;  
 PI Mezes PS, Miller CE, Miller I, Padigaru M, Patuvarajan M, Peyman J;  
 PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
 PI Sukumaran S, Vernet CM, Voss EZ, Zhong M;  
 XX WPI; 2003-697890/66.  
 DR P-PSDB; ADF74846.  
 XX  
 PT New isolated NOXV polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOXV-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 XX  
 PS Claim 20; SEQ ID NO 59; 2822p; English.  
 XX  
 CC This invention relates to a novel nucleic acid, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOXV proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and haematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,  
 CC virocidic, neurotropic, antiinflammatory, neuroprotective, antilipemic,  
 CC anabolic and cardiant. Furthermore, they are useful in screening assays  
 CC to identify small molecules that modulate or inhibit, for example,  
 CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
 CC used as in chromosome mapping, tissue typing, preventive medicine and  
 CC pharmacogenomics. This polynucleotide is a murine NOXV cDNA of the  
 CC invention.  
 XX  
 SQ Sequence 1399 BP; 289 A; 401 C; 420 G; 289 T; 0 U; 0 Other;  
 Query Match 14.3%; Score 16; DB 10; Length 1399;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Murine NOXV cDNA to treat human pathological conditions (SeqID 41).  
 XX  
 KW gene; ss; mouse; murine; NOXV; metabolic disorder; diabetes; anorexia;  
 KW cancer; cardiovascular; infectious; neurodegenerative; immune;  
 KW haematopoietic disease; dyslipidaemia; anorectic; virocidic; neurotropic;  
 KW antiinflammatory; neuroprotective; antilipemic; anabolic; cardiant;  
 KW neurogenesis; wound healing; angiogenesis; chromosome mapping;  
 KW tissue typing; preventive medicine; pharmacogenomic.  
 XX  
 OS Mus musculus.  
 XX  
 WO2003076578-A2.  
 XX  
 XX  
 PD 18-SEP-2003.  
 XX  
 XX  
 PF 06-MAR-2003; 2003WO-US006794.  
 XX  
 XX 06-MAR-2002; 2002US-0361974P.  
 PR 08-MAR-2002; 2002US-00093463.  
 PR 08-MAR-2002; 2002WO-US007288.  
 PR 15-MAR-2002; 2002US-0365034P.  
 PR 19-MAR-2002; 2002US-0365477P.  
 PR 20-MAR-2002; 2002US-0365884P.  
 PR 20-MAR-2002; 2002US-0365984P.  
 PR 20-MAR-2002; 2002US-0365985P.  
 PR 22-MAR-2002; 2002US-036928P.  
 PR 12-APR-2002; 2002US-0372018P.  
 PR 12-APR-2002; 2002US-0372022P.  
 PR 23-APR-2002; 2002US-0374682P.  
 PR 12-JUN-2002; 2002US-0388096P.  
 PR 14-JUN-2002; 2002US-0389143P.  
 PR 26-JUN-2002; 2002US-0391779P.  
 PR 15-AUG-2002; 2002US-0403743P.  
 PR 13-SEP-2002; 2002US-0410755P.  
 PR 23-SEP-2002; 2002US-0412957P.  
 PR 22-OCT-2002; 2002US-0420382P.  
 PR 05-MAR-2003; 2003US-00420382.  
 XX  
 PA (CURA-) CURAGEN CORP.  
 XX  
 PI Alabrook JP, Anderson DM, Boldog FL, Burgess CE, Chaudhuri A;  
 PI Colman SD, Edinger SR, Ettenberg S, Gangoli EA, Gerlach VL;  
 PI Gorman L, Guo X, Kekuda R, Li L, MacLachlan T, Malayanar UM;  
 PI Mezes PS, Miller CE, Miller I, Padigaru M, Patuvarajan M, Peyman J;  
 PI Qian X, Rastelli L, Rieger DK, Smithson G, Spytek KA, Stone DJ;  
 PI Sukumaran S, Vernet CM, Voss EZ, Zhong M;  
 XX WPI; 2003-697890/66.  
 DR P-PSDB; ADF74828.  
 XX  
 PT New isolated NOXV polypeptides and polynucleotides, useful for  
 PT preventing, diagnosing or treating NOXV-associated disorders, e.g.  
 PT osteoarthritis, obesity, atherosclerosis, cancer, Parkinson's disease,  
 PT asthma, or infections.  
 XX  
 PS Claim 20; SEQ ID NO 41; 2822p; English.  
 XX  
 CC This invention relates to a novel nucleic acid, and encoded polypeptides  
 CC thereof, which have properties related to the stimulation of biochemical  
 CC or physiological responses in a cell, tissue, organ or organism.  
 CC Specifically, it refers to the use of biologically active fragments for  
 CC diagnostic and prognostic assays and furthermore in the treatment of  
 CC diverse pathological conditions. The present invention describes novel  
 CC human and murine NOXV proteins, as well as methods to modulate their  
 CC expression using antisense oligos, ribozymes and peptide nucleic acids.  
 CC The polypeptides, nucleic acid molecules and antibodies are useful in the  
 CC manufacture of a medicament for treating metabolic disorders, diabetes,  
 CC anorexia, cancer, cardiovascular, infectious, neurodegenerative, immune  
 CC and haematopoietic diseases as well as various dyslipidaemias.  
 CC Accordingly, these molecules have many activities including anorectic,



CC vlnuclide, nootropic, antiinflammatory, neuroprotective, antilipemic,  
CC anabolic and cardiant. Furthermore, they are useful in screening assays  
CC to identify small molecules that modulate or inhibit, for example,  
CC neurogenesis, wound healing and angiogenesis. The nucleic acids are also  
CC used as in chromosome mapping, tissue typing, preventive medicine and  
CC pharmacogenomics. This polynucleotide is a murine NOVX cDNA of the  
CC invention.  
XX  
SQ Sequence 1476 BP; 309 A; 407 C; 457 G; 303 T; 0 U; 0 Other;  
Query Match 14.3%; Score 16; DB 10; Length 1476;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 91 AGGGTAGTTAAAGAGC 106  
Db 1354 AGGGTAGTTAAAGAGC 1369  
RESULT 32  
ADL45295/C  
ID ADL45295 standard; DNA; 1665 BP.  
XX  
AC ADL45295;  
XX  
DT 20-MAY-2004 (first entry)  
XX  
DE Human ovarian cancer DNA marker #19185.  
XX  
KW Human; ovarian cancer; ds; tumour; cytostatic; DNA marker.  
XX  
OS Homo sapiens.  
XX  
PN WO200170979-A2.  
XX  
PD 27-SEP-2001.  
XX  
PP 21-MAR-2001; 2001MO-US009126.  
XX  
PR 21-MAR-2000; 2000US-0191031P.  
PR 25-MAY-2000; 2000US-0207124P.  
PR 15-JUN-2000; 2000US-0211940P.  
PR 07-JUL-2000; 2000US-0216820P.  
PR 25-JUL-2000; 2000US-0220661P.  
PR 21-DEC-2000; 2000US-0257672P.  
XX  
PA (MILL-) MILLENNIUM PREDICTIVE MEDICINE INC.  
XX  
PI Lee J, Lillie J;  
XX  
XX WPI; 2001-611502/70.  
XX  
DR WPI; 2001-611502/70.  
XX  
PT Novel isolated nucleic acid molecules (markers) overexpressed in ovarian  
PT cancer cells as compared to their normal non-cancerous ovarian cells are  
PT used to characterize stage, grade, histological type of ovarian cancer.  
XX  
PS Disclosure; SEQ ID NO 19185; 106pp; English.  
XX  
XX The invention relates to nucleic acid markers which are overexpressed in  
CC ovarian cancer cells as compared to their expression in normal (i.e. non-  
CC cancerous) ovarian cells. The invention also relates to polypeptides  
CC encoded by the markers, antibodies that selectively bind to the  
CC polypeptides, a method of inhibiting ovarian cancer in a patient at risk  
CC of developing ovarian cancer involving inhibiting expression of a gene  
CC corresponding to a marker of the invention and a method of treating a  
CC patient afflicted with ovarian cancer comprising providing to cells of  
CC the patient an antisense oligonucleotide complementary to a marker of the  
CC invention. The markers are useful for assessing if a patient is afflicted  
CC with ovarian cancer, which involves comparing the level of expression of  
CC a marker in a patient sample and a normal level of expression of the  
CC marker in a control non-ovarian cancer sample. A difference between the  
CC expression levels indicates ovarian cancer. The level of expression of a  
CC marker corresponds to a secreted protein or to a transcribed

CC polynucleotide or its portion. The level of expression of the marker is  
CC assessed by detecting the presence in the sample, a protein or protein  
CC fragment corresponding to the marker. The presence of protein or protein  
CC fragment detected using an antibody that specifically binds with the  
CC protein or protein fragment. Alternatively, the level of expression of  
CC the marker is assessed by detecting the presence of a transcribed  
CC polynucleotide which anneals with the marker or anneals with a portion of  
CC the polynucleotide comprising the marker, under stringent conditions. The  
CC marker is also used for monitoring the progression of ovarian cancer in a  
CC patient which involves detecting expression of the marker in a patient  
CC sample at a first point in time, repeating the method at a subsequent  
CC time and comparing the level of expression. The method is carried out  
CC using an ovarian tissue sample. A composition comprising a marker,  
CC polypeptide or antibody of the invention is used to treat ovarian cancer.  
CC This sequence represents a human ovarian cancer DNA marker of the  
CC invention. Note: The sequence data for this patent did not form part of  
CC the printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
SQ Sequence 1665 BP; 567 A; 305 C; 322 G; 467 T; 0 U; 4 Other;  
Query Match 14.3%; Score 16; DB 5; Length 1665;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 15 AATGATATATGGTTT 30  
Db 1172 AATGATATATGGTTT 1157  
RESULT 33  
ACL37062/C  
ID ACL37062 standard; cDNA; 2000 BP.  
XX  
AC ACL37062;  
XX  
DT 02-JUN-2005 (first entry)  
XX  
DE Rice stress-regulated promoter SEQ ID NO:15625.  
XX  
KW ss; abiotic stress tolerance; transgenic plant; plant; cereal;  
XX agriculture.  
XX  
OS Oryza sativa.  
XX  
PN WO2003008540-A2.  
XX  
PD 30-JAN-2003.  
XX  
PP 21-JUN-2002; 2002MO-US019668.  
XX  
PR 22-JUN-2001; 2001US-0300112P.  
PR 24-AUG-2001; 2001US-0314662P.  
PR 26-SEP-2001; 2001US-0325277P.  
PR 21-NOV-2001; 2001US-0332132P.  
XX  
PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
XX  
PI Kreps J, Briggs SP, Cooper B, Glazebrook J, Goff SA, Katagiri F;  
PI Moughamer T, Provart N, Riecke D, Zhu T;  
XX  
XX WPI; 2003-248011/24.  
XX  
DR WPI; 2003-248011/24.  
XX  
PT New stress-responsive nucleic acid, useful for altering the  
PT responsiveness of a plant, e.g. cereal, to an abiotic stress such as cold  
PT stress, salt stress or osmotic stress.  
XX  
PS Claim 48; SEQ ID NO 15625; 89pp; English.  
XX  
XX The invention relates to novel abiotic stress responsive polynucleotides  
CC and polypeptides. Also disclosed are vectors, expression cassettes, host  
CC cells, and plants containing such polynucleotides. Also disclosed are  
CC methods for using the polynucleotides and polypeptides to alter the



CC responsiveness of a plant to abiotic stress. The invention is useful in  
CC agriculture. The nucleic acid is useful for determining whether a test  
CC plant has been exposed to an abiotic stress condition. It is also useful  
CC for selecting an agent that alters abiotic stress regulated  
CC polynucleotide expression in a plant cell, and to identify a homolog or  
CC ortholog to an abiotic stress responsive polynucleotide. The nucleic acid  
CC molecule and the polypeptide encoded by it are useful in altering the  
CC responsiveness of a plant to an abiotic stress, such as cold stress, salt  
CC stress, osmotic stress or any of their combinations. The present sequence  
CC is used in the exemplification of the invention  
XX  
SQ Sequence 2000 BP; 534 A; 422 C; 481 G; 561 T; 0 U; 2 Other;  
Query Match 14.3%; Score 16; DB 11; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 73 AATATCGGTGAGCAAC 88  
|||||  
Db 1087 AATATCGGTGAGCAAC 1072  
|||||

## RESULT 34

ADJ41001  
ID ADJ41001 standard; cDNA; 2000 BP.

XX AC ADJ41001;

XX DT 06-MAY-2004 (first entry)

XX DE Plant cDNA #2001.

XX KW Plant; gene; ss; transcription; plant genome augmentation; cereal;  
KW soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;  
KW maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;  
KW stress tolerance; salt tolerance; cold tolerance; drought tolerance;  
KW plant nutrition; apical dominance; dwarfism; early flowering; antiviral;  
KW antifungal.

XX OS Bukaryota.

XX PN US2004016025-A1.

XX PD 22-JAN-2004.

XX PF 26-SEP-2002; 2002US-00260238.

XX PR 26-SEP-2001; 2001US-0325277P.

XX PR 26-SEP-2001; 2001US-0325448P.

XX PR 04-APR-2002; 2002US-0370620P.

XX PA (BUDW/) BUDWORTH P.  
XX PA (MOUG/) MOUGHAMER T.  
XX PA (BRIG/) BRIGGS S P.  
XX PA (COOP/) COOPER B.  
XX PA (GLAZ/) GLAZEBROOK J.  
XX PA (GOFF/) GOFF S A.  
XX PA (KATA/) KATAGIRI F.  
XX PA (KREP/) KREPS J.  
XX PA (PROV/) PROVART N.  
XX PA (RICK/) RICHE D.  
XX PA (ZHUT/) ZHU T.  
XX PI Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;  
XX PI Goff SA, Katagiri F, Kreps J, Provart N, Riche D, Zhu T;  
XX DR WPI; 2004-190374/18.

XX PT New rice promoter, useful for manipulating crop plants to alter or  
XX PT improve phenotypic characteristics, e.g. produce large quantities of oil  
XX PT or proteins, resistance to insecticides, virus or fungi, stress tolerance  
XX PT or high nutritional value.

PS Claim 44; SEQ ID NO 2001; 230bp; English.

XX The invention relates to plant nucleotide sequences that direct seed-,  
XX leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential  
XX or constitutive transcription of an operatively linked nucleic acid  
XX segment. The invention also relates to a method for augmenting a plant  
XX genome and a method of identifying a gene, where its expression is  
XX altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
XX in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
XX canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
XX sorghum, rice or wheat. The polynucleotides and the polypeptides they  
XX encode are useful for manipulating crop plants to alter or improve  
XX phenotypic characteristics, to produce large quantities of oil or  
XX proteins, to incur resistance to insecticides, viruses or fungi, and to  
XX incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
XX have a high nutritional value with reduced apical dominance or dwarfism,  
XX early flowering or altered metabolic pathways. This sequence represents a  
XX plant nucleic acid of the invention. Note: The sequence data for this  
XX patent did not form part of the printed specification but was obtained in  
XX electronic format directly from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).

SQ Sequence 2000 BP; 474 A; 492 C; 539 G; 484 T; 0 U; 11 Other;  
Query Match 14.3%; Score 16; DB 12; Length 2000;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 TATATGGTTTACTGA 35  
|||||  
Db 226 TATATGGTTTACTGA 241  
|||||

## RESULT 35

ABL10239  
ID ABL10239 standard; cDNA; 2084 BP.

XX AC ABL10239;

XX DT 26-MAR-2002 (first entry)

XX DE Drosophila melanogaster expressed polynucleotide SEQ ID NO 25199.

XX KW Drosophila; developmental biology; cell signalling; insecticide;

XX KW pharmaceutical; gene; ss.

XX OS Drosophila melanogaster.

XX PN WO200171042-A2.

XX PD 27-SEP-2001.

XX PF 23-MAR-2001; 2001WO-US009231.

XX PR 23-MAR-2000; 2000US-0191637P.

XX PR 11-JUL-2000; 2000US-00614150.

XX PA (PEKE ) PE CORP NY.

XX PI Venter JC, Adams M, Li PWD, Myers EW;

XX DR WPI; 2001-656860/75.

XX DR P-PSDB; ABB66136.

XX PT New isolated nucleic acid detection reagent for detecting 1000 or more  
XX PT genes from Drosophila and for elucidating cell signalling and cell-cell  
XX PT interactions.

XX PS Claim 1; SEQ ID NO 25199; 21bp + Sequence Listing; English.

XX The invention relates to an isolated nucleic acid detection reagent  
XX capable of detecting 1000 or more genes from Drosophila. The invention is  
XX useful in developmental biology and in elucidating cell signalling and  
XX cell-cell interactions in higher eukaryotes for the development of



CC insecticides, therapeutics and pharmaceutical drugs. The invention  
CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA  
CC sequences (AB101840-AB16175) and the encoded proteins (ABBS7737-  
CC ABBS72072). The sequence data for this patent did not form part of the  
CC printed specification, but was obtained in electronic format directly  
CC from WIPO at ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 2084 BP; 579 A; 527 C; 459 G; 519 T; 0 U; 0 Other;  
Query Match 14.3%; Score 16; DB 4; Length 2084;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 31 ACTGACGAGGAGCAGC 46  
DB 1473 ACTGACGAGGAGCAGC 1488  
RESULT 36  
ADJ40194  
ID ADJ40194 standard; CDNA; 2307 BP.  
XX  
AC ADJ40194;  
DT 06-MAY-2004 (first entry)  
XX  
XX Plant CDNA #1194.  
DE  
XX Plant; gene; ss; transcription; plant genome augmentation; cereal;  
KM soybean; alfalfa; sunflower; canola; cotton; peanut; tobacco; sugar beet;  
KM maize; barley; sorghum; rice; wheat; crop plant; insecticide resistance;  
KM stress tolerance; salt tolerance; cold tolerance; drought tolerance;  
KM plant nutrition; apical dominance; dwarfism; early flowering; antiviral;  
KM antifungal.  
XX  
OS Eukaryota.  
XX  
XX US2004016025-A1.  
PN  
XX 22-JAN-2004.  
PD  
XX 26-SEP-2002; 2002US-00260238.  
PF  
XX 26-SEP-2001; 2001US-0325277P.  
PR 26-SEP-2001; 2001US-0325448P.  
PR 04-APR-2002; 2002US-0370620P.  
XX  
XX (BUDW/) BUDWORTH P.  
PA (MOUG/) MOUGHAMER T.  
PA (BRIG/) BRIGGS S. P.  
PA (COOP/) COOPER B.  
PA (GLAZ/) GLAZEBROOK J.  
PA (GOFF/) GOFF S. A.  
PA (KATA/) KATAGIRI F.  
PA (KREP/) KREPS J.  
PA (PROV/) PROVART N.  
PA (RICK/) RICHKE D.  
PA (ZHUT/) ZHU T.  
XX  
XX Budworth P, Moughamer T, Briggs SP, Cooper B, Glazebrook J;  
PI Goff SA, Katagiri F, Kreps J, Provart N, Ricke D, Zhu T;  
XX  
XX WPI; 2004-190374/18.  
DR  
XX  
XX New rice promoter; useful for manipulating crop plants to alter or  
PT improve phenotypic characteristics, e.g. produce large quantities of oil  
PT or proteins, resistance to insecticides, virus or fungi, stress tolerance  
PT or high nutritional value.  
XX  
PS Claim 25; SEQ ID NO 1194; 230bp; English.  
XX  
XX The invention relates to plant nucleotide sequences that direct seed-,  
CC leaf- and/or stem-, panicle-, root- or pollen-specific or -preferential

CC or constitutive transcription of an operatively linked nucleic acid  
CC segment. The invention also relates to a method for augmenting a plant  
CC genome and a method of identifying a gene, where its expression is  
CC altered in the seed, leaf, stem, panicle, pollen, root or is constitutive  
CC in a plant cell. The plant is a cereal, e.g. soybean, alfalfa, sunflower,  
CC canola, cotton, peanut, tobacco or sugar beet, preferably maize, barley,  
CC sorghum, rice or wheat. The polynucleotides and the polypeptides they  
CC encode are useful for manipulating crop plants to alter or improve  
CC phenotypic characteristics, to produce large quantities of oil or  
CC proteins, to incur resistance to insecticides, viruses or fungi, and to  
CC incur stress tolerance (e.g. salt, cold or drought) to ensure the plants  
CC have a high nutritional value with reduced apical dominance or dwarfism,  
CC early flowering or altered metabolic pathways. This sequence represents a  
CC plant nucleic acid of the invention. Note: The sequence data for this  
CC patent did not form part of the printed specification but was obtained in  
CC electronic format directly from USPTO at seqdata.uspto.gov/sequence.html.  
XX  
SQ Sequence 2307 BP; 519 A; 617 C; 570 G; 599 T; 0 U; 2 Other;  
Query Match 14.3%; Score 16; DB 12; Length 2307;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
CY 26 GGTTTACTGACGAGCA 41  
DB 803 GGTTTACTGACGAGCA 818  
RESULT 37  
ACN91623/C  
ID ACN91623 standard; DNA; 2517 BP.  
XX  
XX ACN91623;  
AC  
XX 02-DEC-2004 (first entry)  
DT  
XX  
XX Breast cancer related marker, seq id 12773.  
DE  
XX  
XX Cancer; breast; tumour; cytostatic; marker; detection; therapy; ds.  
KM  
XX  
XX Homo sapiens.  
OS  
XX  
XX US2003099974-A1.  
PN  
XX 29-MAY-2003.  
PD  
XX 18-JUL-2002; 2002US-00198846.  
PF  
XX 18-JUL-2001; 2001US-0306220P.  
PR 18-JUL-2001; 2001US-0306220P.  
PR  
XX (MILL-) MILLENNIUM PHARM INC.  
XX  
XX Lillie J, Xu Y, Wang Y, Steinmann K;  
PI WPI; 2003-787014/74.  
DR  
XX  
XX Novel isolated polypeptide associated with breast cancer; useful for  
PT detecting presence of polypeptide in sample, as a marker for breast  
PT cancer.  
XX  
XX Disclosure; SEQ ID NO 12773; 36bp; English.  
XX  
XX The invention relates to an isolated polypeptide (I) associated with  
CC breast cancer which is encoded by a nucleic acid molecule comprising a  
CC nucleotide sequence (SI). Further disclosed is an antibody that binds to  
CC the polypeptide of the invention. The activity of the polypeptide of the  
CC invention may be described as cytostatic. The antibody is useful for  
CC detecting the presence of (I) in a sample. Nucleic acid molecules of the  
CC invention are useful in the detection of breast tumours. (I) is useful as  
CC a marker for breast cancer and in breast cancer therapy. Sequences given  
CC in records ACN78851-ACN92934 represent nucleic acid markers associated  
CC with breast cancer. Note: The sequence listing does not form part of the  
CC specification but may be obtained in electronic format from the USPTO web



CC site at seqdata.uspto.gov/sequence.html?docid=2003009974  
XX Sequence 2517 BP; 701 A; 516 C; 557 G; 735 T; 0 U; 8 Other;  
SQ Query Match 14.3%; Score 16; DB 11; Length 2517;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTT 30  
DB 2024 AATGATATATTGTTT 2009

RESULT 38  
AAFI6046  
ID AAFI6046 standard; cDNA; 2995 BP.  
XX AAFI6046;  
AC AAFI6046;  
XX 13-MAR-2001 (first entry)  
DT 13-MAR-2001 (first entry)  
XX Human prostate cancer antigen nucleotide sequence SEQ ID NO:481.  
DE Human prostate cancer antigen nucleotide sequence SEQ ID NO:481.  
XX Human; prostate cancer; prostate cancer antigen; detection; diagnosis;  
KW neuroprotective; cytosolic; cardioactive; immunomodulatory; muscular;  
KW vulnary; gastrointestinal; nephrotropic; antiinfective; gynaecological;  
KW antibacterial; gene therapy; neural; immune; reproductive; renal;  
KW gastrointestinal; pulmonary; cardiovascular; proliferative disorder;  
KW wound; infectious disease; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX MO200055174-A1.  
PN 21-SEP-2000.  
PD 21-SEP-2000.  
XX 08-MAR-2000; 2000WO-US005988.  
PF 08-MAR-2000; 2000WO-US005988.  
XX 12-MAR-1999; 99US-0124270P.  
PR 12-MAR-1999; 99US-0124270P.  
XX (HUMA-) HUMAN GENOME SCI INC.  
PA (ROSE/) ROSEN C A.  
XX Rosen CA, Ruben SM;  
PI WPI; 2000-587513/55.  
DR P-PSDB; AAB56843.  
XX Prostate cancer associated gene sequences, referred to as prostate cancer  
PT antigens, useful for treatment, prevention, and diagnosis of disorders  
PT such as prostate cancer.  
XX Claim 1; Page 953; 2338pp; English.

AAFI5566 to AAFI6505 encode the human prostate cancer associated  
CC proteins, called prostate cancer antigens, given in AAB56363 to AAB57302.  
CC The prostate cancer antigens can have neuroprotective, cytosolic,  
CC cardioactive, immunomodulatory, muscular, vulnary, gastrointestinal,  
CC nephrotropic, antiinfective, gynaecological and antibacterial activities,  
CC and can be used in gene therapy. The prostate cancer antigen  
CC polynucleotides may be used for detection of prostate cancer, chromosome  
CC identification, as chromosome markers, and for numerous other diagnostic  
CC or research purposes. The prostate cancer antigens may be used to treat  
CC disorders such as neural, immune, muscular, reproductive,  
CC gastrointestinal, pulmonary, cardiovascular, renal, and proliferative  
CC disorders, wounds, and infectious diseases. AAFI6506 to AAFI6514 to  
CC AAB57303 represent sequences used in the exemplification of the present  
CC invention  
XX Sequence 2995 BP; 961 A; 572 C; 526 G; 934 T; 0 U; 2 Other;  
SQ Query Match 14.3%; Score 16; DB 3; Length 2995;  
Best Local Similarity 100.0%; Pred. No. 91;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTT 30  
DB 1552 AATGATATATTGTTT 1567

RESULT 39  
AAKS2850/C  
ID AAKS2850 standard; cDNA; 3880 BP.  
XX AAKS2850;  
AC AAKS2850;  
XX 06-NOV-2001 (first entry)  
DT 06-NOV-2001 (first entry)  
XX Human polynucleotide SEQ ID NO 2379.  
DE Human polynucleotide SEQ ID NO 2379.  
XX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; hematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX Homo sapiens.  
OS Homo sapiens.  
XX MO200157190-A2.  
PN 09-AUG-2001.  
PD 09-AUG-2001.  
XX 05-FEB-2001; 2001WO-US004098.  
PF 05-FEB-2001; 2001WO-US004098.  
XX 03-FEB-2000; 2000US-00496914.  
PR 27-APR-2000; 2000US-00560875.  
PR 20-JUN-2000; 2000US-00598075.  
PR 19-JUL-2000; 2000US-00620325.  
PR 01-SEP-2000; 2000US-00654936.  
PR 15-SEP-2000; 2000US-00663561.  
PR 20-OCT-2000; 2000US-00693325.  
PR 30-NOV-2000; 2000US-00728422.  
XX (HYSE-) HYSEQ INC.  
PA (HYSE-) HYSEQ INC.  
XX Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Gao Y;  
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren P, Chen R, Wang ZW;  
PI Xue AJ, Yang Y, Weinman T, Goodrich R;  
XX WPI; 2001-476283/51.  
DR P-PSDB; AAM79717.  
XX Nucleic acids encoding polypeptides with cytokine-like activities, useful  
PT in diagnosis and gene therapy.  
PT Claim 1; Page 4670-4671; 6221pp; English.

The invention relates to polynucleotides (AAK51456-AAK51435) and the  
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to  
CC cytokine, cell proliferation or cell differentiation or which may induce  
CC production of other cytokines in other cell populations. The  
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or  
CC peptide therapy. The polypeptides have various cytokine-like activities,  
CC e.g. stem cell growth factor activity, haematopoiesis regulating  
CC activity, tissue growth factor activity, immunomodulatory activity and  
CC activin/inhibin activity and may be useful in the diagnosis and/or  
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and  
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111  
CC (AAK5582) and 3666 (AAM80020) are omitted as the relevant pages from the  
CC sequence listing were missing at the time of publication  
XX Sequence 3880 BP; 1121 A; 763 C; 761 G; 1235 T; 0 U; 0 Other;  
SQ Query Match 14.3%; Score 16; DB 4; Length 3880;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 15 AATGATATATTGGTTT 30  
 ||||||||||||||||  
 Db 861 AATGATATATTGGTTT 846

## RESULT 40

AAKS1866  
 ID AAKS1866 standard; cDNA, 4021 BP.

AAKS1866;

DT 06-NOV-2001 (first entry)

DE Human polynucleotide SEQ ID NO 411.

KX Human; cytokine; cell proliferation; cell differentiation; gene therapy;  
 KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
 KM tissue growth factor; immunomodulatory; cancer; leukaemia;  
 nervous system disorder; arthritis; inflammation; ss.

OS Homo sapiens.

PN WO200157190-A2.

PD 09-AUG-2001.

PF 05-FEB-2001; 2001WO-US004098.

PR 03-FEB-2000; 2000US-00496914.

PR 27-APR-2000; 2000US-00560875.

PR 20-JUN-2000; 2000US-00598075.

PR 19-JUL-2000; 2000US-00620325.

PR 01-SEP-2000; 2000US-00654936.

PR 15-SEP-2000; 2000US-00663561.

PR 20-OCT-2000; 2000US-00693325.

PR 30-NOV-2000; 2000US-00728422.

DR WPI; 2001-476283/51.

PI P-PSDB; AAM78733.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

PI WPI; 2001-476283/51.

PI P-PSDB; AAM78733.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

PI WPI; 2001-476283/51.

PI P-PSDB; AAM78733.

PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;

PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;

PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

PI WPI; 2001-476283/51.

PI P-PSDB; AAM78733.

Db 3161 AATGATATATTGGTTT 3176

Search completed: April 11, 2006, 16:25:20  
 Job time : 182.046 secs

Query Match 14.3%; Score 16; DB 4; Length 4021;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGGTTT 30  
 ||||||||||||||||



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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 45.4595 Seconds  
(without alignments)  
4379.433 Million cell updates/sec

Title: US-10-712-654-25

Perfect score: 112

Sequence: 1 ggtacatctgcgcgaatgat.....ggtacgtaagaagcgtcgtg 112

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Issued Patents NA: \*  
1: /cgn2\_6/ptodata/1/ina/1 COMB.seq: \*  
2: /cgn2\_6/ptodata/1/ina/5 COMB.seq: \*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq: \*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq: \*  
5: /cgn2\_6/ptodata/1/ina/H COMB.seq: \*  
6: /cgn2\_6/ptodata/1/ina/PCRTUS COMB.seq: \*  
7: /cgn2\_6/ptodata/1/ina/PP COMB.seq: \*  
8: /cgn2\_6/ptodata/1/ina/RE COMB.seq: \*  
9: /cgn2\_6/ptodata/1/ina/backfile1.seq: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	17	15.2 122626	3 US-09-949-016-17524	Sequence 17524, A
2	16	14.3 434	3 US-10-131-827-8493	Sequence 8493, Ap
3	16	14.3 825	3 US-08-998-416-525	Sequence 525, App
4	15	13.4 255	3 US-09-270-767-25671	Sequence 25671, A
5	15	13.4 321	3 US-09-107-532A-1330	Sequence 1330, Ap
6	15	13.4 332	3 US-09-270-767-10299	Sequence 10299, A
7	15	13.4 403	3 US-09-513-999C-3060	Sequence 3060, Ap
8	15	13.4 537	3 US-09-107-532A-2913	Sequence 2913, Ap
9	15	13.4 537	3 US-09-134-000C-2403	Sequence 2403, Ap
10	15	13.4 549	3 US-09-710-279-3099	Sequence 3099, Ap
11	15	13.4 552	3 US-09-248-796A-179	Sequence 179, App
12	15	13.4 558	3 US-09-107-433-2198	Sequence 2198, App
13	15	13.4 558	3 US-09-134-001C-456	Sequence 456, App
14	15	13.4 601	3 US-09-949-016-84995	Sequence 84995, A
15	15	13.4 601	3 US-09-949-016-85146	Sequence 85146, A
16	15	13.4 601	3 US-09-949-016-150903	Sequence 150903, A
17	15	13.4 601	3 US-09-949-016-153570	Sequence 153570, A
18	15	13.4 655	3 US-09-023-655-98	Sequence 98, Appl
19	15	13.4 1159	3 US-08-858-207A-29	Sequence 29, Appl
20	15	13.4 1281	3 US-09-327-487A-3	Sequence 3, Appl1
21	15	13.4 1284	3 US-09-327-487A-4	Sequence 4, Appl1
22	15	13.4 1458	3 US-09-334-938-9	Sequence 9, Appl1
23	15	13.4 2112	3 US-09-710-279-4414	Sequence 4414, Ap
24	15	13.4 2872	3 US-09-327-487A-2	Sequence 2, Appl1



C 98	14	12.5	621	3	US-09-621-976-9731	Sequence 9731, Ap	C 171	14	12.5	5115	3	US-09-723-890-19	Sequence 19, Appl
C 99	14	12.5	639	3	US-09-533-559-5539	Sequence 5539, Ap	C 172	14	12.5	5115	3	US-09-723-901-19	Sequence 19, Appl
C 100	14	12.5	700	3	US-09-735-271-1060	Sequence 1060, Ap	C 173	14	12.5	5115	3	US-09-723-547-19	Sequence 19, Appl
C 101	14	12.5	711	3	US-09-543-681A-3012	Sequence 3012, Ap	C 174	14	12.5	5115	3	US-09-724-127-19	Sequence 19, Appl
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C 105	14	12.5	757	2	US-07-989-845-27	Sequence 27, Appl	C 178	14	12.5	5115	3	US-09-723-913-19	Sequence 19, Appl
C 106	14	12.5	757	2	US-07-989-844-11	Sequence 11, Appl	C 179	14	12.5	5115	3	US-09-723-912-19	Sequence 19, Appl
C 107	14	12.5	757	2	US-08-161-044-11	Sequence 11, Appl	C 180	14	12.5	5115	3	US-09-724-095-19	Sequence 19, Appl
C 108	14	12.5	757	2	US-08-240-121-11	Sequence 11, Appl	C 181	14	12.5	5115	3	US-09-724-157-19	Sequence 19, Appl
C 109	14	12.5	757	2	US-08-451-241-11	Sequence 11, Appl	C 182	14	12.5	5115	3	US-09-724-062-19	Sequence 19, Appl
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C 111	14	12.5	757	6	PCT-US93-11297-11	Sequence 11, Appl	C 184	14	12.5	5115	3	US-09-724-461-19	Sequence 19, Appl
C 112	14	12.5	757	6	PCT-US93-11298-27	Sequence 27, Appl	C 185	14	12.5	5140	3	US-08-825-852-20	Sequence 20, Appl
C 113	14	12.5	759	3	US-09-543-681A-73	Sequence 73, Appl	C 186	14	12.5	5140	3	US-09-723-890-20	Sequence 20, Appl
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C 115	14	12.5	822	3	US-09-107-433-1681	Sequence 1681, Ap	C 188	14	12.5	5140	3	US-09-723-547-20	Sequence 20, Appl
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C 118	14	12.5	879	2	US-08-249-671A-10	Sequence 10, Appl	C 191	14	12.5	5140	3	US-09-723-917-20	Sequence 20, Appl
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C 130	14	12.5	1215	3	US-09-270-767-13069	Sequence 13069, A	C 203	14	12.5	5586	3	US-09-357-206A-19	Sequence 19, Appl
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C 132	14	12.5	1431	3	US-08-443-568B-15	Sequence 901, App	C 205	14	12.5	5718	3	US-09-265-315-48	Sequence 48, Appl
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C 138	14	12.5	1742	3	US-09-073-010-3	Sequence 3, Appl	C 211	14	12.5	6095	3	US-09-357-206A-18	Sequence 18, Appl
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C 406	13	11.6	558	3	US-09-919-039-194	Sequence 194, App
C 407	13	11.6	576	4	US-09-605-703B-1847	Sequence 1847, App
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537	13	11.6	911	2	US-08-393-985-5	Sequence 5, Appl1	610	13	11.6	1425	2	US-07-876-280-6	Sequence 6, Appl1
538	13	11.6	915	2	US-09-252-991A-323	Sequence 323, App	611	13	11.6	1425	2	US-07-876-280-27	Sequence 27, Appl1
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542	13	11.6	933	3	US-09-252-991A-343	Sequence 343, App	615	13	11.6	1425	2	US-08-147-189-1	Sequence 1, Appl1
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547	13	11.6	972	3	US-09-583-110-1979	Sequence 1979, Ap	620	13	11.6	1425	3	US-09-222-553-1	Sequence 1, Appl1
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556	13	11.6	1038	3	US-09-134-000C-2250	Sequence 2250, Ap	629	13	11.6	1452	3	US-09-252-991A-9237	Sequence 9237, Ap
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558	13	11.6	1047	3	US-09-533-559-7024	Sequence 7024, Ap	631	13	11.6	1495	3	US-09-902-540-311	Sequence 311, App
559	13	11.6	1050	3	US-09-769-787-271	Sequence 5, Appl1	632	13	11.6	1495	3	US-09-902-540-6176	Sequence 67, Appl1
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561	13	11.6	1059	3	US-09-328-352-2421	Sequence 2421, Ap	634	13	11.6	1509	3	US-09-071-035-321	Sequence 321, App
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563	13	11.6	1076	3	US-09-716-964B-143	Sequence 143, App	636	13	11.6	1521	3	US-09-023-655-179	Sequence 179, App
564	13	11.6	1098	3	US-09-270-767-15028	Sequence 15028, A	637	13	11.6	1534	3	US-09-949-016-2104	Sequence 2104, App
565	13	11.6	1113	3	US-09-859-822-3	Sequence 3, Appl1	638	13	11.6	1547	3	US-09-828-995B-4-104	Sequence 49, Appl1
566	13	11.6	1113	3	US-09-248-796A-3645	Sequence 3645, Ap	639	13	11.6	1547	3	US-09-828-995B-5-1	Sequence 51, Appl1
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568	13	11.6	1126	3	US-08-781-986A-28	Sequence 28, Appl1	641	13	11.6	1548	3	US-09-270-767-2246	Sequence 2246, A
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570	13	11.6	1136	3	US-09-270-767-15218	Sequence 15218, A	643	13	11.6	1593	3	US-09-774-528-228	Sequence 228, App
571	13	11.6	1138	3	US-09-489-039A-6844	Sequence 6844, Ap	644	13	11.6	1595	3	US-10-120-988-128	Sequence 128, App
572	13	11.6	1146	3	US-09-328-352-209	Sequence 209, App	645	13	11.6	1599	3	US-09-252-991A-9152	Sequence 10717, A
573	13	11.6	1149	3	US-09-248-796A-2916	Sequence 2916, Ap	646	13	11.6	1608	3	US-09-489-039A-4290	Sequence 4290, Ap
574	13	11.6	1149	3	US-09-134-001C-2539	Sequence 2539, Ap	647	13	11.6	1674	2	US-08-793-410-311	Sequence 4290, Ap
575	13	11.6	1182	3	US-09-134-001C-2757	Sequence 2757, Ap	648	13	11.6	1676	2	US-10-418-036-15	Sequence 31, Appl1
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577	13	11.6	1215	3	US-09-828-995B-53	Sequence 53, Appl1	650	13	11.6	1698	3	US-09-949-016-5642	Sequence 5642, Ap
578	13	11.6	1242	3	US-09-248-796A-6696	Sequence 6696, Ap	651	13	11.6	1700	2	US-08-539-1004-3	Sequence 3, Appl1
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580	13	11.6	1251	3	US-09-107-532A-1897	Sequence 1897, Ap	653	13	11.6	1720	3	US-09-205-258-133	Sequence 133, App
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852	13	11.6	21526	3	US-09-949-016-13567	Sequence 13567, A	925	13	11.6	51928	3	US-09-949-016-13184	Sequence 13184, A
853	13	11.6	21525	3	US-09-949-016-13568	Sequence 13568, A	926	13	11.6	52494	3	US-09-949-016-16448	Sequence 16448, A
854	13	11.6	23925	3	US-09-949-016-11797	Sequence 11797, A	927	13	11.6	54245	3	US-09-949-016-13439	Sequence 13439
855	13	11.6	23929	3	US-09-949-016-13301	Sequence 13301, A	928	13	11.6	54550	3	US-10-327-189-42	Sequence 42, App1
856	13	11.6	24018	3	US-09-949-016-17114	Sequence 17114, A	929	13	11.6	54576	3	US-09-949-016-15954	Sequence 15954, A
857	13	11.6	24671	3	US-09-949-016-12842	Sequence 12842, A	930	13	11.6	54576	3	US-09-949-016-15994	Sequence 15994, A
858	13	11.6	25590	3	US-09-949-002-377	Sequence 377, App	931	13	11.6	56832	3	US-09-949-016-12976	Sequence 12976, A
859	13	11.6	25709	3	US-09-949-016-13338	Sequence 13338, A	932	13	11.6	57218	3	US-09-949-016-16512	Sequence 16512, A
860	13	11.6	26274	3	US-09-949-016-12841	Sequence 12841, A	933	13	11.6	58014	3	US-09-949-016-17448	Sequence 17448, A
861	13	11.6	26276	3	US-09-949-016-15026	Sequence 15026, A	934	13	11.6	59719	3	US-09-949-016-15616	Sequence 15616, A
862	13	11.6	26276	3	US-09-949-016-15027	Sequence 15027, A	935	13	11.6	61108	3	US-09-949-002-608	Sequence 608, App
863	13	11.6	26276	3	US-09-949-016-15028	Sequence 15028, A	936	13	11.6	63760	3	US-09-949-016-14087	Sequence 14087, A
864	13	11.6	26276	3	US-09-949-016-15029	Sequence 15029, A	937	13	11.6	63760	3	US-09-949-016-14088	Sequence 14088, A
865	13	11.6	26684	3	US-09-949-016-15109	Sequence 15109, A	938	13	11.6	63783	3	US-09-949-016-13576	Sequence 13576, A
866	13	11.6	26684	3	US-09-949-016-15110	Sequence 15110, A	939	13	11.6	64984	3	US-09-949-016-15234	Sequence 15234, A
867	13	11.6	26684	3	US-09-949-016-17409	Sequence 17409, A	940	13	11.6	65445	3	US-09-949-016-16699	Sequence 16699, A
868	13	11.6	26684	3	US-09-949-016-17410	Sequence 17410, A	941	13	11.6	65518	3	US-09-949-016-12421	Sequence 12421, A
869	13	11.6	27903	3	US-09-902-540-1235	Sequence 1235, Ap	942	13	11.6	65518	3	US-09-949-016-14101	Sequence 14101, A
870	13	11.6	27910	3	US-09-949-016-15020	Sequence 15020, A	943	13	11.6	65848	3	US-09-949-016-13285	Sequence 13285, A
871	13	11.6	27910	3	US-09-949-016-15021	Sequence 15021, A	944	13	11.6	65966	3	US-09-949-016-17152	Sequence 17152, A
872	13	11.6	27910	3	US-09-949-016-15022	Sequence 15022, A	945	13	11.6	66986	3	US-09-596-002-29	Sequence 29, App1
873	13	11.6	27910	3	US-09-949-016-15023	Sequence 15023, A	946	13	11.6	67745	3	US-09-949-016-17821	Sequence 17251, A
874	13	11.6	27910	3	US-09-949-016-15024	Sequence 15024, A	947	13	11.6	68580	3	US-09-949-016-15844	Sequence 15844, A
875	13	11.6	27910	3	US-09-949-016-15025	Sequence 15025, A	948	13	11.6	69924	3	US-09-949-016-15367	Sequence 15367, A
876	13	11.6	27970	3	US-09-949-016-15314	Sequence 15314, A	949	13	11.6	70559	3	US-09-409-800B-1	Sequence 1, App1
877	13	11.6	28791	3	US-09-949-016-15366	Sequence 15366, A	950	13	11.6	70559	3	US-09-409-800B-1	Sequence 1, App1
878	13	11.6	29742	3	US-09-949-016-15650	Sequence 15650, A	951	13	11.6	70828	3	US-09-949-016-12122	Sequence 12122, A
879	13	11.6	30221	3	US-09-949-016-12577	Sequence 12577, A	952	13	11.6	72278	3	US-09-949-016-16113	Sequence 16113, A
880	13	11.6	30222	3	US-09-949-016-17299	Sequence 17299, A	953	13	11.6	72662	3	US-09-949-016-17073	Sequence 17073, A
881	13	11.6	30444	3	US-09-949-016-14997	Sequence 14997, A	954	13	11.6	73757	3	US-09-949-016-15369	Sequence 15369, A
882	13	11.6	32584	3	US-09-949-016-16766	Sequence 16766, A	955	13	11.6	76553	3	US-09-949-016-17099	Sequence 17099, A
883	13	11.6	32998	3	US-08-408-020-1	Sequence 1, App1	956	13	11.6	78269	3	US-09-949-016-12497	Sequence 12497, A
884	13	11.6	34534	3	US-09-949-016-15141	Sequence 15141, A	957	13	11.6	80430	3	US-09-949-002-733	Sequence 733, App
885	13	11.6	34762	3	US-09-902-540-1261	Sequence 1261, Ap	958	13	11.6	80706	3	US-09-949-016-15347	Sequence 15347, A
886	13	11.6	34762	3	US-09-949-002-665	Sequence 665, App	959	13	11.6	81701	3	US-09-949-016-14891	Sequence 14891, A
887	13	11.6	34726	3	US-09-949-002-857	Sequence 857, App	960	13	11.6	82048	3	US-09-949-002-696	Sequence 696, App
888	13	11.6	35064	3	US-09-949-016-12778	Sequence 12778, A	961	13	11.6	82619	3	US-09-949-016-12797	Sequence 799, App
889	13	11.6	35065	3	US-09-949-016-13136	Sequence 13136, A	962	13	11.6	83343	3	US-09-949-016-12242	Sequence 12242, A
890	13	11.6	36016	3	US-09-949-016-14223	Sequence 14223, A	963	13	11.6	83439	3	US-09-949-016-17149	Sequence 17149, A
891	13	11.6	36023	3	US-09-949-016-15577	Sequence 15577, A	964	13	11.6	83439	3	US-09-949-016-15517	Sequence 15517, A
892	13	11.6	36221	3	US-09-954-556-29	Sequence 29, App1	965	13	11.6	84425	3	US-09-949-016-15442	Sequence 15442, A
893	13	11.6	36228	3	US-09-949-016-12256	Sequence 12256, A	966	13	11.6	86980	3	US-09-949-016-15344	Sequence 15344, A
894	13	11.6	36228	3	US-09-949-016-15468	Sequence 15468, A	967	13	11.6	88906	3	US-09-949-016-17468	Sequence 17468, A
895	13	11.6	36412	3	US-08-311-731A-132	Sequence 132, App	968	13	11.6	89047	3	US-09-596-002-34	Sequence 34, App1
896	13	11.6	36618	3	US-09-949-016-16935	Sequence 16935, A	969	13	11.6	90876	3	US-09-949-016-13271	Sequence 13271, A
897	13	11.6	36791	3	US-09-949-016-17451	Sequence 17451, A	970	13	11.6	91665	3	US-09-949-016-12234	Sequence 12234, A
898	13	11.6	37068	3	US-09-949-016-12543	Sequence 12543, A	971	13	11.6	91831	3	US-09-949-016-13694	Sequence 13694, A
899	13	11.6	37068	3	US-09-949-016-17376	Sequence 17376, A	972	13	11.6	94855	3	US-09-949-016-12264	Sequence 12264, A
900	13	11.6	37269	3	US-09-949-016-16672	Sequence 16672, A	973	13	11.6	94987	3	US-09-949-016-12510	Sequence 12510, A



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C 974 13 11.6 94987 3 US-09-949-016-12510 Sequence 12510, A
C 975 13 11.6 95122 3 US-09-949-016-17235 Sequence 17235, A
C 976 13 11.6 96327 3 US-09-949-016-16541 Sequence 16541, A
C 977 13 11.6 96690 3 US-09-949-016-17103 Sequence 17103, A
C 978 13 11.6 96987 3 US-09-949-016-14429 Sequence 14429, A
C 979 13 11.6 96987 3 US-09-949-016-14429 Sequence 14429, A
C 980 13 11.6 98701 3 US-09-949-016-15898 Sequence 15898, A
C 981 13 11.6 98701 3 US-09-949-016-15899 Sequence 15899, A
C 982 13 11.6 99370 3 US-09-949-016-12816 Sequence 12816, A
C 983 13 11.6 99370 3 US-09-949-016-17540 Sequence 17540, A
C 984 13 11.6 102008 3 US-09-949-016-16617 Sequence 16617, A
C 985 13 11.6 102520 3 US-09-949-016-17367 Sequence 17367, A
C 986 13 11.6 102526 3 US-09-949-016-12448 Sequence 12448, A
C 987 13 11.6 103447 3 US-09-949-016-16320 Sequence 16320, A
C 988 13 11.6 105055 3 US-09-949-016-14001 Sequence 14001, A
C 989 13 11.6 107329 3 US-09-949-016-12663 Sequence 12663, A
C 990 13 11.6 107329 3 US-09-949-016-12664 Sequence 12664, A
C 991 13 11.6 107330 3 US-09-949-016-15408 Sequence 15408, A
C 992 13 11.6 107330 3 US-09-949-016-15409 Sequence 15409, A
C 993 13 11.6 107330 3 US-09-949-016-15410 Sequence 15410, A
C 994 13 11.6 107330 3 US-09-949-016-15411 Sequence 15411, A
C 995 13 11.6 107458 3 US-09-949-016-15687 Sequence 15687, A
C 996 13 11.6 107750 3 US-09-949-016-12662 Sequence 12662, A
C 997 13 11.6 107751 3 US-09-949-016-15412 Sequence 15412, A
C 998 13 11.6 107751 3 US-09-949-016-15413 Sequence 15413, A
C 999 13 11.6 107751 3 US-09-949-016-15414 Sequence 15414, A
C1000 13 11.6 107751 3 US-09-949-016-15415 Sequence 15415, A
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## ALIGNMENTS

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RESULT 1
US-09-949-016-17524
; Sequence 17524, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17524
; LENGTH: 122626
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-17524
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Query Match 15.2%; Score 17; DB 3; Length 122626;
Best Local Similarity 100.0%; Pred. No. 7.5;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 14 GAATGATATATTTGGTTT 30
DB 106624 GAATGATATATTTGGTTT 106640
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RESULT 2
US-10-131-827-8493
; Sequence 8493, Application US/10131827
; Patent No. 6905827
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
```

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; APPLICANT: Woodward, Robert
; APPLICANT: Lv, Nnoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
; PRIOR FILING DATE: 2001-06-08
; NUMBER OF SEQ ID NOS: 9090
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8493
; LENGTH: 434
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-131-827-8493
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Query Match 14.3%; Score 16; DB 3; Length 434;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 16 ATGATATATTTGGTTTA 31
DB 378 ATGATATATTTGGTTTA 393
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RESULT 3
US-08-998-416-525
; Sequence 525, Application US/08998416
; Patent No. 6239264
; GENERAL INFORMATION:
; APPLICANT: Philippen, Peter
; APPLICANT: Fohlmann, Rainer
; APPLICANT: Steiner, Sabine
; APPLICANT: Mohr, Christine
; APPLICANT: Wendland, Jürgen
; APPLICANT: Knechtle, Philipp
; APPLICANT: Redischung, Corinne
; TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSPYII
; NUMBER OF SEQUENCES: 1152
; CORRESPONDENCE ADDRESS:
; ADDRESS: No. 6239264rtlis Corporation
; STREET: 3054 Cornwalls Road
; CITY: Research Triangle Park
; STATE: No. 6239264th Carolina
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/998,416
; FILING DATE: 24-DEC-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: CH 0016/97
; FILING DATE: 31-DEC-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38, 241
; REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 525:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 825 base pairs
; TYPE: nucleic acid
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STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
ORGANISM: PAG1368RP  
US-08-998-416-525

Query Match 14.4%; Score 16; DB 3; Length 825;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 79 GGTGAGCAACGACGG 94  
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Db 83 GGTGAGCAACGACGG 98

RESULT 4  
US-09-270-767-25671  
Sequence 25671, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 25671  
LENGTH: 255  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-25671

Query Match 13.4%; Score 15; DB 3; Length 255;  
Best Local Similarity 100.0%; Pred. No. 77;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGATATATGGTTTA 31  
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Db 97 TGATATATGGTTTA 111

RESULT 5  
US-09-107-532A-1330  
Sequence 1330, Application US/09107532A  
Patent No. 6583275  
GENERAL INFORMATION:  
APPLICANT: Lynn A Doucette-Stamm and David Bush  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO  
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS  
NUMBER OF SEQUENCES: 7310  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
STREET: 100 Beaver Street  
CITY: Waltham  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02354  
COMPUTER READABLE FORM:  
MEDIUM TYPE: CD-ROM ISO9660  
COMPUTER: PC  
OPERATING SYSTEM: <Unknown>  
SOFTWARE: ASCII  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/107,532A  
FILING DATE: 30-Jun-1998  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/085,598  
FILING DATE: 14 May 1998  
APPLICATION NUMBER: 60/051571  
FILING DATE: July 2, 1997  
ATTORNEY/AGENT INFORMATION:

NAME: Arinello, Pamela Deneke  
REGISTRATION NUMBER: 40,489  
REFERENCE/DOCKET NUMBER: GTC-012  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (781)893-5007  
TELEFAX: (781)893-8277  
INFORMATION FOR SEQ ID NO: 1330:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 321 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHEetical: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Enterococcus faecium  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...321  
SEQUENCE DESCRIPTION: SEQ ID NO: 1330:  
US-09-107-532A-1330

Query Match 13.4%; Score 15; DB 3; Length 321;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 19 ATATATTTGGTTTACT 33  
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Db 69 ATATATTTGGTTTACT 83

RESULT 6  
US-09-270-767-10299  
Sequence 10299, Application US/09270767  
Patent No. 6703491  
GENERAL INFORMATION:  
APPLICANT: Homburger et al.  
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster  
FILE REFERENCE: File Reference: 7326-094  
CURRENT APPLICATION NUMBER: US/09/270,767  
CURRENT FILING DATE: 1999-03-17  
NUMBER OF SEQ ID NOS: 62517  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 10299  
LENGTH: 332  
TYPE: DNA  
ORGANISM: Drosophila melanogaster  
US-09-270-767-10299

Query Match 13.4%; Score 15; DB 3; Length 332;  
Best Local Similarity 100.0%; Pred. No. 78;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGATATATGGTTTA 31  
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Db 174 TGATATATGGTTTA 188

RESULT 7  
US-09-513-999C-3060  
Sequence 3060, Application US/09513999C  
Patent No. 6783961  
GENERAL INFORMATION:  
APPLICANT: Dumas Milne Edwards, J. B.  
APPLICANT: Duclert, A.  
APPLICANT: Giordano, J. Y.  
TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.  
PATENT NO. 6783961  
FILE REFERENCE: 59.US2.REG  
CURRENT APPLICATION NUMBER: US/09/513,999C  
CURRENT FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/122,487



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PRIORITY FILING DATE: 1999-02-26
NUMBER OF SEQ ID NOS: 36681
SOFTWARE: Patent.pm
SEQ ID NO 3060
LENGTH: 403
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: 26..403
FEATURE:
NAME/KEY: misc_feature
LOCATION: 171
OTHER INFORMATION: s=g or c
FEATURE:
NAME/KEY: UNSURE
LOCATION: 49
OTHER INFORMATION: Xaa=Ser or Thr
US-09-513-999C-3060

Query Match      13.4% Score 15; DB 3; Length 403;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      95 TAGTTAAAGAGCGTG 109
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Db      282 TAGTTAAAGAGCGTG 296

RESULT 8
US-09-107-532A-2913
; Sequence 2913, Application US/09107532A
; Patent No. 6583275
; GENERAL INFORMATION:
; APPLICANT: Lytn A Doucette-Stamm and David Bush
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS
; NUMBER OF SEQUENCES: 7310
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION
; STREET: 100 Beaver Street
; CITY: Waltham
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02354
; COMPUTER READABLE FORM:
; MEDIUM TYPE: CD/ROM ISO9660
; COMPUTER: PC
; OPERATING SYSTEM: <Unknown>
; SOFTWARE: ASCII
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/107,532A
; FILING DATE: 30-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/085,598
; FILING DATE: 14 May 1998
; APPLICATION NUMBER: 60/051571
; FILING DATE: July 2, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Arinello, Pamela Deneka
; REGISTRATION NUMBER: 40,489
; REFERENCE/DOCKET NUMBER: GTC-012
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (781)893-8277
; TELEFAX: (781)893-8277
; INFORMATION FOR SEQ ID NO: 2913:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 537 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEICAL: NO

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: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Enterococcus faecium
:
: FEATURE:
:   NAME/KEY: misc_feature
:   LOCATION: (B) LOCATION 1...537
: SEQUENCE DESCRIPTION: SEQ ID NO: 2913:
US-09-107-532A-2913

Query Match      13.4%; Score 15; DB 3; Length 537;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55 CGCGCTAAGAAGGT 69
      |||||
Db      508 CGCGCTAAGAAGGT 522

RESULT 9
US-09-134-000C-2403
: Sequence 2403, Application US/09134000C
: Patent No. 6617156
: GENERAL INFORMATION:
:   APPLICANT: Lynn Doucelte-Stamm et al
:   TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
:   TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
:   FILE REFERENCE: 032796-032
:   CURRENT APPLICATION NUMBER: US/09/134,000C
:   CURRENT FILING DATE: 1998-08-13
:   PRIOR APPLICATION NUMBER: US 60/055,778
:   PRIOR FILING DATE: 1997-08-15
:   NUMBER OF SEQ ID NOS: 6812
: SOFTWARE: PatentIn version 3.1
: SEQ ID NO 2403
: LENGTH: 537
: TYPE: DNA
: ORGANISM: Enterococcus faecalis
US-09-134-000C-2403

Query Match      13.4%; Score 15; DB 3; Length 537;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55 CGCGCTAAGAAGGT 69
      |||||
Db      508 CGCGCTAAGAAGGT 522

RESULT 10
US-09-710-279-3099
: Sequence 3099, Application US/09710279
: Patent No. 6703492
: GENERAL INFORMATION:
:   APPLICANT: KIMMERLY, WILLIAM JOHN
:   TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
:   FILE REFERENCE: PU3480US
:   CURRENT APPLICATION NUMBER: US/09/710,279
:   CURRENT FILING DATE: 2000-11-09
:   PRIOR APPLICATION NUMBER: 60/164,258
:   PRIOR FILING DATE: 1999-11-09
:   NUMBER OF SEQ ID NOS: 4472
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3099
: LENGTH: 537
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURE:
:   OTHER INFORMATION: Description of Artificial Sequence: synthetic
:   OTHER INFORMATION: nucleic acid sequence
US-09-710-279-3099

Query Match      13.4%; Score 15; DB 3; Length 537;
Best Local Similarity 100.0%; Pred. No. 80;

```



Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCGTAAGAAGT 69  
|||||  
Db 508 CGCGTAAGAAGT 522

RESULT 11  
US-09-248-796A-179/c  
; Sequence 179, Application US/09248796A  
; Patent No. 6747137  
; GENERAL INFORMATION:  
; APPLICANT: Keith Weinstein et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICAN  
; TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: 107196.132  
; CURRENT APPLICATION NUMBER: US/09/248,796A  
; CURRENT FILING DATE: 1999-02-12  
; PRIOR APPLICATION NUMBER: US 60/074,725  
; PRIOR FILING DATE: 1998-02-13  
; PRIOR APPLICATION NUMBER: US 60/096,409  
; PRIOR FILING DATE: 1998-08-13  
; NUMBER OF SEQ ID NOS: 28208  
; SEQ ID NO 179  
; LENGTH: 549  
; TYPE: DNA  
; ORGANISM: Candida albicans  
US-09-248-796A-179

Query Match 13.4%; Score 15; DB 3; Length 549;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 GAATGATATATTGCT 28  
|||||  
Db 51 GAATGATATATTGCT 37

RESULT 12  
US-09-107-433-2198  
; Sequence 2198, Application US/09107433  
; Patent No. 6800744  
; GENERAL INFORMATION:  
; APPLICANT: Lynn A Doucette-Stamm and David Bush  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID  
; SEQUENCES RELATING TO STREPTOCOCCUS PNEUMONIAE FOR DIAGN  
; THERAPEUTICS  
; NUMBER OF SEQUENCES: 5206  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: GENOME THERAPEUTICS CORPORATION  
; STREET: 100 Beaver Street  
; CITY: Waltham  
; STATE: Massachusetts  
; COUNTRY: USA  
; ZIP: 02354  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: CD-ROM ISO9660  
; COMPUTER: <Unknown>  
; OPERATING SYSTEM: <Unknown>  
; SOFTWARE: <Unknown>  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/107,433  
; FILING DATE: 30-Jun-1998  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 60/ 085131  
; FILING DATE: May 12, 1998  
; APPLICATION NUMBER: 60/051553  
; FILING DATE: July 2, 1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Arinello, Pamela Deneke  
; REGISTRATION NUMBER: 40,489  
; REFERENCE/DOCKET NUMBER: GTC-011  
; TELECOMMUNICATION INFORMATION:

TELEPHONE: (781) 893-5007  
TELEFAX: (781) 893-8277  
INFORMATION FOR SEQ ID NO: 2198:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 552 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: circular  
MOLECULE TYPE: DNA (genomic)  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Streptococcus pneumoniae  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: (B) LOCATION 1...552  
SEQUENCE DESCRIPTION: SEQ ID NO: 2198:  
US-09-107-433-2198

Query Match 13.4%; Score 15; DB 3; Length 552;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCGTAAGAAGT 69  
|||||  
Db 523 CGCGTAAGAAGT 537

RESULT 13  
US-09-134-001C-456  
; Sequence 456, Application US/09134001C  
; Patent No. 6380370  
; GENERAL INFORMATION:  
; APPLICANT: Lynn Doucette-Stamm et al  
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCI  
; TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS  
; FILE REFERENCE: GTC-007  
; CURRENT APPLICATION NUMBER: US/09/134,001C  
; CURRENT FILING DATE: 1998-08-13  
; PRIOR APPLICATION NUMBER: US 60/064,964  
; PRIOR FILING DATE: 1997-11-08  
; PRIOR APPLICATION NUMBER: US 60/055,779  
; PRIOR FILING DATE: 1997-08-14  
; NUMBER OF SEQ ID NOS: 5674  
; SEQ ID NO 456  
; LENGTH: 558  
; TYPE: DNA  
; ORGANISM: Staphylococcus epidermidis  
US-09-134-001C-456

Query Match 13.4%; Score 15; DB 3; Length 558;  
Best Local Similarity 100.0%; Pred. No. 80;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCGTAAGAAGT 69  
|||||  
Db 529 CGCGTAAGAAGT 543

RESULT 14  
US-09-949-016-84995/c  
; Sequence 84995, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CU001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768



```

; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 84995
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-84995

Query Match      13.4%; Score 15; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      61 AAAGAAGTCTTAAT 75
DB      411 AAAGAAGTCTTAAT 397

RESULT 15
US-09-949-016-85146/c
; Sequence 85146, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 85146
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-85146

Query Match      13.4%; Score 15; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      61 AAAGAAGTCTTAAT 75
DB      411 AAAGAAGTCTTAAT 397

RESULT 16
US-09-949-016-150903
; Sequence 150903, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

; SEQ ID NO 150903
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-150903

Query Match      13.4%; Score 15; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 ATATTGGTTACTGA 35
DB      409 ATATTGGTTACTGA 423

RESULT 17
US-09-949-016-153570
; Sequence 153570, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153570
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-153570

Query Match      13.4%; Score 15; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 80;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      19 ATATTGGTTACT 33
DB      532 ATATTGGTTACT 546

RESULT 18
US-09-023-655-98/c
; Sequence 98, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocke, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Selhammer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESS: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
```



```

; APPLICATION NUMBER: US/09/023,655
; FILING DATE: HEREMITH
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 98:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 655 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: HUVELPBO1
; CLONE: 015937
; US-09-023-655-98

Query Match 13.4%; Score 15; DB 3; Length 655;
Best Local Similarity 100.0%; Pred. No. 81;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 49 ATTAAGCGCCGTAA 63
Db 130 ATTAAGCGCCGTAA 116

RESULT 19
US-08-858-207A-29/c
; Sequence 29, Application US/08858207A
; Patent No. 6348328
; GENERAL INFORMATION:
; APPLICANT: Black, Michael
; APPLICANT: Hodgson, John
; APPLICANT: Knowles, David
; APPLICANT: Nicholas, Richard
; APPLICANT: Stodola, Robert
; TITLE OF INVENTION: No. 6348328el Compounds
; NUMBER OF SEQUENCES: 552
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406-0939
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/858,207A
; FILING DATE: 09-MAY-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/017670
; FILING DATE: 14-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Gimml, Edward R
; REGISTRATION NUMBER: 38,891
; REFERENCE/DOCKET NUMBER: P50475
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-4478
; TELEFAX: 610-270-5090
; TELEX:
```

```

; INFORMATION FOR SEQ ID NO: 29:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1159 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-858-207A-29

Query Match 13.4%; Score 15; DB 3; Length 1159;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 55 CGCGTAAGAAGGT 69
Db 444 CGCGTAAGAAGGT 430

RESULT 20
US-09-327-487A-3
; Sequence 3, Application US/09327487A
; Patent No. 6352847
; GENERAL INFORMATION:
; APPLICANT: MATSUKAWA, Hirokazu
; APPLICANT: OKA, Osamu
; APPLICANT: FUJITA, Tsyosi
; APPLICANT: MIYAZAKI, Kentaro
; TITLE OF INVENTION: AMMONIA ELIMINATION LIQUID REAGENT
; FILE REFERENCE: 028022-013
; CURRENT APPLICATION NUMBER: US/09/327,487A
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: JP 10-176643
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 1281
; TYPE: DNA
; ORGANISM: Thermus aquaticus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(1281)
; US-09-327-487A-3

Query Match 13.4%; Score 15; DB 3; Length 1281;
Best Local Similarity 100.0%; Pred. No. 84;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 59 GTAAAGAGTCTTA 73
Db 517 GTAAAGAGTCTTA 531

RESULT 21
US-09-327-487A-4
; Sequence 4, Application US/09327487A
; Patent No. 6352847
; GENERAL INFORMATION:
; APPLICANT: MATSUKAWA, Hirokazu
; APPLICANT: OKA, Osamu
; APPLICANT: FUJITA, Tsyosi
; APPLICANT: MIYAZAKI, Kentaro
; TITLE OF INVENTION: AMMONIA ELIMINATION LIQUID REAGENT
; FILE REFERENCE: 028022-013
; CURRENT APPLICATION NUMBER: US/09/327,487A
; CURRENT FILING DATE: 1999-06-08
; PRIOR APPLICATION NUMBER: JP 10-176643
; PRIOR FILING DATE: 1998-06-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 1284
; TYPE: DNA
; ORGANISM: Thermus aquaticus
```







Patent No. 6703492  
GENERAL INFORMATION:  
APPLICANT: KIMBERLY, WILLIAM JOHN  
TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS  
FILE REFERENCE: P0348005  
CURRENT APPLICATION NUMBER: US/09/710,279  
CURRENT FILING DATE: 2000-11-09  
PRIOR APPLICATION NUMBER: 60/164,258  
PRIOR FILING DATE: 1999-11-09  
NUMBER OF SEQ ID NOS: 4472  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4016  
LENGTH: 3302  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: synthetic  
US-09-710-279-4016

Query Match 13.4%; Score 15; DB 3; Length 3302;  
Best Local Similarity 100.0%; Pred. No. 88;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 55 CGCGTAAAGAGGT 69  
|||||  
Db 2191 CGCGTAAAGAGGT 2205

RESULT 27  
US-08-770-544-1  
Sequence 1, Application US/08770544  
Patent No. 5907085  
GENERAL INFORMATION:  
APPLICANT: Gonsalves, Dennis  
APPLICANT: Ling, Kai-Shu  
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND  
TITLE OF INVENTION: THEIR USES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/770,544  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60009008  
FILING DATE: 21-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/621  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4173 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-770-544-1

Query Match 13.4%; Score 15; DB 2; Length 4173;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGATATATTGTTT 30  
|||||  
Db 3155 ATGATATATTGTTT 3169

RESULT 28  
US-09-579-259-1  
Sequence 1, Application US/09579259  
Patent No. 6558953  
GENERAL INFORMATION:  
APPLICANT: Gonsalves, Dennis  
APPLICANT: Ling, Kai-Shu  
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS  
PROTEINS AND THEIR USES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon, Hargrave, Devans & Doyle LLP  
STREET: Clinton Square, P.O. Box 1051  
CITY: Rochester  
STATE: New York  
COUNTRY: U.S.A.  
ZIP: 14603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/579,259  
FILING DATE: 25-May-2000  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60009008  
FILING DATE: 21-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldman, Michael L.  
REGISTRATION NUMBER: 30,727  
REFERENCE/DOCKET NUMBER: 19603/621  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (716) 263-1304  
TELEFAX: (716) 263-1600  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4173 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-579-259-1

Query Match 13.4%; Score 15; DB 3; Length 4173;  
Best Local Similarity 100.0%; Pred. No. 89;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGATATATTGTTT 30  
|||||  
Db 3155 ATGATATATTGTTT 3169

RESULT 29  
US-09-650-324A-1  
Sequence 1, Application US/09650324A  
Patent No. 6638720  
GENERAL INFORMATION:  
APPLICANT: GONSALVES, DENNIS  
APPLICANT: LING, KAI-SHU  
TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND



```
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: 07678/025006
; CURRENT APPLICATION NUMBER: US/09/650,324A
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 09/579,259
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/224,898
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 08/770,544
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/009,008
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4173
; TYPE: DNA
; ORGANISM: Grapevine Leafroll Virus
US-09-650-324A-1

Query Match      13.4%; Score 15; DB 3; Length 4173;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGATATATTGGTTT 30
      |||||
Db      3155 ATGATATATTGGTTT 3169

RESULT 30
US-10-039-112A-1
; Sequence 1, Application US/10039112A
; Patent No. 6916617
; GENERAL INFORMATION:
; APPLICANT: GONSALVES, DENNIS
; APPLICANT: LING, KAI-SHU
; TITLE OF INVENTION: GRAPEVINE LEAFROLL VIRUS PROTEINS AND
; TITLE OF INVENTION: THEIR USES
; FILE REFERENCE: 07678/025007
; CURRENT APPLICATION NUMBER: US/10/039,112A
; CURRENT FILING DATE: 2002-12-31
; PRIOR APPLICATION NUMBER: US 09/650,324
; PRIOR FILING DATE: 2000-08-29
; PRIOR APPLICATION NUMBER: US 09/579,259
; PRIOR FILING DATE: 2000-05-25
; PRIOR APPLICATION NUMBER: US 09/224,898
; PRIOR FILING DATE: 1998-12-31
; PRIOR APPLICATION NUMBER: US 08/770,544
; PRIOR FILING DATE: 1996-12-20
; PRIOR APPLICATION NUMBER: US 60/009,008
; PRIOR FILING DATE: 1995-12-21
; NUMBER OF SEQ ID NOS: 67
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4173
; TYPE: DNA
; ORGANISM: Grapevine Leafroll Virus
US-10-039-112A-1

Query Match      13.4%; Score 15; DB 3; Length 4173;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      16 ATGATATATTGGTTT 30
      |||||
Db      3155 ATGATATATTGGTTT 3169

RESULT 31
US-08-961-527-65
; Sequence 65, Application US/08961527
; Patent No. 6420135
; GENERAL INFORMATION:
```

```
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Streptococcus pneumoniae Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 391
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/961,527
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brookes, A. Anders
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PB340P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 65:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11831 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
US-08-961-527-65

Query Match      13.4%; Score 15; DB 3; Length 11831;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55 CGCCGTAAGAAGGT 69
      |||||
Db      7738 CGCCGTAAGAAGGT 7752

RESULT 32
US-08-956-171E-205/C
; Sequence 205, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; Gail H. Choi
; Patrick S. Dillon
; Craig A. Rosen
; Steven C. Barash
; Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
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: FILING DATE: 20-Oct-1997
: CLASSIFICATION: <Unknown>
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 60/009,861
: FILING DATE: January 5, 1996
: APPLICATION NUMBER: 08/781,986
: FILING DATE: January 3, 1997
: ATTORNEY/AGENT INFORMATION:
: NAME: Mark J. Hyman
: REGISTRATION NUMBER: 46,789
: REFERENCE/DOCKET NUMBER: PB248P1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (240) 314-1224
: TELEFAX: (301) 309-8439
: INFORMATION FOR SEQ ID NO: 205:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 16397 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
:
: SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-08-956-171E-205
Query Match          13.4%; Score 15; DB 3; Length 16397;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55  CGCCGTAAGAAGT 69
Db      8528  CGCCGTAAGAAGT 8514

RESULT 33
US-08-781-986A-205/c
: Sequence 205, Application US/08781986A
: Patent No. 6737248
: GENERAL INFORMATION:
: APPLICANT: Charles Kunach
: TITLE OF INVENTION: Stephylococcus aureus Polynucleotides and Sequences
: NUMBER OF SEQUENCES: 5255
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Human Genome Sciences, Inc.
: STREET: 9410 Key West Avenue
: CITY: Rockville
: STATE: Maryland
: COUNTRY: USA
: ZIP: 20850
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
: COMPUTER: HP Vectra 486/33
: OPERATING SYSTEM: MSDOS version 6.2
: SOFTWARE: ASCII Text
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/781,986A
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Benson, Bob
: REGISTRATION NUMBER: 30,446
: REFERENCE/DOCKET NUMBER: PB248PP
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (301) 309-8504
: TELEFAX: (301) 309-8512
: INFORMATION FOR SEQ ID NO: 205:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 16397 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
US-08-781-986A-205
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Query Match          13.4%; Score 15; DB 3; Length 16397;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      55  CGCCGTAAGAAGT 69
Db      8528  CGCCGTAAGAAGT 8514

RESULT 34
US-09-949-016-15979/c
: Sequence 15979, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 15979
: LENGTH: 21593
: TYPE: DNA
: ORGANISM: Human
: FEATURE:
: NAME/KEY: misc feature
: LOCATION: (1)...(21593)
: OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15979

Query Match          13.4%; Score 15; DB 3; Length 21593;
Best Local Similarity 100.0%; Pred. No. 98;
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21  ATATTGTTTACTGA 35
Db      12092  ATATTGTTTACTGA 12078

RESULT 35
US-09-949-016-17466
: Sequence 17466, Application US/09949016
: Patent No. 6812339
: GENERAL INFORMATION:
: APPLICANT: VENTER, J. Craig et al.
: TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
: WITH INFECTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: CLO01307
: CURRENT APPLICATION NUMBER: US/09/949,016
: PRIOR FILING DATE: 2000-04-14
: PRIOR APPLICATION NUMBER: 60/241,755
: PRIOR FILING DATE: 2000-10-20
: PRIOR APPLICATION NUMBER: 60/237,768
: PRIOR FILING DATE: 2000-10-03
: PRIOR APPLICATION NUMBER: 60/231,498
: PRIOR FILING DATE: 2000-09-08
: NUMBER OF SEQ ID NOS: 207012
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 17466
: LENGTH: 27555
: TYPE: DNA
: ORGANISM: Human
US-09-949-016-17466
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Query Match 13.4%; Score 15; DB 3; Length 27555;  
Best Local Similarity 100.0%; Pred. No. 99;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ATATATTGTTTACT 33  
|||||  
Db 18068 ATATATTGTTTACT 18082

RESULT 36  
US-09-949-016-16052  
; Sequence 16052, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 16052  
; LENGTH: 58879  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(58879)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-16052

Query Match 13.4%; Score 15; DB 3; Length 58879;  
Best Local Similarity 100.0%; Pred. No. 1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ATATATTGTTTACT 33  
|||||  
Db 24754 ATATATTGTTTACT 24768

RESULT 37  
US-09-949-016-14890/C  
; Sequence 14890, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14890  
; LENGTH: 93364  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(93364)

; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-14890

Query Match 13.4%; Score 15; DB 3; Length 93364;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 TAAAGAGTCTCTAA 74  
|||||  
Db 30957 TAAAGAGTCTCTAA 30943

RESULT 38  
US-09-949-016-12551/C  
; Sequence 12551, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12551  
; LENGTH: 96878  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc\_feature  
; LOCATION: (1)...(96878)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12551

Query Match 13.4%; Score 15; DB 3; Length 96878;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 ATATTGTTTACTGA 35  
|||||  
Db 89420 ATATTGTTTACTGA 89406

RESULT 39  
US-09-949-016-14169/C  
; Sequence 14169, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; PRIOR FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14169  
; LENGTH: 109159  
; TYPE: DNA  
; ORGANISM: Human



US-09-949-016-14169

Query Match 13.4%; Score 15; DB 3; Length 109159;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AAAGAGGTCTTAAT 75  
|||||  
Db 30192 AAAGAGGTCTTAAT 30178

RESULT 40

US-09-949-016-14170/c  
; Sequence 14170, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14170  
; LENGTH: 109159  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-14170

Query Match 13.4%; Score 15; DB 3; Length 109159;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 AAAGAGGTCTTAAT 75  
|||||  
Db 30192 AAAGAGGTCTTAAT 30178

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Job time : 82.4595 secs



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GenCore version 5.1.7  
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Run on: April 12, 2006, 04:34:31 ; Search time 303.376 Seconds  
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Title: US-10-712-654-25

Perfect score: 112

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Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 413468905 residues

Word size : 1

Total number of hits satisfying chosen parameters: 19584538

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

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- 9: /cgn2\_6/ptodata/1/pubpna/US10E\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	25	22.3	25	5	US-10-068-238-13
5	18	16.1	1042	7	US-10-260-228-3339
6	18	16.1	2782	7	US-10-437-963-44672
7	17	15.2	551	4	US-09-925-065A-626524
8	17	15.2	787	8	US-10-425-115-26871
9	17	15.2	830	8	US-10-425-115-26868
10	17	15.2	855	7	US-10-425-114-4342
11	17	15.2	973	7	US-10-425-114-12904
12	17	15.2	974	7	US-10-425-114-21001
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15	17	15.2	4224	7	US-10-437-963-44719
16	16	14.3	25	10	US-11-036-317-201076
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18	16	14.3	25	10	US-11-036-317-351958
19	16	14.3	142	7	US-10-437-963-80382
20	16	14.3	403	6	US-10-424-599-9960
21	16	14.3	434	6	US-10-131-827-8493
22	16	14.3	472	5	US-10-027-632-57063
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C 24	16	14.3	526	5	US-10-198-846-9184	Sequence 9184, Ap
C 25	16	14.3	552	7	US-10-424-599-117489	Sequence 117489, A
C 26	16	14.3	569	6	US-10-029-886-13425	Sequence 13425, A
C 27	16	14.3	577	4	US-09-925-065A-619252	Sequence 619252, A
C 28	16	14.3	577	4	US-09-925-065A-619253	Sequence 619253, A
C 29	16	14.3	608	7	US-10-021-323-15408	Sequence 15408, A
C 30	16	14.3	623	4	US-09-925-065A-682241	Sequence 682241, A
C 31	16	14.3	624	4	US-09-925-065A-104147	Sequence 104147, A
C 32	16	14.3	642	5	US-10-027-632-1803	Sequence 1803, Ap
C 33	16	14.3	642	5	US-10-027-632-1803	Sequence 1803, Ap
C 34	16	14.3	663	6	US-10-027-632-199517	Sequence 199517, A
C 35	16	14.3	663	5	US-10-027-632-199518	Sequence 199518, A
C 36	16	14.3	663	5	US-10-027-632-199519	Sequence 199519, A
C 37	16	14.3	663	6	US-10-027-632-199517	Sequence 199517, A
C 38	16	14.3	663	6	US-10-027-632-199518	Sequence 199518, A
C 39	16	14.3	663	6	US-10-027-632-199519	Sequence 199519, A
C 40	16	14.3	675	5	US-10-027-632-283608	Sequence 283608, A
C 41	16	14.3	675	6	US-10-027-632-283608	Sequence 283608, A
C 42	16	14.3	759	5	US-10-027-632-4356	Sequence 4356, Ap
C 43	16	14.3	759	6	US-10-027-632-4356	Sequence 4356, Ap
C 44	16	14.3	777	7	US-10-424-599-122751	Sequence 122751, A
C 45	16	14.3	818	5	US-10-027-632-131126	Sequence 131126, A
C 46	16	14.3	818	6	US-10-027-632-131126	Sequence 131126, A
C 47	16	14.3	829	7	US-10-383-201-47	Sequence 47, Appl
C 48	16	14.3	829	7	US-10-383-201-47	Sequence 47, Appl
C 49	16	14.3	832	5	US-10-027-632-173824	Sequence 173824, A
C 50	16	14.3	832	5	US-10-027-632-173825	Sequence 173825, A
C 51	16	14.3	832	6	US-10-027-632-173824	Sequence 173824, A
C 52	16	14.3	832	6	US-10-027-632-173825	Sequence 173825, A
C 53	16	14.3	910	4	US-09-925-065A-952833	Sequence 952833, A
C 54	16	14.3	928	5	US-10-027-632-172683	Sequence 172683, A
C 55	16	14.3	928	5	US-10-027-632-172684	Sequence 172684, A
C 56	16	14.3	928	5	US-10-027-632-172685	Sequence 172685, A
C 57	16	14.3	928	6	US-10-027-632-172683	Sequence 172683, A
C 58	16	14.3	928	6	US-10-027-632-172684	Sequence 172684, A
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C 61	16	14.3	1155	4	US-09-925-065A-84148	Sequence 84148, A
C 62	16	14.3	1155	4	US-09-925-065A-84149	Sequence 84149, A
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C 66	16	14.3	1392	7	US-10-383-201-45	Sequence 45, Appl
C 67	16	14.3	1399	7	US-10-383-201-49	Sequence 49, Appl
C 68	16	14.3	1399	7	US-10-383-201-49	Sequence 49, Appl
C 69	16	14.3	1476	7	US-10-383-201-41	Sequence 41, Appl
C 70	16	14.3	1665	3	US-09-814-353-19185	Sequence 19185, A
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C 72	16	14.3	2084	10	US-11-097-143-12599	Sequence 12599, A
C 73	16	14.3	2307	7	US-10-260-238-1194	Sequence 1194, Ap
C 74	16	14.3	2517	5	US-10-198-846-12773	Sequence 12773, A
C 75	16	14.3	2995	3	US-09-925-065A-481	Sequence 481, Ap
C 76	16	14.3	4525	9	US-10-887-553A-759	Sequence 759, Ap
C 77	16	14.3	8354	7	US-10-383-201-43	Sequence 43, Appl
C 78	16	14.3	8354	7	US-10-029-020-13	Sequence 13, Appl
C 79	16	14.3	8395	6	US-10-311-435-148	Sequence 148, Ap
C 80	16	14.3	8645	6	US-10-467-535-52	Sequence 52, Appl
C 81	16	14.3	11365	7	US-10-433-311A-1	Sequence 1, Appl
C 82	16	14.3	12044	10	US-11-097-143-12598	Sequence 12598, A
C 83	15	13.4	25	10	US-11-036-317-333354	Sequence 333354, A
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C 85	15	13.4	170	3	US-09-815-242-2743	Sequence 2743, Ap
C 86	15	13.4	170	7	US-10-282-122A-5261	Sequence 5261, Ap
C 87	15	13.4	170	7	US-10-282-122A-6087	Sequence 6087, Ap
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C 89	15	13.4	221	3	US-10-424-599-1500	Sequence 1500, Ap
C 90	15	13.4	223	3	US-10-424-599-16354	Sequence 16354, A
C 91	15	13.4	246	3	US-09-815-242-1274	Sequence 1274, Ap
C 92	15	13.4	246	7	US-10-282-122A-4782	Sequence 4782, Ap
C 93	15	13.4	250	3	US-09-887-577-54	Sequence 54, Appl
C 94	15	13.4	250	3	US-10-796-174-54	Sequence 54, Appl
C 95	15	13.4	261	9	US-10-839-227-1	Sequence 1, Appl
C 96	15	13.4	264	7	US-10-424-599-28115	Sequence 28115, A



C 97	15	13.4	294	3	US-09-815-242-817	Sequence 817, App	170	15	13.4	642	4	US-09-925-065A-294710	Sequence 294710,
C 98	15	13.4	294	7	US-10-282-122A-814	Sequence 814, App	171	15	13.4	642	4	US-09-925-065A-294711	Sequence 294711,
C 99	15	13.4	321	7	US-10-282-122A-35081	Sequence 35081, A	172	15	13.4	642	4	US-09-925-065A-294712	Sequence 294712,
C 100	15	13.4	331	7	US-10-469-285-305	Sequence 305, App	173	15	13.4	646	4	US-09-925-065A-880693	Sequence 880693,
C 101	15	13.4	341	8	US-10-425-115-125769	Sequence 125769,	174	15	13.4	646	4	US-09-925-065A-908433	Sequence 908433,
C 102	15	13.4	357	8	US-10-357-930-18498	Sequence 18498, A	175	15	13.4	650	5	US-10-027-632-112711	Sequence 213711,
C 103	15	13.4	370	7	US-10-242-535A-43133	Sequence 24313, A	176	15	13.4	650	5	US-10-027-632-212712	Sequence 212712,
C 104	15	13.4	370	7	US-10-085-783A-43133	Sequence 24313, A	177	15	13.4	650	6	US-10-027-632-212711	Sequence 212711,
C 105	15	13.4	377	3	US-09-918-995-35262	Sequence 36262, A	178	15	13.4	651	6	US-10-027-632-212712	Sequence 212712,
C 106	15	13.4	416	4	US-09-925-065A-154516	Sequence 154516, A	179	15	13.4	651	4	US-09-925-065A-698557	Sequence 698557,
C 107	15	13.4	426	8	US-10-357-930-48309	Sequence 48309, A	180	15	13.4	655	7	US-10-641-643-98	Sequence 98, App1
C 108	15	13.4	431	3	US-09-864-761-2457	Sequence 2457, App	181	15	13.4	657	5	US-10-027-632-215358	Sequence 215358,
C 109	15	13.4	440	7	US-10-424-599-30955	Sequence 30955, A	182	15	13.4	657	6	US-10-027-632-215358	Sequence 215358,
C 110	15	13.4	453	4	US-09-925-065A-379196	Sequence 379196,	183	15	13.4	676	5	US-10-027-632-112880	Sequence 112880,
C 111	15	13.4	453	4	US-09-925-065A-379197	Sequence 379197,	184	15	13.4	676	5	US-10-027-632-112880	Sequence 112880,
C 112	15	13.4	467	3	US-09-918-995-25526	Sequence 25526, A	185	15	13.4	677	5	US-10-027-632-278788	Sequence 278788,
C 113	15	13.4	468	3	US-09-918-995-25241	Sequence 25241, A	186	15	13.4	677	6	US-10-027-632-278788	Sequence 278788,
C 114	15	13.4	469	9	US-10-450-763-25866	Sequence 25866, A	187	15	13.4	759	7	US-10-027-632-278788	Sequence 278788,
C 115	15	13.4	486	5	US-10-027-632-81193	Sequence 81193, A	188	15	13.4	795	8	US-10-689-006-21	Sequence 21,
C 116	15	13.4	486	5	US-10-027-632-292781	Sequence 292781, A	189	15	13.4	810	5	US-10-027-632-154075	Sequence 154075,
C 117	15	13.4	486	6	US-10-027-632-81193	Sequence 81193, A	190	15	13.4	810	5	US-10-027-632-154076	Sequence 154076,
C 118	15	13.4	486	6	US-10-027-632-292781	Sequence 292781, A	191	15	13.4	810	5	US-10-027-632-154076	Sequence 154076,
C 119	15	13.4	526	4	US-09-925-065A-376838	Sequence 376838,	192	15	13.4	810	6	US-10-027-632-154075	Sequence 154075,
C 120	15	13.4	528	3	US-09-815-242-3885	Sequence 3885, App	193	15	13.4	810	6	US-10-027-632-154076	Sequence 154076,
C 121	15	13.4	531	3	US-09-864-761-12334	Sequence 12334, A	194	15	13.4	883	7	US-10-437-963-26854	Sequence 26854,
C 122	15	13.4	534	7	US-10-282-122A-6243	Sequence 6243, App	195	15	13.4	883	3	US-09-770-445-517	Sequence 517, App
C 123	15	13.4	534	7	US-10-282-122A-11588	Sequence 21588, A	196	15	13.4	888	7	US-10-437-963-38121	Sequence 38121, A
C 124	15	13.4	534	7	US-10-282-122A-4353	Sequence 34353, A	197	15	13.4	900	7	US-10-437-963-47839	Sequence 47839, A
C 125	15	13.4	534	7	US-10-282-122A-36030	Sequence 36030, A	198	15	13.4	926	3	US-09-864-761-19188	Sequence 19188, A
C 126	15	13.4	534	8	US-10-472-928-265	Sequence 265, App	199	15	13.4	956	8	US-10-425-115-42439	Sequence 42439, A
C 127	15	13.4	537	3	US-09-815-242-6432	Sequence 6432, App	200	15	13.4	960	8	US-10-425-115-42439	Sequence 42439, A
C 128	15	13.4	537	3	US-09-815-242-8132	Sequence 8132, App	201	15	13.4	964	4	US-09-925-065A-702729	Sequence 702729,
C 129	15	13.4	537	3	US-09-815-242-8732	Sequence 8732, App	202	15	13.4	964	4	US-09-925-065A-702730	Sequence 702730,
C 130	15	13.4	537	3	US-09-815-242-9473	Sequence 9473, App	203	15	13.4	990	9	US-10-508-768A-24	Sequence 24, App1
C 131	15	13.4	537	7	US-10-282-122A-8015	Sequence 8015, App	204	15	13.4	1034	7	US-10-437-963-35360	Sequence 35360, A
C 132	15	13.4	537	7	US-10-282-122A-24649	Sequence 24649, A	205	15	13.4	1162	7	US-10-425-114-23994	Sequence 23994, A
C 133	15	13.4	537	8	US-10-857-625-475	Sequence 475, App	206	15	13.4	1194	7	US-10-437-963-81739	Sequence 81739, A
C 134	15	13.4	540	5	US-10-027-632-62132	Sequence 62132, A	207	15	13.4	1210	8	US-10-425-115-12869	Sequence 12869, A
C 135	15	13.4	540	5	US-10-027-632-297955	Sequence 297955, A	208	15	13.4	1211	8	US-10-425-115-12869	Sequence 12869, A
C 136	15	13.4	540	6	US-10-027-632-62132	Sequence 62132, A	209	15	13.4	1212	7	US-10-767-701-13756	Sequence 13756, A
C 137	15	13.4	540	6	US-10-027-632-297955	Sequence 297955, A	210	15	13.4	1350	6	US-09-925-065A-702728	Sequence 702728,
C 138	15	13.4	543	5	US-10-027-632-219781	Sequence 219781, A	211	15	13.4	1384	4	US-09-925-065A-702729	Sequence 702729,
C 139	15	13.4	552	6	US-10-027-632-219781	Sequence 219781, A	212	15	13.4	1384	4	US-09-925-065A-702730	Sequence 702730,
C 140	15	13.4	552	9	US-10-474-776-446	Sequence 446, App	213	15	13.4	1384	4	US-09-925-065A-702730	Sequence 702730,
C 141	15	13.4	552	9	US-10-617-320-2198	Sequence 2198, App	214	15	13.4	1400	9	US-10-955-157-7724	Sequence 7724, App
C 142	15	13.4	558	7	US-10-724-972A-2659	Sequence 2659, App	215	15	13.4	1431	6	US-10-369-493-27156	Sequence 27156, A
C 143	15	13.4	563	4	US-09-925-065A-334863	Sequence 334863, App	216	15	13.4	1631	10	US-11-097-143-37475	Sequence 37475, A
C 144	15	13.4	570	9	US-09-925-065A-878817	Sequence 878817, A	217	15	13.4	1655	10	US-11-097-143-35363	Sequence 35363, App
C 145	15	13.4	577	4	US-09-925-065A-878817	Sequence 878817, A	218	15	13.4	1916	7	US-10-424-599-59459	Sequence 59459, A
C 146	15	13.4	577	4	US-09-925-065A-878819	Sequence 878819, A	219	15	13.4	1928	9	US-10-450-763-21992	Sequence 21992, A
C 147	15	13.4	577	4	US-09-925-065A-907243	Sequence 907243, A	220	15	13.4	1939	8	US-10-425-115-12880	Sequence 12880, A
C 148	15	13.4	580	4	US-09-925-065A-334862	Sequence 334862, A	221	15	13.4	1964	9	US-10-956-157-2489	Sequence 2489, App
C 149	15	13.4	581	4	US-09-925-065A-58455	Sequence 58455, A	222	15	13.4	1964	9	US-10-631-467-238	Sequence 238, App
C 150	15	13.4	581	4	US-09-925-065A-58455	Sequence 58455, A	223	15	13.4	1968	3	US-09-991-936-1910	Sequence 1910, App
C 151	15	13.4	595	5	US-10-027-632-34402	Sequence 34402, A	224	15	13.4	1968	3	US-09-991-936-1911	Sequence 1911, App
C 152	15	13.4	595	6	US-10-027-632-34402	Sequence 34402, A	225	15	13.4	1968	3	US-10-978-246-1910	Sequence 1910, App
C 153	15	13.4	599	4	US-09-925-065A-248965	Sequence 248965, A	226	15	13.4	1968	9	US-10-978-246-1911	Sequence 1911, App
C 154	15	13.4	600	9	US-10-972-079-32280	Sequence 32280, A	227	15	13.4	2051	7	US-10-437-963-2707	Sequence 2707, App
C 155	15	13.4	600	9	US-10-972-079-61737	Sequence 61737, A	228	15	13.4	2066	7	US-10-437-963-74019	Sequence 74019, A
C 156	15	13.4	600	9	US-10-972-079-70973	Sequence 70973, A	229	15	13.4	2117	6	US-10-108-260A-2250	Sequence 2250, App
C 157	15	13.4	600	9	US-10-972-079-79702	Sequence 79702, A	230	15	13.4	2158	7	US-10-767-701-11871	Sequence 11871, A
C 158	15	13.4	602	5	US-10-027-632-205606	Sequence 205606, A	231	15	13.4	2191	3	US-09-991-936-1908	Sequence 1908, App
C 159	15	13.4	602	5	US-10-027-632-205607	Sequence 205607, A	232	15	13.4	2191	3	US-09-991-936-1909	Sequence 1909, App
C 160	15	13.4	602	5	US-10-027-632-205608	Sequence 205608, A	233	15	13.4	2191	9	US-10-978-246-1908	Sequence 1908, App
C 161	15	13.4	602	5	US-10-027-632-205609	Sequence 205609, A	234	15	13.4	2191	9	US-10-978-246-1909	Sequence 1909, App
C 162	15	13.4	602	6	US-10-027-632-205606	Sequence 205606, A	235	15	13.4	2370	7	US-10-398-221-2028	Sequence 2028, App
C 163	15	13.4	602	6	US-10-027-632-205607	Sequence 205607, A	236	15	13.4	2453	10	US-11-097-143-29167	Sequence 29167, A
C 164	15	13.4	602	6	US-10-027-632-205608	Sequence 205608, A	237	15	13.4	2553	3	US-09-991-936-1917	Sequence 1917, App
C 165	15	13.4	602	6	US-10-027-632-205609	Sequence 205609, A	238	15	13.4	2553	3	US-09-991-936-1918	Sequence 1918, App
C 166	15	13.4	605	4	US-09-925-065A-437982	Sequence 437982, A	239	15	13.4	2553	9	US-10-978-246-1917	Sequence 1917, App
C 167	15	13.4	633	4	US-09-925-065A-311111	Sequence 311111, A	240	15	13.4	2559	9	US-10-978-246-1918	Sequence 1918, App
C 168	15	13.4	633	4	US-09-925-065A-628926	Sequence 628926, A	241	15	13.4	2559	9	US-10-282-122A-17735	Sequence 17735, A
C 169	15	13.4	637	10	US-11-097-143-52480	Sequence 52480, App	242	15	13.4	2567	7	US-10-398-221-3724	Sequence 3724, App



C 243	15	13.4	2696	10	US-11-097-143-5239	Sequence 5239, Ap	316	14	12.5	25	9	US-10-843-527-144801	Sequence 144801,
C 244	15	13.4	2724	10	US-11-097-143-1196	Sequence 1196, Ap	317	14	12.5	25	10	US-11-036-317-334079	Sequence 334079,
C 245	15	13.4	2853	9	US-10-450-763-25875	Sequence 25875, A	318	14	12.5	25	10	US-11-036-317-81648	Sequence 81648,
C 246	15	13.4	2917	10	US-11-097-143-5647	Sequence 5647, Ap	319	14	12.5	25	10	US-11-060-756-273479	Sequence 273479,
C 247	15	13.4	2939	10	US-11-097-143-1346	Sequence 1346, Ap	320	14	12.5	60	3	US-09-908-575-1965	Sequence 7965, Ap
C 248	15	13.4	3016	10	US-11-097-143-5233	Sequence 5233, Ap	321	14	12.5	145	7	US-10-424-599-133000	Sequence 133000,
C 249	15	13.4	3050	10	US-11-097-143-12595	Sequence 12595, A	322	14	12.5	180	5	US-10-083-357-145	Sequence 145, Ap
C 250	15	13.4	3126	3	US-09-991-936-1914	Sequence 1914, Ap	323	14	12.5	201	8	US-10-719-993-40273	Sequence 40273, A
C 251	15	13.4	3126	3	US-10-978-245-1914	Sequence 1914, Ap	324	14	12.5	201	8	US-10-719-993-40275	Sequence 40275, A
C 252	15	13.4	3126	3	US-10-978-245-1916	Sequence 1916, Ap	325	14	12.5	201	8	US-10-741-600-28923	Sequence 28923, A
C 253	15	13.4	3126	7	US-10-978-245-1916	Sequence 1916, Ap	326	14	12.5	201	8	US-10-741-600-51730	Sequence 51730, A
C 254	15	13.4	3159	7	US-10-437-963-59602	Sequence 59602, A	327	14	12.5	216	8	US-10-425-115-174413	Sequence 174413,
C 255	15	13.4	3409	10	US-11-097-143-5536	Sequence 5536, Ap	328	14	12.5	216	8	US-10-425-115-179579	Sequence 179579,
C 256	15	13.4	3723	10	US-11-097-143-5362	Sequence 5362, Ap	329	14	12.5	234	7	US-10-242-535A-23134	Sequence 23134, A
C 257	15	13.4	3723	10	US-11-097-143-27241	Sequence 27241, A	330	14	12.5	234	7	US-10-085-783A-23134	Sequence 23134, A
C 258	15	13.4	3834	10	US-11-097-143-5371	Sequence 5371, Ap	331	14	12.5	241	7	US-10-242-535A-15403	Sequence 15403, A
C 259	15	13.4	3906	10	US-11-097-143-9448	Sequence 9448, Ap	332	14	12.5	241	7	US-10-085-783A-15403	Sequence 15403, A
C 260	15	13.4	4116	10	US-11-097-143-27661	Sequence 27661, A	333	14	12.5	241	7	US-10-085-783A-15403	Sequence 15403, A
C 261	15	13.4	4173	6	US-10-039-112-1	Sequence 1, Appl1	334	14	12.5	253	3	US-10-425-115-110629	Sequence 110629,
C 262	15	13.4	4173	6	US-10-761-983-1	Sequence 1, Appl1	335	14	12.5	253	3	US-10-425-115-110629	Sequence 110629,
C 263	15	13.4	4212	10	US-11-097-143-16712	Sequence 16712, A	336	14	12.5	277	8	US-10-425-115-178744	Sequence 178744,
C 264	15	13.4	5205	10	US-11-097-143-37474	Sequence 37474, A	337	14	12.5	286	7	US-10-424-599-106893	Sequence 106893,
C 265	15	13.4	5645	9	US-10-764-420-1126	Sequence 2126, Ap	338	14	12.5	303	7	US-10-424-599-120544	Sequence 120544,
C 266	15	13.4	5818	7	US-10-398-221-3827	Sequence 3827, Ap	339	14	12.5	308	3	US-09-967-899-6408	Sequence 6408, Ap
C 267	15	13.4	6661	3	US-09-873-367C-257	Sequence 257, Ap	340	14	12.5	318	5	US-10-083-357-146	Sequence 146, Ap
C 268	15	13.4	6661	3	US-10-843-641A-257	Sequence 257, Ap	341	14	12.5	318	7	US-10-424-599-103068	Sequence 103068,
C 269	15	13.4	6697	10	US-11-097-143-20158	Sequence 20158, A	342	14	12.5	318	7	US-10-424-599-103068	Sequence 103068,
C 270	15	13.4	7554	10	US-11-097-143-9994	Sequence 9994, Ap	343	14	12.5	319	8	US-10-425-115-129995	Sequence 129995,
C 271	15	13.4	9306	10	US-11-097-143-16711	Sequence 16711, A	344	14	12.5	328	7	US-10-242-535A-11440	Sequence 11440, A
C 272	15	13.4	9613	10	US-11-097-143-1195	Sequence 1195, A	345	14	12.5	341	8	US-10-085-783A-11440	Sequence 11440, A
C 273	15	13.4	11831	2	US-08-961-527-65	Sequence 65, Appl	346	14	12.5	344	8	US-10-425-115-62023	Sequence 62023, A
C 274	15	13.4	11831	7	US-10-158-844-65	Sequence 65, Appl	347	14	12.5	344	7	US-10-437-963-96034	Sequence 96034, A
C 275	15	13.4	12676	10	US-11-097-143-27994	Sequence 27994, A	348	14	12.5	359	8	US-10-674-124A-928	Sequence 928, Ap
C 276	15	13.4	13916	8	US-10-857-625-138	Sequence 138, Ap	349	14	12.5	359	8	US-10-425-115-182000	Sequence 182000,
C 277	15	13.4	14141	10	US-11-097-143-7474	Sequence 7474, Ap	350	14	12.5	359	8	US-10-425-115-172310	Sequence 172310,
C 278	15	13.4	14557	3	US-09-070-927A-367	Sequence 367, Ap	351	14	12.5	363	8	US-10-425-115-156551	Sequence 156551, A
C 279	15	13.4	16397	2	US-08-781-986A-205	Sequence 205, Ap	352	14	12.5	368	3	US-09-867-701-10350	Sequence 10350, A
C 280	15	13.4	16397	7	US-10-329-624-305	Sequence 205, Ap	353	14	12.5	378	7	US-10-437-963-688721	Sequence 688721, A
C 281	15	13.4	22281	5	US-10-087-192-1153	Sequence 1153, Ap	354	14	12.5	388	7	US-10-424-599-100643	Sequence 100643,
C 282	15	13.4	24227	10	US-11-097-143-1345	Sequence 1345, Ap	355	14	12.5	389	8	US-10-425-115-85857	Sequence 85857, A
C 283	15	13.4	27324	6	US-10-238-075-993	Sequence 993, Ap	356	14	12.5	390	8	US-10-425-115-184278	Sequence 184278,
C 284	15	13.4	32591	6	US-10-085-117-55	Sequence 55, Appl	357	14	12.5	391	8	US-10-425-115-179486	Sequence 179486,
C 285	15	13.4	40766	10	US-11-097-143-42070	Sequence 40270, A	358	14	12.5	396	3	US-09-918-995-4695	Sequence 4695, Ap
C 286	15	13.4	42429	10	US-11-097-143-24106	Sequence 24106, A	359	14	12.5	402	10	US-11-029-984-405	Sequence 405, Ap
C 287	15	13.4	68611	6	US-10-085-959-182	Sequence 182, Ap	360	14	12.5	402	10	US-11-029-984-406	Sequence 406, Ap
C 288	15	13.4	106664	5	US-10-175-523-97	Sequence 97, Appl	361	14	12.5	402	10	US-11-029-984-407	Sequence 407, Ap
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C 290	15	13.4	133955	5	US-10-087-192-1984	Sequence 1984, Ap	363	14	12.5	406	3	US-09-764-869-75	Sequence 75, Appl
C 291	15	13.4	134442	9	US-10-461-862-23	Sequence 23, Appl	364	14	12.5	406	5	US-10-091-504-75	Sequence 75, Appl
C 292	15	13.4	164875	6	US-10-085-117-322	Sequence 322, Ap	365	14	12.5	406	6	US-10-227-577-75	Sequence 75, Appl
C 293	15	13.4	207542	9	US-10-893-315-348	Sequence 148, Ap	366	14	12.5	407	7	US-10-424-599-1	Sequence 1, Appl1
C 294	15	13.4	207557	9	US-10-893-315-348	Sequence 148, Ap	367	14	12.5	408	3	US-09-728-445-687	Sequence 687, Ap
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C 296	15	13.4	268685	6	US-10-025-966A-22	Sequence 22, Appl	369	14	12.5	411	8	US-10-653-407-2068	Sequence 2068, Ap
C 297	15	13.4	339234	7	US-10-332-696-73	Sequence 73, Appl	370	14	12.5	417	3	US-09-764-869-1398	Sequence 1398, Ap
C 298	15	13.4	350570	8	US-10-417-375-146	Sequence 146, Ap	371	14	12.5	417	5	US-10-091-504-1398	Sequence 1398, Ap
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C 300	15	13.4	495269	7	US-10-398-221-8	Sequence 8, Appl1	373	14	12.5	418	4	US-10-424-599-80899	Sequence 80899, A
C 301	15	13.4	510510	8	US-10-741-600-17606	Sequence 17606, A	374	14	12.5	418	7	US-10-424-599-80899	Sequence 80899, A
C 302	15	13.4	684707	7	US-10-398-221-9	Sequence 9, Appl1	375	14	12.5	421	7	US-10-424-599-80899	Sequence 80899, A
C 303	15	13.4	786431	6	US-10-412-277-3	Sequence 3, Appl1	376	14	12.5	425	4	US-09-925-065A-608436	Sequence 608436,
C 304	15	13.4	1163020	7	US-10-398-221-10	Sequence 10, Appl	377	14	12.5	427	8	US-10-425-115-1677	Sequence 1677, Ap
C 305	15	13.4	1754382	9	US-10-501-282-6651	Sequence 6651, Ap	378	14	12.5	433	7	US-10-424-599-117685	Sequence 117685,
C 306	15	13.4	2162598	8	US-10-472-928-4979	Sequence 4979, Ap	379	14	12.5	440	4	US-09-925-065A-197704	Sequence 197704,
C 307	15	13.4	3011208	7	US-10-398-221-2058	Sequence 2058, Ap	380	14	12.5	440	5	US-10-027-632-94549	Sequence 94549, A
C 308	15	13.4	3011208	7	US-10-398-221-2058	Sequence 2058, Ap	381	14	12.5	440	5	US-10-027-632-305091	Sequence 305091,
C 309	15	13.4	9025608	6	US-10-156-761-1	Sequence 1, Appl1	382	14	12.5	440	6	US-10-027-632-94549	Sequence 94549, A
C 310	14	12.5	25	7	US-10-719-956-449959	Sequence 449959,	383	14	12.5	443	3	US-09-861-893-46	Sequence 861, Appl
C 311	14	12.5	25	7	US-10-719-956-587101	Sequence 587101,	384	14	12.5	443	3	US-10-308-863-26	Sequence 308, Appl
C 312	14	12.5	25	8	US-10-719-900-100687	Sequence 100687,	385	14	12.5	443	6	US-10-296-862-46	Sequence 296, Appl
C 313	14	12.5	25	8	US-10-719-900-574568	Sequence 574568,	386	14	12.5	444	7	US-10-282-122A-36386	Sequence 282, A
C 314	14	12.5	25	8	US-10-719-900-784758	Sequence 784758,	387	14	12.5	448	7	US-10-282-122A-36386	Sequence 282, A
C 315	14	12.5	25	9	US-10-843-527-93376	Sequence 93376, A	388	14	12.5	448	8	US-10-425-115-19707	Sequence 19707, A



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C 390	14	12.5	451	7	US-10-437-963-79407	Sequence 79407, A
C 391	14	12.5	457	8	US-10-425-115-48005	Sequence 48005, A
C 392	14	12.5	459	6	US-10-300-341-9	Sequence 9, Appl1
C 393	14	12.5	460	3	US-09-918-995-9688	Sequence 9688, Ap
C 394	14	12.5	466	4	US-09-925-065A-187488	Sequence 187488, Ap
C 395	14	12.5	467	3	US-09-764-877-2059	Sequence 2059, Ap
C 396	14	12.5	467	3	US-09-764-877-2060	Sequence 2060, Ap
C 397	14	12.5	467	6	US-10-242-515-2059	Sequence 2059, Ap
C 398	14	12.5	467	6	US-10-242-515-2060	Sequence 2060, Ap
C 399	14	12.5	478	8	US-10-425-115-37722	Sequence 37722, A
C 400	14	12.5	481	8	US-10-425-115-142236	Sequence 142236, A
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C 402	14	12.5	493	7	US-10-021-323-2657	Sequence 2657, Ap
C 403	14	12.5	495	4	US-09-925-065A-192242	Sequence 192242, A
C 404	14	12.5	497	4	US-09-925-065A-241433	Sequence 241433, A
C 405	14	12.5	497	4	US-09-925-065A-241434	Sequence 241434, A
C 406	14	12.5	498	3	US-09-070-927A-509	Sequence 509, App
C 407	14	12.5	500	3	US-09-991-936-399	Sequence 399, App
C 408	14	12.5	500	7	US-10-621-901-46	Sequence 46, Appl
C 409	14	12.5	500	9	US-10-978-245-399	Sequence 399, App
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C 419	14	12.5	507	5	US-10-027-632-194624	Sequence 194624, A
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C 423	14	12.5	509	6	US-10-300-341-6	Sequence 6, Appl1
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C 426	14	12.5	514	6	US-10-027-632-286874	Sequence 286874, A
C 427	14	12.5	515	4	US-10-767-701-17824	Sequence 17824, A
C 428	14	12.5	516	4	US-09-925-065A-665586	Sequence 665586, A
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C 430	14	12.5	520	5	US-10-171-581-318	Sequence 318, App
C 431	14	12.5	529	5	US-10-027-632-241642	Sequence 241642, A
C 432	14	12.5	529	6	US-10-027-632-241642	Sequence 241642, A
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C 434	14	12.5	532	4	US-09-925-065A-348406	Sequence 348406, A
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C 436	14	12.5	532	8	US-10-363-345A-34531	Sequence 34531, A
C 437	14	12.5	532	8	US-10-363-345A-34532	Sequence 34532, A
C 438	14	12.5	532	9	US-10-363-483A-34531	Sequence 34531, A
C 439	14	12.5	532	9	US-10-363-483A-34532	Sequence 34532, A
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C 447	14	12.5	555	4	US-09-925-065A-95108	Sequence 95108, A
C 448	14	12.5	555	7	US-10-021-323-16893	Sequence 16893, A
C 449	14	12.5	556	4	US-09-925-065A-171930	Sequence 171930, A
C 450	14	12.5	556	4	US-09-925-065A-766568	Sequence 766568, A
C 451	14	12.5	557	4	US-09-925-065A-18063	Sequence 18063, A
C 452	14	12.5	559	4	US-09-925-065A-488650	Sequence 488650, A
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C 454	14	12.5	561	4	US-09-925-065A-239716	Sequence 239716, A
C 455	14	12.5	561	4	US-09-925-065A-239717	Sequence 239717, A
C 456	14	12.5	562	4	US-09-925-065A-764381	Sequence 764381, A
C 457	14	12.5	562	4	US-09-925-065A-580419	Sequence 580419, A
C 458	14	12.5	566	4	US-09-925-065A-410238	Sequence 410238, A
C 459	14	12.5	566	4	US-09-925-065A-410239	Sequence 410239, A
C 460	14	12.5	567	4	US-09-925-065A-497093	Sequence 497093, A
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C 463	14	12.5	572	4	US-09-925-065A-102440	Sequence 102440, A
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C 468	14	12.5	574	4	US-09-925-065A-103995	Sequence 103995, A
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C 470	14	12.5	575	4	US-09-925-065A-286900	Sequence 286900, A
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C 483	14	12.5	582	8	US-10-425-115-63190	Sequence 63190, A
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C 485	14	12.5	584	4	US-09-925-065A-932359	Sequence 932359, A
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C 487	14	12.5	585	5	US-10-027-632-279421	Sequence 279421, A
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C 489	14	12.5	585	6	US-10-027-632-279421	Sequence 279421, A
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C 491	14	12.5	586	5	US-10-027-632-37	Sequence 37, Appl
C 492	14	12.5	586	6	US-10-027-632-36	Sequence 36, Appl
C 493	14	12.5	586	6	US-10-027-632-16	Sequence 16, Appl
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C 496	14	12.5	588	4	US-09-925-065A-210262	Sequence 210262, A
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C 498	14	12.5	591	4	US-09-925-065A-584590	Sequence 584590, A
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C 518	14	12.5	600	9	US-10-972-079-71709	Sequence 71709, A
C 519	14	12.5	600	9	US-10-972-079-79058	Sequence 79058, A
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C 522	14	12.5	602	4	US-09-925-065A-789306	Sequence 789306, A
C 523	14	12.5	603	4	US-09-925-065A-650471	Sequence 650471, A
C 524	14	12.5	603	4	US-09-925-065A-650472	Sequence 650472, A
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C 526	14	12.5	603	5	US-10-027-632-64679	Sequence 64679, A
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C 530	14	12.5	605	4	US-09-925-065A-975757	Sequence 975757, A
C 531	14	12.5	605	4	US-09-925-065A-975757	Sequence 975757, A
C 532	14	12.5	606	4	US-09-925-065A-674170	Sequence 674170, A
C 533	14	12.5	610	4	US-09-925-065A-748703	Sequence 748703, A
C 534	14	12.5	610	4	US-09-925-065A-902578	Sequence 902578, A



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C 537	14	12.5	611	5	US-10-027-632-272215	Sequence 272215, A	C 610	14	12.5	712	5	US-10-027-632-99362	Sequence 99362, A
C 538	14	12.5	611	6	US-10-027-632-272215	Sequence 272215, A	C 611	14	12.5	712	6	US-10-027-632-99362	Sequence 99362, A
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C 541	14	12.5	613	4	US-09-925-065A-826012	Sequence 826012, A	C 614	14	12.5	722	6	US-10-027-632-99362	Sequence 99362, A
C 542	14	12.5	613	7	US-10-437-963-100078	Sequence 100078, A	C 615	14	12.5	729	4	US-09-925-065A-932739	Sequence 932739, A
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C 546	14	12.5	616	4	US-09-925-065A-792680	Sequence 792680, A	C 619	14	12.5	729	6	US-10-027-632-26515	Sequence 26515, A
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C 550	14	12.5	619	4	US-09-925-065A-660412	Sequence 660412, A	C 623	14	12.5	732	9	US-10-755-415-160	Sequence 160, App
551	14	12.5	619	4	US-09-925-065A-796258	Sequence 796258, A	C 624	14	12.5	741	5	US-10-027-632-126561	Sequence 126561, A
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C 556	14	12.5	621	4	US-10-437-963-69937	Sequence 933357, A	C 629	14	12.5	752	4	US-09-925-065A-548590	Sequence 548590, A
C 557	14	12.5	623	7	US-10-437-963-69937	Sequence 933357, A	C 630	14	12.5	762	4	US-10-437-963-100139	Sequence 100139, A
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C 564	14	12.5	629	8	US-10-363-345A-36934	Sequence 36934, A	C 637	14	12.5	794	6	US-10-012-697-18	Sequence 18, App1
565	14	12.5	629	9	US-10-363-483A-36933	Sequence 36933, A	C 638	14	12.5	794	7	US-10-779-543-12018	Sequence 12018, A
C 566	14	12.5	630	4	US-09-925-065A-533709	Sequence 533709, A	639	14	12.5	798	7	US-10-282-122A-18586	Sequence 18586, A
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C 570	14	12.5	631	4	US-09-925-065A-125552	Sequence 125552, A	643	14	12.5	808	8	US-10-767-705-1008	Sequence 1008, A
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C 573	14	12.5	632	4	US-10-027-632-187836	Sequence 187836, A	646	14	12.5	825	8	US-10-472-632-159453	Sequence 159453, A
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C 575	14	12.5	638	4	US-09-925-065A-694729	Sequence 694729, A	648	14	12.5	827	6	US-10-027-632-159454	Sequence 159454, A
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577	14	12.5	638	4	US-09-925-065A-694731	Sequence 694731, A	650	14	12.5	834	3	US-09-738-636-1216	Sequence 1216, Ap
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C 579	14	12.5	638	5	US-10-027-632-287777	Sequence 287777, A	C 652	14	12.5	840	9	US-10-779-543-12019	Sequence 12019, A
C 580	14	12.5	638	6	US-10-653-047-5539	Sequence 5539, Ap	C 653	14	12.5	841	8	US-10-425-115-116616	Sequence 116616, A
C 581	14	12.5	645	4	US-09-925-065A-789659	Sequence 789659, A	C 654	14	12.5	851	5	US-10-027-632-172515	Sequence 172515, A
C 582	14	12.5	645	4	US-10-027-632-197491	Sequence 197491, A	655	14	12.5	851	5	US-10-027-632-172516	Sequence 172516, A
C 583	14	12.5	645	4	US-10-027-632-197491	Sequence 197491, A	656	14	12.5	851	5	US-10-027-632-172516	Sequence 172516, A
C 584	14	12.5	645	4	US-10-027-632-197491	Sequence 197491, A	657	14	12.5	851	6	US-10-027-632-172516	Sequence 172516, A
C 585	14	12.5	645	4	US-10-027-632-197491	Sequence 197491, A	658	14	12.5	851	6	US-10-027-632-172516	Sequence 172516, A
C 586	14	12.5	645	4	US-10-027-632-197491	Sequence 197491, A	659	14	12.5	858	6	US-10-027-632-172516	Sequence 172516, A
C 587	14	12.5	654	6	US-11-097-143-38348	Sequence 38348, A	660	14	12.5	879	7	US-10-282-122A-21105	Sequence 21105, A
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C 593	14	12.5	663	4	US-09-925-065A-904129	Sequence 904129, A	666	14	12.5	915	5	US-10-027-632-145513	Sequence 145513, A
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C 597	14	12.5	663	6	US-10-027-632-197491	Sequence 197491, A	C 670	14	12.5	942	4	US-10-450-763-13543	Sequence 13543, A
C 598	14	12.5	663	7	US-10-021-333-17301	Sequence 17301, A	C 671	14	12.5	960	4	US-09-925-065A-79204	Sequence 79204, A
C 599	14	12.5	666	4	US-09-925-065A-742986	Sequence 742986, A	C 672	14	12.5	960	4	US-09-925-065A-79205	Sequence 79205, A
C 600	14	12.5	669	6	US-10-204-887-6	Sequence 6, App1	C 673	14	12.5	960	4	US-09-925-065A-79206	Sequence 79206, A
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C 602	14	12.5	671	8	US-10-363-345A-31027	Sequence 31027, A	C 675	14	12.5	963	3	US-09-738-636-724	Sequence 724, App
C 603	14	12.5	671	9	US-10-363-483A-31027	Sequence 31027, A	676	14	12.5	965	6	US-10-029-386-20207	Sequence 20207, A
C 604	14	12.5	671	9	US-10-363-483A-31028	Sequence 31028, A	677	14	12.5	993	3	US-09-974-300-1743	Sequence 1743, Ap
C 605	14	12.5	681	9	US-10-450-763-1504	Sequence 4504, Ap	C 678	14	12.5	1017	7	US-10-282-122A-34219	Sequence 34219, A
C 606	14	12.5	681	9	US-10-450-763-17941	Sequence 17941, A	C 679	14	12.5	1033	4	US-09-925-065A-93034	Sequence 93034, A
C 607	14	12.5	683	8	US-10-425-115-181726	Sequence 181726, A	680	14	12.5	1054	8	US-10-425-115-105557	Sequence 105557, A



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683	14	12.5	1075	4	US-09-925-065A-93810	Sequence 93810, A	C 756	14	12.5	1994	3	US-10-786-970A-298	Sequence 298, App
684	14	12.5	1080	9	US-10-450-763-28482	Sequence 28482, A	C 757	14	12.5	2000	3	US-09-938-842A-5177	Sequence 5117, App
685	14	12.5	1088	8	US-10-425-115-144265	Sequence 144265, A	C 758	14	12.5	2000	3	US-09-938-842A-5117	Sequence 5117, App
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688	14	12.5	1105	3	US-09-995-494-56	Sequence 56, App1	C 761	14	12.5	2001	7	US-10-282-122A-18861	Sequence 18861, A
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691	14	12.5	1114	7	US-10-425-114-5551	Sequence 5551, App	C 764	14	12.5	2038	6	US-10-062-614-1524	Sequence 1524, App
692	14	12.5	1115	8	US-10-653-047-477	Sequence 477, App	C 765	14	12.5	2085	6	US-09-940-166A-5	Sequence 5, App11
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695	14	12.5	1227	7	US-10-424-599-15670	Sequence 35670, A	C 768	14	12.5	2149	7	US-10-437-963-9923	Sequence 9923, A
696	14	12.5	1262	7	US-10-424-599-3486	Sequence 3486, App	C 769	14	12.5	2163	7	US-10-437-963-9923	Sequence 9923, A
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704	14	12.5	1377	6	US-10-369-493-35629	Sequence 35629, A	C 777	14	12.5	2339	9	US-10-764-899-1607	Sequence 1607, App
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727	14	12.5	1674	10	US-11-097-143-10154	Sequence 10154, A	C 800	14	12.5	2700	5	US-10-727-694-3	Sequence 3, App11
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742	14	12.5	1820	4	US-09-925-065A-722747	Sequence 722747, A	C 815	14	12.5	2906	9	US-10-887-553A-944	Sequence 944, App
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747	14	12.5	1838	7	US-10-425-114-16672	Sequence 16672, A	C 820	14	12.5	3106	5	US-10-425-114-28626	Sequence 2626, App
748	14	12.5	1854	9	US-10-501-282-4183	Sequence 4183, App	C 821	14	12.5	3106	8	US-10-227-69A-6	Sequence 6, App11
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C 828	14	12.5	3224	7	US-10-342-887-1782	Sequence 1782, App	C 901	14	12.5	3244	5	US-10-187-596-571	Sequence 571, App
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C 835	14	12.5	3244	5	US-10-175-737-571	Sequence 571, App	C 908	14	12.5	3244	5	US-10-176-751-571	Sequence 571, App
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C 838	14	12.5	3244	5	US-10-176-748-571	Sequence 571, App	C 911	14	12.5	3244	5	US-10-180-544-571	Sequence 571, App
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C 842	14	12.5	3244	5	US-10-175-738-571	Sequence 571, App	C 915	14	12.5	3244	5	US-10-180-999-571	Sequence 571, App
C 843	14	12.5	3244	5	US-10-175-752-571	Sequence 571, App	C 916	14	12.5	3244	5	US-10-180-999-571	Sequence 571, App
C 844	14	12.5	3244	5	US-10-176-483-571	Sequence 571, App	C 917	14	12.5	3244	5	US-10-183-013-571	Sequence 571, App
C 845	14	12.5	3244	5	US-10-176-757-571	Sequence 571, App	C 918	14	12.5	3244	5	US-10-184-612-571	Sequence 571, App
C 846	14	12.5	3244	5	US-10-176-913-571	Sequence 571, App	C 919	14	12.5	3244	5	US-10-184-616-571	Sequence 571, App
C 847	14	12.5	3244	5	US-10-180-552-571	Sequence 571, App	C 920	14	12.5	3244	5	US-10-184-616-571	Sequence 571, App
C 848	14	12.5	3244	5	US-10-180-557-571	Sequence 571, App	C 921	14	12.5	3244	5	US-10-184-622-571	Sequence 571, App
C 849	14	12.5	3244	5	US-10-173-700-571	Sequence 571, App	C 922	14	12.5	3244	5	US-10-184-628-571	Sequence 571, App
C 850	14	12.5	3244	5	US-10-174-572-571	Sequence 571, App	C 923	14	12.5	3244	5	US-10-184-632-571	Sequence 571, App
C 851	14	12.5	3244	5	US-10-174-579-571	Sequence 571, App	C 924	14	12.5	3244	5	US-10-184-630-571	Sequence 571, App
C 852	14	12.5	3244	5	US-10-174-582-571	Sequence 571, App	C 925	14	12.5	3244	5	US-10-184-631-571	Sequence 571, App
C 853	14	12.5	3244	5	US-10-174-588-571	Sequence 571, App	C 926	14	12.5	3244	5	US-10-184-653-571	Sequence 571, App
C 854	14	12.5	3244	5	US-10-175-739-571	Sequence 571, App	C 927	14	12.5	3244	5	US-10-184-638-571	Sequence 571, App
C 855	14	12.5	3244	5	US-10-175-740-571	Sequence 571, App	C 928	14	12.5	3244	5	US-10-184-646-571	Sequence 571, App
C 856	14	12.5	3244	5	US-10-175-743-571	Sequence 571, App	C 929	14	12.5	3244	5	US-10-184-650-571	Sequence 571, App
C 857	14	12.5	3244	5	US-10-176-488-571	Sequence 571, App	C 930	14	12.5	3244	5	US-10-184-651-571	Sequence 571, App
C 858	14	12.5	3244	5	US-10-176-492-571	Sequence 571, App	C 931	14	12.5	3244	5	US-10-187-588-571	Sequence 571, App
C 859	14	12.5	3244	5	US-10-176-747-571	Sequence 571, App	C 932	14	12.5	3244	5	US-10-187-597-571	Sequence 571, App
C 860	14	12.5	3244	5	US-10-176-750-571	Sequence 571, App	C 933	14	12.5	3244	5	US-10-187-598-571	Sequence 571, App
C 861	14	12.5	3244	5	US-10-176-985-571	Sequence 571, App	C 934	14	12.5	3244	5	US-10-187-600-571	Sequence 571, App
C 862	14	12.5	3244	5	US-10-176-987-571	Sequence 571, App	C 935	14	12.5	3244	5	US-10-187-601-571	Sequence 571, App
C 863	14	12.5	3244	5	US-10-176-989-571	Sequence 571, App	C 936	14	12.5	3244	5	US-10-187-602-571	Sequence 571, App
C 864	14	12.5	3244	5	US-10-176-993-571	Sequence 571, App	C 937	14	12.5	3244	5	US-10-187-603-571	Sequence 571, App
C 865	14	12.5	3244	5	US-10-184-658-571	Sequence 571, App	C 938	14	12.5	3244	5	US-10-187-741-571	Sequence 571, App
C 866	14	12.5	3244	5	US-10-176-991-571	Sequence 571, App	C 939	14	12.5	3244	5	US-10-187-743-571	Sequence 571, App
C 867	14	12.5	3244	5	US-10-173-695-571	Sequence 571, App	C 940	14	12.5	3244	5	US-10-187-746-571	Sequence 571, App
C 868	14	12.5	3244	5	US-10-173-697-571	Sequence 571, App	C 941	14	12.5	3244	5	US-10-187-747-571	Sequence 571, App
C 869	14	12.5	3244	5	US-10-173-705-571	Sequence 571, App	C 942	14	12.5	3244	5	US-10-187-751-571	Sequence 571, App
C 870	14	12.5	3244	5	US-10-174-585-571	Sequence 571, App	C 943	14	12.5	3244	5	US-10-187-753-571	Sequence 571, App
C 871	14	12.5	3244	5	US-10-174-585-571	Sequence 571, App	C 944	14	12.5	3244	5	US-10-187-754-571	Sequence 571, App
C 872	14	12.5	3244	5	US-10-174-586-571	Sequence 571, App	C 945	14	12.5	3244	5	US-10-187-757-571	Sequence 571, App
C 873	14	12.5	3244	5	US-10-175-747-571	Sequence 571, App	C 946	14	12.5	3244	5	US-10-187-888-571	Sequence 571, App
C 874	14	12.5	3244	5	US-10-176-481-571	Sequence 571, App	C 947	14	12.5	3244	5	US-10-188-767-571	Sequence 571, App
C 875	14	12.5	3244	5	US-10-176-485-571	Sequence 571, App	C 948	14	12.5	3244	5	US-10-188-769-571	Sequence 571, App
C 876	14	12.5	3244	5	US-10-176-487-571	Sequence 571, App	C 949	14	12.5	3244	5	US-10-188-770-571	Sequence 571, App
C 877	14	12.5	3244	5	US-10-176-493-571	Sequence 571, App	C 950	14	12.5	3244	5	US-10-188-773-571	Sequence 571, App
C 878	14	12.5	3244	5	US-10-176-756-571	Sequence 571, App	C 951	14	12.5	3244	5	US-10-188-781-571	Sequence 571, App
C 879	14	12.5	3244	5	US-10-176-911-571	Sequence 571, App	C 952	14	12.5	3244	5	US-10-194-361-571	Sequence 571, App
C 880	14	12.5	3244	5	US-10-176-919-571	Sequence 571, App	C 953	14	12.5	3244	5	US-10-194-423-571	Sequence 571, App
C 881	14	12.5	3244	5	US-10-176-925-571	Sequence 571, App	C 954	14	12.5	3244	5	US-10-195-897-571	Sequence 571, App
C 882	14	12.5	3244	5	US-10-176-978-571	Sequence 571, App	C 955	14	12.5	3244	5	US-10-195-901-571	Sequence 571, App
C 883	14	12.5	3244	5	US-10-179-510-571	Sequence 571, App	C 956	14	12.5	3244	5	US-10-195-902-571	Sequence 571, App
C 884	14	12.5	3244	5	US-10-180-543-571	Sequence 571, App	C 957	14	12.5	3244	5	US-10-196-740-571	Sequence 571, App
C 885	14	12.5	3244	5	US-10-180-544-571	Sequence 571, App	C 958	14	12.5	3244	5	US-10-196-760-571	Sequence 571, App
C 886	14	12.5	3244	5	US-10-180-546-571	Sequence 571, App	C 959	14	12.5	3244	5	US-10-173-708-571	Sequence 571, App
C 887	14	12.5	3244	5	US-10-180-547-571	Sequence 571, App	C 960	14	12.5	3244	5	US-10-176-479-571	Sequence 571, App
C 888	14	12.5	3244	5	US-10-180-549-571	Sequence 571, App	C 961	14	12.5	3244	5	US-10-176-748-571	Sequence 571, App
C 889	14	12.5	3244	5	US-10-180-555-571	Sequence 571, App	C 962	14	12.5	3244	5	US-10-176-916-571	Sequence 571, App
C 890	14	12.5	3244	5	US-10-180-559-571	Sequence 571, App	C 963	14	12.5	3244	5	US-10-179-507-571	Sequence 571, App
C 891	14	12.5	3244	5	US-10-181-000-571	Sequence 571, App	C 964	14	12.5	3244	5	US-10-179-516-571	Sequence 571, App
C 892	14	12.5	3244	5	US-10-183-010-571	Sequence 571, App	C 965	14	12.5	3244	5	US-10-179-519-571	Sequence 571, App
C 893	14	12.5	3244	5	US-10-183-012-571	Sequence 571, App	C 966	14	12.5	3244	5	US-10-179-525-571	Sequence 571, App
C 894	14	12.5	3244	5	US-10-184-614-571	Sequence 571, App	C 967	14	12.5	3244	5	US-10-180-540-571	Sequence 571, App
C 895	14	12.5	3244	5	US-10-184-623-571	Sequence 571, App	C 968	14	12.5	3244	5	US-10-180-545-571	Sequence 571, App
C 896	14	12.5	3244	5	US-10-184-633-571	Sequence 571, App	C 969	14	12.5	3244	5	US-10-183-006-571	Sequence 571, App
C 897	14	12.5	3244	5	US-10-184-637-571	Sequence 571, App	C 970	14	12.5	3244	5	US-10-183-008-571	Sequence 571, App
C 898	14	12.5	3244	5	US-10-184-646-571	Sequence 571, App	C 971	14	12.5	3244	5	US-10-183-017-571	Sequence 571, App
C 899	14	12.5	3244	5	US-10-184-646-571	Sequence 571, App	C 972	14	12.5	3244	5	US-10-183-019-571	Sequence 571, App



```
c 973 14 12.5 3244 5 US-10-184-618-571 Sequence 571, App
c 974 14 12.5 3244 5 US-10-184-625-571 Sequence 571, App
c 975 14 12.5 3244 5 US-10-184-626-571 Sequence 571, App
c 976 14 12.5 3244 5 US-10-184-627-571 Sequence 571, App
c 977 14 12.5 3244 5 US-10-184-645-571 Sequence 571, App
c 978 14 12.5 3244 5 US-10-184-654-571 Sequence 571, App
c 979 14 12.5 3244 5 US-10-184-655-571 Sequence 571, App
c 980 14 12.5 3244 5 US-10-188-774-571 Sequence 571, App
c 981 14 12.5 3244 5 US-10-188-775-571 Sequence 571, App
c 982 14 12.5 3244 5 US-10-194-462-571 Sequence 571, App
c 983 14 12.5 3244 5 US-10-196-745-571 Sequence 571, App
c 984 14 12.5 3244 5 US-10-196-762-571 Sequence 571, App
c 985 14 12.5 3244 5 US-10-197-695-571 Sequence 571, App
c 986 14 12.5 3244 5 US-10-195-894-571 Sequence 571, App
c 987 14 12.5 3244 5 US-10-176-484-571 Sequence 571, App
c 988 14 12.5 3244 5 US-10-176-753-571 Sequence 571, App
c 989 14 12.5 3244 5 US-10-176-917-571 Sequence 571, App
c 990 14 12.5 3244 5 US-10-176-982-571 Sequence 571, App
c 991 14 12.5 3244 5 US-10-179-506-571 Sequence 571, App
c 992 14 12.5 3244 5 US-10-179-513-571 Sequence 571, App
c 993 14 12.5 3244 5 US-10-179-514-571 Sequence 571, App
c 994 14 12.5 3244 5 US-10-179-522-571 Sequence 571, App
c 995 14 12.5 3244 5 US-10-180-556-571 Sequence 571, App
c 996 14 12.5 3244 5 US-10-180-560-571 Sequence 571, App
c 997 14 12.5 3244 5 US-10-183-015-571 Sequence 571, App
c 998 14 12.5 3244 5 US-10-184-615-571 Sequence 571, App
c 999 14 12.5 3244 5 US-10-184-620-571 Sequence 571, App
c1000 14 12.5 3244 5 US-10-184-643-571 Sequence 571, App
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## ALIGNMENTS

```
RESULT 1
US-10-068-238-3
; Sequence 3, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-3

Query Match 28.6%; Score 32; DB 5; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.1e-08;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-4

Query Match 26.8%; Score 30; DB 5; Length 30;
Best Local Similarity 100.0%; Pred. No. 4.7e-07;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
RESULT 3
US-10-068-238-14
; Sequence 14, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-14

Query Match 23.2%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0001;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
RESULT 4
US-10-068-238-13
; Sequence 13, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
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; NUMBER OF SEQ ID NOS: 16  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 13  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Oligonucleotide  
US-10-066-238-13

Query Match 22.3%; Score 25; DB 5; Length 25;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 55 CGCGTAAAGAGCTCTAATATCG 79  
Db 1 CGCGTAAAGAGCTCTAATATCG 25

## RESULT 5

US-10-260-238-3339  
; Sequence 3339, Application US/10260238  
; Publication No. US20040016025A1  
; GENERAL INFORMATION:  
; APPLICANT: Budworth, Paul R.  
; APPLICANT: Moughamer, Todd G.  
; APPLICANT: Briggs, Steven P.  
; APPLICANT: Cooper, Bret  
; APPLICANT: Glazebrook, Jane  
; APPLICANT: Goff, Stephen A.  
; APPLICANT: Katsagiri, Pamiyaki  
; APPLICANT: Kreps, Joel  
; APPLICANT: Provart, Nicholas  
; APPLICANT: Ricke, Darrell  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: PROMOTERS FOR REGULATION OF PLANT EXPRESSION  
; FILE REFERENCE: 60111-NP  
; CURRENT APPLICATION NUMBER: US/10/260,238  
; PRIOR FILING DATE: 2002-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,448  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/325,277  
; PRIOR FILING DATE: 2001-09-26  
; PRIOR APPLICATION NUMBER: US 60/370,620  
; PRIOR FILING DATE: 2002-04-04  
; NUMBER OF SEQ ID NOS: 6077  
; SEQ ID NO 3339  
; LENGTH: 1042  
; TYPE: DNA  
; ORGANISM: Triticum aestivum  
US-10-260-238-3339

Query Match 16.1%; Score 18; DB 7; Length 1042;  
Best Local Similarity 100.0%; Pred. No. 6.6;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 CGGTGACGACGACGGGT 95  
Db 586 CGGTGACGACGACGGGT 603

## RESULT 6

US-10-437-963-44672/c  
; Sequence 44672, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad

; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437,963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 44672  
; LENGTH: 2782  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_4770C.1  
US-10-437-963-44672

Query Match 16.1%; Score 18; DB 7; Length 2782;  
Best Local Similarity 100.0%; Pred. No. 7;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GATATATTGCTTACTGA 35  
Db 721 GATATATTGCTTACTGA 704

## RESULT 7

US-09-925-065A-626524  
; Sequence 626524, Application US/09925065A  
; Publication No. US20050228172A9  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 626524  
; LENGTH: 551  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-626524

Query Match 15.2%; Score 17; DB 4; Length 551;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGATATATTGCTTACT 33  
Db 101 TGATATATTGCTTACT 117

## RESULT 8

US-10-425-115-26871  
; Sequence 26871, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovacic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With



```
FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26871
; LENGTH: 787
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124517C.1
US-10-425-115-26871

Query Match          15.2%; Score 17; DB 8; Length 787;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      32 CTGACGAGAGCAACCG 48
        |||||||
Db      372 CTGACGAGAGCAACCG 388

RESULT 9
US-10-425-115-26868
; Sequence 26868, Application US/10425115
; Publication No. US2004021472A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53222)B
; CURRENT APPLICATION NUMBER: US/10/425,115
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 369326
; SEQ ID NO 26868
; LENGTH: 830
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: MRT4577_124514C.1
US-10-425-115-26868

Query Match          15.2%; Score 17; DB 8; Length 830;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      32 CTGACGAGAGCAACCG 48
        |||||||
Db      609 CTGACGAGAGCAACCG 625

RESULT 10
US-10-425-114-4342
; Sequence 4342, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 4342
; LENGTH: 855
; TYPE: DNA
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ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: 700354483_FLI
US-10-425-114-4342

Query Match          15.2%; Score 17; DB 7; Length 855;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      32 CTGACGAGAGCAACCG 48
        |||||||
Db      613 CTGACGAGAGCAACCG 629

RESULT 11
US-10-425-114-12904
; Sequence 12904, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 12904
; LENGTH: 973
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: CC-ZMPO148046E06_FLI
US-10-425-114-12904

Query Match          15.2%; Score 17; DB 7; Length 973;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      32 CTGACGAGAGCAACCG 48
        |||||||
Db      603 CTGACGAGAGCAACCG 619

RESULT 12
US-10-425-114-21001
; Sequence 21001, Application US/10425114
; Publication No. US2004003488A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 21001
; LENGTH: 974
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3245-572-A10_FLI
US-10-425-114-21001
```



Query Match 15.2%; Score 17; DB 7; Length 974;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGACGAGGACCAACCG 48  
DB 610 CTGACGAGGACCAACCG 626

RESULT 13  
US-10-424-599-36472  
; Sequence 36472, Application US/10424599  
; Publication No. US20040031072A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J  
; APPLICANT: Kovalic, David K  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53223)B  
; CURRENT APPLICATION NUMBER: US/10/424, 599  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 285684  
; SEQ ID NO 36472  
; LENGTH: 1099  
; TYPE: DNA  
; ORGANISM: Glycine max  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT3847\_132937C.1  
US-10-424-599-36472

Query Match 15.2%; Score 17; DB 7; Length 1099;  
Best Local Similarity 100.0%; Pred. No. 25;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 37 GAGGAGCAACCGATTAA 53  
DB 808 GAGGAGCAACCGATTAA 824

RESULT 14  
US-10-425-115-26873  
; Sequence 26873, Application US/10425115  
; Publication No. US20040214272A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants  
; FILE REFERENCE: 38-21(53222)B  
; CURRENT APPLICATION NUMBER: US/10/425, 115  
; CURRENT FILING DATE: 2003-04-28  
; NUMBER OF SEQ ID NOS: 369326  
; SEQ ID NO 26873  
; LENGTH: 1652  
; TYPE: DNA  
; ORGANISM: Zea mays  
; FEATURE:  
; NAME/KEY: unsure  
; LOCATION: (1)..(1652)  
; OTHER INFORMATION: unsure at all n locations  
; FEATURE:  
; OTHER INFORMATION: Clone ID: MRT4577\_124519C.1  
US-10-425-115-26873

Query Match 15.2%; Score 17; DB 8; Length 1652;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 CTGACGAGGACCAACCG 48

DB 871 CTGACGAGGACCAACCG 887

RESULT 15  
US-10-437-963-44719  
; Sequence 44719, Application US/10437963  
; Publication No. US20040123343A1  
; GENERAL INFORMATION:  
; APPLICANT: La Rosa, Thomas J.  
; APPLICANT: Kovalic, David K.  
; APPLICANT: Zhou, Yihua  
; APPLICANT: Cao, Yongwei  
; APPLICANT: Wu, Wei  
; APPLICANT: Boukharov, Andrey A.  
; APPLICANT: Barbazuk, Brad  
; APPLICANT: Li, Ping  
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With  
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement  
; FILE REFERENCE: 38-21(53221)B  
; CURRENT APPLICATION NUMBER: US/10/437, 963  
; CURRENT FILING DATE: 2003-05-14  
; NUMBER OF SEQ ID NOS: 204966  
; SEQ ID NO 44719  
; LENGTH: 4224  
; TYPE: DNA  
; ORGANISM: Oryza sativa  
; FEATURE:  
; OTHER INFORMATION: Clone ID: PAT\_MRT4530\_47752C.1  
US-10-437-963-44719

Query Match 15.2%; Score 17; DB 7; Length 4224;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGATATATTTGGTTTAC 32  
DB 2132 ATGATATTTGGTTTAC 2148

RESULT 16  
US-11-036-317-201076  
; Sequence 201076, Application US/11036317  
; Publication No. US20050214823A1  
; GENERAL INFORMATION:  
; APPLICANT: Williams, Alan  
; APPLICANT: Blume, John  
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse  
; FILE REFERENCE: 3654.1  
; CURRENT APPLICATION NUMBER: US/11/036, 317  
; CURRENT FILING DATE: 2005-01-13  
; PRIOR APPLICATION NUMBER: US 60/536, 639  
; NUMBER OF SEQ ID NOS: 991174  
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1  
; SEQ ID NO 201076  
; LENGTH: 25  
; TYPE: DNA  
; ORGANISM: Mus musculus  
US-11-036-317-201076

Query Match 14.3%; Score 16; DB 10; Length 25;  
Best Local Similarity 100.0%; Pred. No. 79;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGGTAAGTTAAAGAGG 106  
DB 1 AGGTAAGTTAAAGAGG 16

RESULT 17  
US-11-036-317-206258  
; Sequence 206258, Application US/11036317



```
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; PRIOR FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 206258
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-206258

Query Match          14.3%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGGGTAGTTAAAGAGG 106
DB 3 AGGGTAGTTAAAGAGG 18

RESULT 18
US-11-036-317-351958
; Sequence 351958, Application US/11036317
; Publication No. US20050214823A1
; GENERAL INFORMATION:
; APPLICANT: Williams, Alan
; APPLICANT: Blume, John
; TITLE OF INVENTION: Method of Analysis of Alternative Splicing in Mouse
; FILE REFERENCE: 3654.1
; CURRENT APPLICATION NUMBER: US/11/036,317
; CURRENT FILING DATE: 2005-01-13
; PRIOR APPLICATION NUMBER: US 60/536,639
; NUMBER OF SEQ ID NOS: 991174
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 351958
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Mus musculus
; US-11-036-317-351958

Query Match          14.3%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 91 AGGGTAGTTAAAGAGG 106
DB 2 AGGGTAGTTAAAGAGG 17

RESULT 19
US-10-437-963-80382
; Sequence 80382, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovacic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Mu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Bardazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
```

```
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 80382
; LENGTH: 142
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_8000C.1
; US-10-437-963-80382

Query Match          14.3%; Score 16; DB 7; Length 142;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 70 CCTAATATCGGTGAGC 85
DB 116 CCTAATATCGGTGAGC 131

RESULT 20
US-10-424-599-9960
; Sequence 9960, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovacic, David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 9960
; LENGTH: 403
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(403)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_109003C.1
; US-10-424-599-9960

Query Match          14.3%; Score 16; DB 7; Length 403;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 41 AGCAACCGATTAAAGG 56
DB 189 AGCAACCGATTAAAGG 204

RESULT 21
US-10-131-827-8493
; Sequence 8493, Application US/10131827
; Publication No. US20040009479A1
; GENERAL INFORMATION:
; APPLICANT: Wohlgemuth, Jay
; APPLICANT: Fry, Kirk
; APPLICANT: Woodward, Robert
; APPLICANT: Ly, Ngoc
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DIAGNOSING AND MONITORING AUTOIMMUN
; TITLE OF INVENTION: CHRONIC INFLAMMATORY DISEASES
; FILE REFERENCE: 506612000120
; CURRENT APPLICATION NUMBER: US/10/131,827
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: US 10/006,290
; PRIOR FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: US 60/296,764
```



; PRIOR FILING DATE: 2001-06-08  
; NUMBER OF SEQ ID NOS: 9090  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8493  
; LENGTH: 434  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-131-827-8493

Query Match 14.3%; Score 16; DB 6; Length 434;  
Best Local Similarity 100.0%; Pred. No. 93;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGATATATGCTTTA 31  
|||  
Db 378 ATGATATATGCTTTA 393

## RESULT 22

US-10-027-632-57063  
; Sequence 57063, Application US/10027632  
; Publication No. US2002019837A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027, 632

; PRIOR FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218, 006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198, 676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193, 483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185, 218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167, 363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156, 358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146, 002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 57063

; LENGTH: 472

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-57063

Query Match 14.3%; Score 16; DB 5; Length 472;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 CCGTAAAGAGTCTCT 72  
|||||  
Db 40 CCGTAAAGAGTCTCT 55

## RESULT 23

US-10-027-632-57063  
; Sequence 57063, Application US/10027632  
; Publication No. US20030204075A9  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; TITLE OF INVENTION: Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.129

; CURRENT APPLICATION NUMBER: US/10/027, 632

; PRIOR FILING DATE: 2002-04-30

; PRIOR APPLICATION NUMBER: US 60/218, 006

; PRIOR FILING DATE: 2000-07-12

; PRIOR APPLICATION NUMBER: US 60/198, 676

; PRIOR FILING DATE: 2000-04-20

; PRIOR APPLICATION NUMBER: US 60/193, 483

; PRIOR FILING DATE: 2000-03-29

; PRIOR APPLICATION NUMBER: US 60/185, 218

; PRIOR FILING DATE: 2000-02-24

; PRIOR APPLICATION NUMBER: US 60/167, 363

; PRIOR FILING DATE: 1999-11-23

; PRIOR APPLICATION NUMBER: US 60/156, 358

; PRIOR FILING DATE: 1999-09-28

; PRIOR APPLICATION NUMBER: US 60/146, 002

; PRIOR FILING DATE: 1999-08-09

; NUMBER OF SEQ ID NOS: 325720

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 57063

; LENGTH: 472

; TYPE: DNA

; ORGANISM: Human

US-10-027-632-57063

Query Match 14.3%; Score 16; DB 6; Length 472;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 57 CCGTAAAGAGTCTCT 72  
|||||  
Db 40 CCGTAAAGAGTCTCT 55

## RESULT 24

US-10-198-846-9184/C  
; Sequence 9184, Application US/10198846  
; Publication No. US2003009974A1  
; GENERAL INFORMATION:

; APPLICANT: Lillie, James  
; APPLICANT: Xu, Yongyao  
; APPLICANT: Wang, Youzhen

; APPLICANT: Steinmann, Kathleen

; TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND METHODS

; TITLE OF INVENTION: FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND

; FILE REFERENCE: MRI-049

; CURRENT APPLICATION NUMBER: US/10/198, 846

; PRIOR FILING DATE: 2002-07-18

; PRIOR APPLICATION NUMBER: 60/306, 220

; PRIOR FILING DATE: 2001-07-18

; NUMBER OF SEQ ID NOS: 14084

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9184

; LENGTH: 526

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; LOCATION: 1, 4\_5, 12, 13, 14, 15, 16, 17

; OTHER INFORMATION: n = A,T,C or G

US-10-198-846-9184

Query Match 14.3%; Score 16; DB 5; Length 526;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATGCTTT 30  
|||||  
Db 520 AATGATATATGCTTT 505

## RESULT 25

US-10-424-599-117489

; Sequence 117489, Application US/10424599

; Publication No. US20040031072A1

; GENERAL INFORMATION:

; APPLICANT: La Rosa Thomas J



```

; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yinhua
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; CURRENT FILING DATE: 2001-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 117489
; LENGTH: 552
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(552)
; OTHER INFORMATION: unsure at all n locations
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_77101C.1
; US-10-424-599-117489
```

```

Query Match          14.3%; Score 16; DB 7; Length 552;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 13 CGAATGATATATTGCT 28
Db 172 CGAATGATATATTGGT 187
```

```

RESULT 26
US-10-029-386-13425
; Sequence 13425, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: A60MICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 13425
; LENGTH: 569
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR14.3
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.1
; OTHER INFORMATION: SWISSPROT HIT: Q58195, EVALU6 4.80e-01
; OTHER INFORMATION: NT HIT: g15834871, EVALU6 1.40e-01
; US-10-029-386-13425
```

```

Query Match          14.3%; Score 16; DB 6; Length 569;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 93 GGTAGTTAAAGAGGCT 108
Db 95 GGTAGTTAAAGAGGCT 110
```

```

RESULT 27
US-09-925-065A-619252/c
; Sequence 619252, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
```

```

; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 619252
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-619252
```

```

Query Match          14.3%; Score 16; DB 4; Length 577;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 17 TGATATATTGGTTAC 32
Db 331 TGATATATTGGTTAC 316
```

```

RESULT 28
US-09-925-065A-619253/c
; Sequence 619253, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 619253
; LENGTH: 577
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-619253
```

```

Query Match          14.3%; Score 16; DB 4; Length 577;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```

Qy 17 TGATATATTGGTTAC 32
Db 331 TGATATATTGGTTAC 316
```

```

RESULT 29
US-10-021-323-15408
; Sequence 15408, Application US/10021323
; Publication No. US20040123340A1
; GENERAL INFORMATION:
```



```
; APPLICANT: Delkman, Jill
; APPLICANT: Feng, Paul C.C.
; APPLICANT: Fincher, Karen L.
; APPLICANT: Ziegler, Todd E.
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(52274)B
; CURRENT APPLICATION NUMBER: US/10/021,323
; CURRENT FILING DATE: 2001-12-12
; PRIOR APPLICATION NUMBER: US 60/255, 619
; PRIOR FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 17880
; SEQ ID NO 15408
; LENGTH: 608
; TYPE: DNA
; ORGANISM: Geesypium hirsutum
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3829-025-Q6-K6-H10
US-10-021-323-15408
```

```
Query Match 14.3%; Score 16; DB 7; Length 608;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 96 AGTTAAGAGGCTGCT 111
Db 206 AGTTAAGAGGCTGCT 221
```

```
RESULT 30
US-09-925-065A-682241
; Sequence 682241, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 682241
; LENGTH: 623
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-682241
```

```
Query Match 14.3%; Score 16; DB 4; Length 623;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 15 AATGATATATTGTTT 30
Db 581 AATGATATATTGTTT 596
```

```
RESULT 31
US-09-925-065A-104147/c
; Sequence 104147, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
```

```
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 104147
; LENGTH: 624
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-104147
```

```
Query Match 14.3%; Score 16; DB 4; Length 624;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 16 ATGATATATTGTTTA 31
Db 395 ATGATATATTGTTTA 380
```

```
RESULT 32
US-10-027-632-1803
; Sequence 1803, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1803
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-1803
```

```
Query Match 14.3%; Score 16; DB 5; Length 642;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 57 CCGTAAGAAGCTCT 72
Db 41 CCGTAAGAAGCTCT 56
```



```
RESULT 33
US-10-027-632-1803
; Sequence 1803, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1803
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-1803
```

```
Query Match      14.3%; Score 16; DB 6; Length 642;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      57 CCGTAAGAAGGTCTT 72
          |||||
Db       41 CCGTAAGAAGGTCTT 56
```

```
RESULT 34
US-10-027-632-199517/c
; Sequence 199517, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199517
; LENGTH: 663
; TYPE: DNA
```

```
; ORGANISM: Human
US-10-027-632-199517
```

```
Query Match      14.3%; Score 16; DB 5; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 AATGATATATTGGTTT 30
          |||||
Db       502 AATGATATATTGGTTT 487
```

```
RESULT 35
US-10-027-632-199518/c
; Sequence 199518, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 199518
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199518
```

```
Query Match      14.3%; Score 16; DB 5; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      15 AATGATATATTGGTTT 30
          |||||
Db       502 AATGATATATTGGTTT 487
```

```
RESULT 36
US-10-027-632-199519/c
; Sequence 199519, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
```



```
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 199519
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199519
```

```
Query Match      14.3%; Score 16; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      15 AATGATATATTGTTT 30
          |||
Db      502 AATGATATATTGTTT 487
```

```
RESULT 37
US-10-027-632-199517/c
; Sequence 199517, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 199517
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199517
```

```
US-10-027-632-199517
```

```
Query Match      14.3%; Score 16; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      15 AATGATATATTGTTT 30
          |||
Db      502 AATGATATATTGTTT 487
```

```
RESULT 38
US-10-027-632-199518/c
; Sequence 199518, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 199519
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199519
```

```
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 199518
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199518
```

```
Query Match      14.3%; Score 16; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      15 AATGATATATTGTTT 30
          |||
Db      502 AATGATATATTGTTT 487
```

```
RESULT 39
US-10-027-632-199519/c
; Sequence 199519, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827,129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 199519
; LENGTH: 663
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-199519
```

```
Query Match      14.3%; Score 16; DB 6; Length 663;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      15 AATGATATATTGTTT 30
          |||
```



Db 502 AATGATATATTGTTT 487

```
RESULT 40
US-10-027-632-283608
; Sequence 283608, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 283608
; LENGTH: 675
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-283608
```

```
Query Match 14.3%; Score 16; DB 5; Length 675;
Best Local Similarity 100.0%; Pred. No. 96;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGATATATTGTTTAC 32
|||
Db 381 TGATATATTGTTTAC 396
```

Search completed: April 12, 2006, 06:02:16  
Job time : 332.378 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 05:20:02 ; Search time 457.422 Seconds  
(without alignments)  
986.217 Million cell updates/sec

Title: US-10-712-654-25

Perfect score: 112

Sequence: 1 ggtacatctgcgcgaatgat.....ggtacgtaagaagcgtctgt 112

Scoring table:  
OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0  
9281099 seqs, 2013915447 residues

Searched:

Word size : 1  
Total number of hits satisfying chosen parameters: 18561424

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications NA\_New:\*  
1: /SIDS5/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
2: /SIDS5/ptodata/2/pubpna/US06\_NEW\_PUB.seq:\*  
3: /SIDS5/ptodata/2/pubpna/US07\_NEW\_PUB.seq:\*  
4: /SIDS5/ptodata/2/pubpna/PCT\_NEW\_PUB.seq:\*  
5: /SIDS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
6: /SIDS5/ptodata/2/pubpna/US09\_NEW\_PUB.seq:\*  
7: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
8: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
9: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
10: /SIDS5/ptodata/2/pubpna/US10\_NEW\_PUB.seq:\*  
11: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
12: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
13: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
14: /SIDS5/ptodata/2/pubpna/US11\_NEW\_PUB.seq:\*  
15: /SIDS5/ptodata/2/pubpna/US60\_NEW\_PUB.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	ID	Description
C 1	18	16.1	31737	11 US-11-221-243-111 Sequence 111, App
C 2	17	15.2	551	6 US-09-925-065A-626524 Sequence 626524
C 3	16	14.3	25	9 US-10-932-182A-89126 Sequence 89126, A
C 4	16	14.3	25	9 US-10-932-182A-89126 Sequence 89126, A
C 5	16	14.3	25	9 US-10-934-048A-49740 Sequence 49740, A
C 6	16	14.3	425	9 US-10-301-480-3015 Sequence 3015, App
C 7	16	14.3	425	10 US-10-301-480-616424 Sequence 616424, App
C 8	16	14.3	450	9 US-10-301-480-1889 Sequence 1889, App
C 9	16	14.3	450	10 US-10-301-480-615298 Sequence 615298, App
C 10	16	14.3	577	6 US-09-925-065A-619252 Sequence 619252, App
C 11	16	14.3	577	6 US-09-925-065A-619252 Sequence 619252, App
C 12	16	14.3	623	6 US-09-925-065A-682241 Sequence 682241, App
C 13	16	14.3	624	6 US-09-925-065A-104147 Sequence 104147, App
C 14	16	14.3	634	6 US-10-301-480-204311 Sequence 204311, App
C 15	16	14.3	634	10 US-10-301-480-817730 Sequence 817730, App
C 16	16	14.3	642	9 US-10-301-480-53372 Sequence 53372, A
C 17	16	14.3	642	9 US-10-301-480-53372 Sequence 53372, A
C 18	16	14.3	642	9 US-10-301-480-53373 Sequence 53373, A

C 19	16	14.3	642	10 US-10-301-480-666780 Sequence 666780, App
C 20	16	14.3	642	10 US-10-301-480-666781 Sequence 666781, App
C 21	16	14.3	642	10 US-10-301-480-666782 Sequence 666782, App
C 22	16	14.3	910	6 US-09-925-065A-952833 Sequence 952833, App
C 23	16	14.3	1152	6 US-10-301-480-185389 Sequence 185389, App
C 24	16	14.3	1155	6 US-09-925-065A-84147 Sequence 84147, A
C 25	16	14.3	1155	6 US-09-925-065A-84148 Sequence 84148, A
C 26	16	14.3	1155	6 US-09-925-065A-84149 Sequence 84149, A
C 27	16	14.3	1155	6 US-09-925-065A-84150 Sequence 84150, A
C 28	16	14.3	1155	9 US-10-301-480-185387 Sequence 185387, App
C 29	16	14.3	1155	9 US-10-301-480-185388 Sequence 185388, App
C 30	16	14.3	1155	9 US-10-301-480-185390 Sequence 185390, App
C 31	16	14.3	1155	10 US-10-301-480-798796 Sequence 798796, App
C 32	16	14.3	1155	10 US-10-301-480-798797 Sequence 798797, App
C 33	16	14.3	1155	10 US-10-301-480-798798 Sequence 798798, App
C 34	16	14.3	1155	10 US-10-301-480-798799 Sequence 798799, App
C 35	16	14.3	1293	9 US-10-932-182A-75911 Sequence 75911, A
C 36	16	14.3	1293	9 US-10-932-182A-75911 Sequence 75911, A
C 37	16	14.3	1304	8 US-10-750-185-60365 Sequence 60365, A
C 38	16	14.3	1304	8 US-10-750-185-60365 Sequence 60365, A
C 39	16	14.3	2512	8 US-10-750-185-40273 Sequence 40273, A
C 40	16	14.3	2512	8 US-10-750-185-40273 Sequence 40273, A
C 41	16	14.3	4680	11 US-11-228-659-40 Sequence 40, App1
C 42	16	14.3	8354	14 US-11-113-424-13 Sequence 1254037, App1
C 43	15	13.4	20	8 US-10-310-914A-1254037 Sequence 1254037, App1
C 44	15	13.4	25	14 US-11-121-849-637144 Sequence 637144, App1
C 45	15	13.4	201	14 US-11-124-367A-19861 Sequence 19861, A
C 46	15	13.4	201	14 US-11-124-367A-19861 Sequence 19861, A
C 47	15	13.4	408	10 US-10-301-480-248026 Sequence 248026, App
C 48	15	13.4	408	10 US-10-301-480-861435 Sequence 861435, App
C 49	15	13.4	416	6 US-09-925-065A-154516 Sequence 154516, App
C 50	15	13.4	453	6 US-09-925-065A-379196 Sequence 379196, App
C 51	15	13.4	453	6 US-09-925-065A-379197 Sequence 379197, App
C 52	15	13.4	504	14 US-11-136-527-7893 Sequence 7893, App
C 53	15	13.4	504	14 US-11-136-527-7893 Sequence 7893, App
C 54	15	13.4	524	10 US-10-301-480-446326 Sequence 446326, App
C 55	15	13.4	524	10 US-10-301-480-1059735 Sequence 1059735, App
C 56	15	13.4	526	6 US-09-925-065A-376638 Sequence 376638, App
C 57	15	13.4	537	8 US-10-793-626-3099 Sequence 3099, App
C 58	15	13.4	563	6 US-09-925-065A-334863 Sequence 334863, App
C 59	15	13.4	564	9 US-10-301-480-57441 Sequence 57441, A
C 60	15	13.4	564	9 US-10-301-480-57441 Sequence 57441, A
C 61	15	13.4	564	9 US-10-301-480-57442 Sequence 57442, A
C 62	15	13.4	564	10 US-10-301-480-670849 Sequence 670849, App
C 63	15	13.4	564	10 US-10-301-480-670850 Sequence 670850, App
C 64	15	13.4	564	10 US-10-301-480-670851 Sequence 670851, App
C 65	15	13.4	574	10 US-10-301-480-408360 Sequence 408360, App
C 66	15	13.4	574	10 US-10-301-480-1021769 Sequence 1021769, App
C 67	15	13.4	577	6 US-09-925-065A-878817 Sequence 878817, App
C 68	15	13.4	577	6 US-09-925-065A-878818 Sequence 878818, App
C 69	15	13.4	577	6 US-09-925-065A-878819 Sequence 878819, App
C 70	15	13.4	577	6 US-09-925-065A-907243 Sequence 907243, App
C 71	15	13.4	580	6 US-09-925-065A-334862 Sequence 334862, App
C 72	15	13.4	581	6 US-09-925-065A-58455 Sequence 58455, A
C 73	15	13.4	581	9 US-10-301-480-159693 Sequence 159693, App
C 74	15	13.4	581	10 US-10-301-480-773102 Sequence 773102, App
C 75	15	13.4	584	10 US-10-301-480-406359 Sequence 406359, App
C 76	15	13.4	584	10 US-10-301-480-1021768 Sequence 1021768, App
C 77	15	13.4	589	6 US-09-925-065A-248965 Sequence 248965, App
C 78	15	13.4	601	10 US-10-301-480-499305 Sequence 499305, App
C 79	15	13.4	601	10 US-10-301-480-1112714 Sequence 1112714, App
C 80	15	13.4	605	6 US-09-925-065A-437982 Sequence 437982, App
C 81	15	13.4	606	10 US-10-301-480-328918 Sequence 328918, App
C 82	15	13.4	606	10 US-10-301-480-942327 Sequence 942327, App
C 83	15	13.4	622	9 US-10-301-480-675112 Sequence 675112, App
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C 86	15	13.4	631	10 US-10-301-480-676760 Sequence 676760, App
C 87	15	13.4	633	6 US-09-925-065A-311111 Sequence 311111, App
C 88	15	13.4	633	6 US-09-925-065A-628926 Sequence 628926, App
C 89	15	13.4	642	6 US-09-925-065A-294710 Sequence 294710, App
C 90	15	13.4	642	6 US-09-925-065A-294711 Sequence 294711, App
C 91	15	13.4	642	6 US-09-925-065A-294712 Sequence 294712, App



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93	15	13.4	646	6	US-09-925-065A-808433	Sequence 908433, A
94	15	13.4	649	9	US-10-714-887-93	Sequence 93, App1
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96	15	13.4	649	10	US-10-301-480-371592	Sequence 371592, A
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99	15	13.4	649	10	US-10-301-480-985001	Sequence 985001, A
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103	15	13.4	667	10	US-10-301-480-999941	Sequence 999941, A
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105	15	13.4	737	10	US-10-301-480-1169492	Sequence 1169492, A
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107	15	13.4	964	9	US-10-301-480-185671	Sequence 185671, A
108	15	13.4	964	10	US-10-301-480-799080	Sequence 799080, A
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110	15	13.4	1090	8	US-10-750-623-50880	Sequence 50880, A
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112	15	13.4	1173	8	US-10-750-623-29123	Sequence 29123, A
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117	15	13.4	1496	8	US-10-750-623-38062	Sequence 38062, A
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119	15	13.4	1524	9	US-10-932-182A-77098	Sequence 77098, A
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121	15	13.4	2001	14	US-11-117-187-182	Sequence 182, App
122	15	13.4	2112	8	US-10-793-626-4414	Sequence 4414, App
123	15	13.4	2211	11	US-11-079-463-1885	Sequence 1885, App
124	15	13.4	2597	8	US-10-750-185-28040	Sequence 28040, A
125	15	13.4	2597	8	US-10-750-623-28040	Sequence 28040, A
126	15	13.4	3126	8	US-10-793-626-4371	Sequence 4371, App
127	15	13.4	3302	8	US-10-793-626-4016	Sequence 4016, App
128	15	13.4	84502	14	US-11-124-367A-5057	Sequence 5057, App
129	15	13.4	159146	14	US-11-121-086-49	Sequence 49, App1
130	15	13.4	191231	14	US-11-112-908-50	Sequence 20, App1
131	15	13.4	268685	8	US-10-933-025-22	Sequence 22, App1
132	15	13.4	268685	11	US-11-219-360-22	Sequence 22, App1
133	15	13.4	268685	14	US-11-117-187-211	Sequence 211, App
134	15	13.4	1082144	14	US-10-310-914A-1373855	Sequence 1373855, A
135	15	13.4	20	8	US-10-831-286A-103	Sequence 103, App
136	15	13.4	20	9	US-10-831-286A-197	Sequence 197, App
137	15	13.4	20	9	US-10-831-286A-222	Sequence 222, App
138	15	13.4	20	9	US-10-831-286A-284	Sequence 284, App
139	15	13.4	20	9	US-10-831-286A-329	Sequence 329, App
140	15	13.4	20	9	US-10-831-286A-1149	Sequence 1149, App
141	15	13.4	20	9	US-10-831-286A-1507	Sequence 1507, App
142	15	13.4	21	8	US-10-310-914A-794176	Sequence 794176, App
143	15	13.4	21	14	US-11-009-840A-278	Sequence 278, App
144	15	13.4	21	14	US-11-009-873A-278	Sequence 278, App
145	15	13.4	21	14	US-11-009-769A-278	Sequence 278, App
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149	15	13.4	25	14	US-11-121-849-34875	Sequence 34101, A
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152	15	13.4	25	14	US-11-121-849-211034	Sequence 211034, A
153	15	13.4	25	14	US-11-121-849-257447	Sequence 257447, A
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155	15	13.4	25	14	US-11-121-849-549949	Sequence 549949, A
156	15	13.4	25	14	US-11-121-849-551341	Sequence 551341, A
157	15	13.4	25	14	US-11-121-849-551342	Sequence 551342, A
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159	15	13.4	378	11	US-11-079-463-3008	Sequence 3008, App
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161	15	13.4	425	6	US-09-925-065A-608436	Sequence 608436, A
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163	15	13.4	426	10	US-10-301-480-978496	Sequence 978496, A
164	15	13.4	437	10	US-10-301-480-286618	Sequence 286618, A

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168	14	12.5	466	6	US-09-925-065A-187488	Sequence 187488, A
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175	14	12.5	489	10	US-10-301-480-663969	Sequence 663969, A
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178	14	12.5	496	10	US-10-301-480-322745	Sequence 322745, A
179	14	12.5	496	10	US-10-301-480-326153	Sequence 326153, A
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185	14	12.5	501	6	US-09-925-065A-304672	Sequence 304672, A
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187	14	12.5	504	10	US-10-301-480-380741	Sequence 380741, A
188	14	12.5	504	10	US-10-301-480-994149	Sequence 994149, A
189	14	12.5	504	10	US-10-301-480-994150	Sequence 994150, A
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193	14	12.5	512	6	US-09-925-065A-255254	Sequence 255254, A
194	14	12.5	514	10	US-10-301-480-562136	Sequence 562136, A
195	14	12.5	514	10	US-10-301-480-1175545	Sequence 1175545, A
196	14	12.5	516	6	US-09-925-065A-665586	Sequence 665586, A
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215	14	12.5	547	10	US-10-301-480-917201	Sequence 917201, A
216	14	12.5	547	10	US-10-301-480-917202	Sequence 917202, A
217	14	12.5	551	10	US-10-301-480-76557	Sequence 76557, A
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223	14	12.5	555	9	US-10-301-480-166350	Sequence 166350, A
224	14	12.5	555	6	US-09-925-065A-807959	Sequence 807959, A
225	14	12.5	555	6	US-09-925-065A-171930	Sequence 171930, A
226	14	12.5	556	6	US-09-925-065A-766568	Sequence 766568, A
227	14	12.5	557	6	US-09-925-065A-18063	Sequence 18063, A
228	14	12.5	557	9	US-10-301-480-119300	Sequence 119300, A
229	14	12.5	557	10	US-10-301-480-732709	Sequence 732709, A
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231	14	12.5	561	6	US-09-925-065A-239717	Sequence 239717, A
232	14	12.5	561	9	US-10-301-480-50236	Sequence 50236, A
233	14	12.5	561	10	US-10-301-480-663645	Sequence 663645, A
234	14	12.5	562	6	US-09-925-065A-764361	Sequence 764361, A
235	14	12.5	563	10	US-10-301-480-563652	Sequence 563652, A
236	14	12.5	563	10	US-10-301-480-877061	Sequence 877061, A
237	14	12.5	563	10	US-10-301-480-877061	Sequence 877061, A



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C 239	14	12.5	566	6	US-09-925-065A-410238	Sequence 410238,	C 312	14	12.5	618	6	US-09-925-065A-636885	Sequence 636885,
C 240	14	12.5	566	6	US-09-925-065A-410239	Sequence 410239,	C 313	14	12.5	619	6	US-09-925-065A-860412	Sequence 860412,
C 241	14	12.5	567	6	US-09-925-065A-497093	Sequence 497093,	C 314	14	12.5	619	6	US-09-925-065A-796258	Sequence 796258,
C 242	14	12.5	567	6	US-09-925-065A-497094	Sequence 497094,	C 315	14	12.5	619	6	US-09-925-065A-796259	Sequence 796259,
C 243	14	12.5	567	10	US-10-301-480-321517	Sequence 321517,	C 316	14	12.5	619	6	US-09-925-065A-851397	Sequence 851397,
C 244	14	12.5	567	10	US-10-301-480-321518	Sequence 321518,	C 317	14	12.5	620	6	US-09-925-065A-54234	Sequence 54234, A
C 245	14	12.5	567	10	US-10-301-480-934926	Sequence 934926,	C 318	14	12.5	620	6	US-09-925-065A-54235	Sequence 54235, A
C 246	14	12.5	567	10	US-10-301-480-934927	Sequence 934927,	C 319	14	12.5	620	9	US-10-301-480-155472	Sequence 155472,
C 247	14	12.5	569	9	US-10-301-480-202814	Sequence 202814,	C 320	14	12.5	620	9	US-10-301-480-155473	Sequence 155473,
C 248	14	12.5	569	9	US-10-301-480-202815	Sequence 202815,	C 321	14	12.5	620	10	US-10-301-480-768881	Sequence 768881,
C 249	14	12.5	569	10	US-10-301-480-816223	Sequence 816223,	C 322	14	12.5	620	10	US-10-301-480-768882	Sequence 768882,
C 250	14	12.5	569	10	US-10-301-480-816224	Sequence 816224,	C 323	14	12.5	621	6	US-09-925-065A-932357	Sequence 932357,
C 251	14	12.5	571	9	US-10-301-480-54692	Sequence 54692, A	C 324	14	12.5	624	6	US-09-925-065A-804393	Sequence 804393,
C 252	14	12.5	571	10	US-10-301-480-668101	Sequence 668101,	C 325	14	12.5	624	6	US-09-925-065A-695156	Sequence 695156,
C 253	14	12.5	572	6	US-09-925-065A-102440	Sequence 102440,	C 326	14	12.5	628	6	US-09-925-065A-695156	Sequence 695156,
C 254	14	12.5	572	6	US-09-925-065A-102441	Sequence 102441,	C 327	14	12.5	628	6	US-09-925-065A-695156	Sequence 695156,
C 255	14	12.5	574	6	US-09-925-065A-103993	Sequence 103993,	C 328	14	12.5	628	6	US-09-925-065A-912841	Sequence 912841,
C 256	14	12.5	574	6	US-09-925-065A-103994	Sequence 103994,	C 329	14	12.5	628	6	US-09-925-065A-945546	Sequence 945546,
C 257	14	12.5	574	6	US-09-925-065A-103995	Sequence 103995,	C 330	14	12.5	630	6	US-09-925-065A-533709	Sequence 533709,
C 258	14	12.5	574	6	US-09-925-065A-595183	Sequence 595183,	C 331	14	12.5	630	6	US-09-925-065A-533710	Sequence 533710,
C 259	14	12.5	575	6	US-09-925-065A-286900	Sequence 286900,	C 332	14	12.5	630	6	US-09-925-065A-608534	Sequence 608534,
C 260	14	12.5	576	6	US-09-925-065A-327114	Sequence 327114,	C 333	14	12.5	630	6	US-09-925-065A-608535	Sequence 608535,
C 261	14	12.5	579	6	US-09-925-065A-920560	Sequence 920560,	C 334	14	12.5	631	6	US-09-925-065A-912029	Sequence 912029,
C 262	14	12.5	579	6	US-09-925-065A-920561	Sequence 920561,	C 335	14	12.5	632	6	US-09-925-065A-125352	Sequence 125352,
C 263	14	12.5	580	6	US-09-925-065A-920562	Sequence 920562,	C 336	14	12.5	632	6	US-09-925-065A-869978	Sequence 869978,
C 264	14	12.5	580	6	US-09-925-065A-714350	Sequence 714350,	C 337	14	12.5	632	10	US-10-301-480-222852	Sequence 222852,
C 265	14	12.5	582	10	US-10-301-480-297611	Sequence 297611,	C 338	14	12.5	636	10	US-10-301-480-836261	Sequence 836261,
C 266	14	12.5	582	10	US-10-301-480-363811	Sequence 363811,	C 339	14	12.5	636	10	US-10-301-480-553792	Sequence 553792,
C 267	14	12.5	582	10	US-10-301-480-911020	Sequence 911020,	C 340	14	12.5	638	6	US-09-925-065A-694728	Sequence 694728,
C 268	14	12.5	582	10	US-10-301-480-911020	Sequence 911020,	C 341	14	12.5	638	6	US-09-925-065A-694729	Sequence 694729,
C 269	14	12.5	583	9	US-10-301-480-6900	Sequence 977220, A	C 342	14	12.5	638	6	US-09-925-065A-694730	Sequence 694730,
C 270	14	12.5	583	10	US-10-301-480-401162	Sequence 401162,	C 343	14	12.5	638	6	US-09-925-065A-694731	Sequence 694731,
C 271	14	12.5	583	10	US-10-301-480-620309	Sequence 620309,	C 344	14	12.5	639	9	US-10-301-480-52155	Sequence 52155, A
C 272	14	12.5	583	10	US-10-301-480-1014571	Sequence 1014571,	C 345	14	12.5	639	10	US-10-301-480-665564	Sequence 665564,
C 273	14	12.5	584	6	US-09-925-065A-932358	Sequence 932358,	C 346	14	12.5	645	6	US-09-925-065A-789659	Sequence 789659,
C 274	14	12.5	584	6	US-09-925-065A-932359	Sequence 932359,	C 347	14	12.5	645	6	US-09-925-065A-847486	Sequence 847486,
C 275	14	12.5	585	9	US-10-301-480-204185	Sequence 204185,	C 348	14	12.5	648	9	US-10-932-182A-77172	Sequence 77172, A
C 276	14	12.5	585	9	US-10-301-480-204186	Sequence 204186,	C 349	14	12.5	648	9	US-10-932-182A-77172	Sequence 77172, A
C 277	14	12.5	585	9	US-10-301-480-204187	Sequence 204187,	C 350	14	12.5	648	9	US-10-932-182A-77172	Sequence 77172, A
C 278	14	12.5	585	10	US-10-301-480-817595	Sequence 817595,	C 351	14	12.5	656	6	US-09-925-065A-874378	Sequence 874378,
C 279	14	12.5	585	10	US-10-301-480-817595	Sequence 817595,	C 352	14	12.5	656	6	US-09-925-065A-905741	Sequence 905741,
C 280	14	12.5	585	10	US-10-301-480-817596	Sequence 817596,	C 353	14	12.5	660	6	US-09-925-065A-905741	Sequence 905741,
C 281	14	12.5	588	6	US-09-925-065A-952863	Sequence 952863,	C 354	14	12.5	663	6	US-09-925-065A-904129	Sequence 904129,
C 282	14	12.5	588	6	US-09-925-065A-210262	Sequence 210262,	C 355	14	12.5	666	6	US-09-925-065A-942986	Sequence 942986,
C 283	14	12.5	589	6	US-09-925-065A-746504	Sequence 746504,	C 356	14	12.5	686	10	US-10-301-480-545084	Sequence 545084,
C 284	14	12.5	591	6	US-09-925-065A-584591	Sequence 584591,	C 357	14	12.5	686	10	US-10-301-480-1158493	Sequence 1158493,
C 285	14	12.5	591	6	US-09-925-065A-584591	Sequence 584591,	C 358	14	12.5	712	10	US-10-301-480-575265	Sequence 575265,
C 286	14	12.5	593	6	US-09-925-065A-261027	Sequence 261027,	C 359	14	12.5	712	10	US-10-301-480-1186874	Sequence 1186874,
C 287	14	12.5	595	9	US-10-301-480-4735	Sequence 4735, Ap	C 360	14	12.5	726	9	US-10-932-182A-191105	Sequence 191105,
C 288	14	12.5	595	10	US-10-301-480-618144	Sequence 618144,	C 361	14	12.5	726	9	US-10-932-182A-191105	Sequence 191105,
C 289	14	12.5	596	6	US-09-925-065A-677857	Sequence 677857,	C 362	14	12.5	729	6	US-09-925-065A-932739	Sequence 932739,
C 290	14	12.5	596	6	US-09-925-065A-677858	Sequence 677858,	C 363	14	12.5	732	6	US-09-925-065A-932739	Sequence 932739,
C 291	14	12.5	601	6	US-09-925-065A-932892	Sequence 932892,	C 364	14	12.5	732	6	US-09-925-065A-943963	Sequence 943963,
C 292	14	12.5	602	6	US-09-925-065A-789306	Sequence 789306,	C 365	14	12.5	732	6	US-09-925-065A-943964	Sequence 943964,
C 293	14	12.5	603	6	US-09-925-065A-650471	Sequence 650471,	C 366	14	12.5	749	6	US-09-925-065A-932738	Sequence 932738,
C 294	14	12.5	603	6	US-09-925-065A-650472	Sequence 650472,	C 367	14	12.5	752	6	US-09-925-065A-948590	Sequence 948590,
C 295	14	12.5	603	10	US-10-301-480-567300	Sequence 567300,	C 368	14	12.5	752	10	US-10-301-480-526540	Sequence 526540,
C 296	14	12.5	603	10	US-10-301-480-1180709	Sequence 1180709,	C 369	14	12.5	752	10	US-10-301-480-1139949	Sequence 1139949,
C 297	14	12.5	604	6	US-09-925-065A-916728	Sequence 916728,	C 370	14	12.5	764	6	US-09-925-065A-427773	Sequence 427773, A
C 298	14	12.5	605	6	US-09-925-065A-497575	Sequence 497575,	C 371	14	12.5	764	6	US-09-925-065A-427774	Sequence 427774, A
C 299	14	12.5	605	6	US-09-925-065A-947797	Sequence 947797,	C 372	14	12.5	764	6	US-09-925-065A-427775	Sequence 427775, A
C 300	14	12.5	606	6	US-09-925-065A-674170	Sequence 674170,	C 373	14	12.5	764	9	US-10-301-480-144011	Sequence 144011,
C 301	14	12.5	608	10	US-10-301-480-339351	Sequence 339351,	C 374	14	12.5	764	9	US-10-301-480-144012	Sequence 144012,
C 302	14	12.5	608	10	US-10-301-480-952760	Sequence 952760,	C 375	14	12.5	764	9	US-10-301-480-144013	Sequence 144013,
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C 305	14	12.5	613	6	US-09-925-065A-755654	Sequence 755654,	C 378	14	12.5	774	10	US-10-301-480-582185	Sequence 582185,
C 306	14	12.5	613	6	US-09-925-065A-755655	Sequence 755655,	C 379	14	12.5	774	10	US-10-301-480-582185	Sequence 582185,
C 307	14	12.5	613	6	US-09-925-065A-826012	Sequence 826012,	C 380	14	12.5	774	10	US-10-301-480-1195594	Sequence 1195594,
C 308	14	12.5	615	6	US-09-925-065A-754113	Sequence 754113,	C 381	14	12.5	777	10	US-10-301-480-1195619	Sequence 1195619,
C 309	14	12.5	615	6	US-09-925-065A-754122	Sequence 754122,	C 382	14	12.5	777	10	US-10-301-480-1170028	Sequence 1170028,
C 310	14	12.5	616	6	US-09-925-065A-792680	Sequence 792680,	C 383	14	12.5	804	14	US-11-112-908-289	Sequence 289, App



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C 387	14	12.5	826	10	US-10-301-480-546521	Sequence 546521, A
C 388	14	12.5	826	10	US-10-301-480-1159930	Sequence 1159930, A
C 389	14	12.5	846	11	US-11-079-463-247	Sequence 247, App
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C 393	14	12.5	902	10	US-10-301-480-1221901	Sequence 1221901, A
C 394	14	12.5	903	10	US-10-301-480-594734	Sequence 594734, A
C 395	14	12.5	903	10	US-10-301-480-1208143	Sequence 1208143, A
C 396	14	12.5	957	8	US-10-454-437-75	Sequence 75, App1
C 397	14	12.5	960	6	US-09-925-065A-79204	Sequence 79204, A
C 398	14	12.5	960	6	US-09-925-065A-79205	Sequence 79205, A
C 399	14	12.5	960	6	US-09-925-065A-79206	Sequence 79206, A
C 400	14	12.5	960	6	US-09-925-065A-79207	Sequence 79207, A
C 401	14	12.5	960	9	US-10-301-480-180443	Sequence 180443, A
C 402	14	12.5	960	9	US-10-301-480-180444	Sequence 180444, A
C 403	14	12.5	960	9	US-10-301-480-180445	Sequence 180445, A
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C 405	14	12.5	960	10	US-10-301-480-793852	Sequence 793852, A
C 406	14	12.5	960	10	US-10-301-480-793853	Sequence 793853, A
C 407	14	12.5	960	10	US-10-301-480-793854	Sequence 793854, A
C 408	14	12.5	960	10	US-10-301-480-793855	Sequence 793855, A
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C 410	14	12.5	988	10	US-10-301-480-590365	Sequence 590365, A
C 411	14	12.5	988	10	US-10-301-480-1203773	Sequence 1203773, A
C 412	14	12.5	988	10	US-10-301-480-1203774	Sequence 1203774, A
C 413	14	12.5	991	10	US-10-301-480-579512	Sequence 579512, A
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C 415	14	12.5	992	10	US-10-301-480-1209686	Sequence 1209686, A
C 416	14	12.5	992	10	US-10-301-480-601549	Sequence 601549, A
C 417	14	12.5	998	10	US-10-301-480-606574	Sequence 606574, A
C 418	14	12.5	998	10	US-10-301-480-1214958	Sequence 1214958, A
C 419	14	12.5	998	10	US-10-301-480-1219983	Sequence 1219983, A
C 420	14	12.5	999	10	US-10-301-480-586343	Sequence 586343, A
C 421	14	12.5	999	10	US-10-301-480-1199752	Sequence 1199752, A
C 422	14	12.5	1000	10	US-10-301-480-591255	Sequence 591255, A
C 423	14	12.5	1000	10	US-10-301-480-1144956	Sequence 1144956, A
C 424	14	12.5	1000	10	US-10-301-480-1212534	Sequence 1212534, A
C 425	14	12.5	1000	6	US-09-925-065A-93034	Sequence 93034, A
C 426	14	12.5	1043	9	US-10-301-480-194276	Sequence 194276, A
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C 433	14	12.5	1070	6	US-09-925-065A-40207	Sequence 40207, A
C 434	14	12.5	1070	6	US-10-301-480-141445	Sequence 141445, A
C 435	14	12.5	1070	10	US-10-301-480-754854	Sequence 754854, A
C 436	14	12.5	1075	6	US-09-925-065A-93810	Sequence 93810, A
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C 438	14	12.5	1075	10	US-10-301-480-808461	Sequence 808461, A
C 439	14	12.5	1093	6	US-09-925-065A-554040	Sequence 554040, A
C 440	14	12.5	1093	6	US-10-750-185-33106	Sequence 33106, A
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C 442	14	12.5	1260	9	US-10-932-182A-6066	Sequence 6066, App
C 443	14	12.5	1260	9	US-10-932-182A-6066	Sequence 6066, App
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C 445	14	12.5	1289	9	US-10-932-182A-82160	Sequence 82160, A
C 446	14	12.5	1289	9	US-10-932-182A-82160	Sequence 82160, A
C 447	14	12.5	1289	9	US-10-932-182A-82160	Sequence 82160, A
C 448	14	12.5	1338	9	US-10-932-182A-75667	Sequence 75667, A
C 449	14	12.5	1338	9	US-10-932-182A-75667	Sequence 75667, A
C 450	14	12.5	1390	6	US-09-925-065A-727522	Sequence 727522, A
C 451	14	12.5	1412	8	US-10-750-185-51532	Sequence 51532, A
C 452	14	12.5	1412	8	US-10-750-185-62968	Sequence 62968, A
C 453	14	12.5	1412	8	US-10-750-623-51532	Sequence 51532, A
C 454	14	12.5	1459	6	US-09-925-065A-674978	Sequence 674978, A
C 455	14	12.5	1533	9	US-10-932-182A-173675	Sequence 173675, A
C 456	14	12.5	1533	9	US-10-932-182A-173675	Sequence 173675, A
C 457	14	12.5	1543	6	US-09-925-065A-86320	Sequence 86320, A
C 458	14	12.5	1543	6	US-09-925-065A-86321	Sequence 86321, A
C 459	14	12.5	1543	6	US-10-301-480-187560	Sequence 187560, A
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C 461	14	12.5	1543	10	US-10-301-480-800969	Sequence 800969, A
C 462	14	12.5	1543	10	US-10-301-480-800970	Sequence 800970, A
C 463	14	12.5	1562	8	US-10-750-185-56783	Sequence 56783, A
C 464	14	12.5	1562	8	US-10-750-623-51663	Sequence 51663, A
C 465	14	12.5	1568	8	US-10-750-185-51864	Sequence 51864, A
C 466	14	12.5	1568	8	US-10-750-623-51864	Sequence 51864, A
C 467	14	12.5	1735	6	US-09-925-065A-714259	Sequence 714259, A
C 468	14	12.5	1735	6	US-09-925-065A-714260	Sequence 714260, A
C 469	14	12.5	1735	6	US-09-925-065A-714261	Sequence 714261, A
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C 471	14	12.5	1741	8	US-10-750-623-52668	Sequence 52668, A
C 472	14	12.5	1750	8	US-10-750-185-12931	Sequence 12931, A
C 473	14	12.5	1750	8	US-10-750-623-12931	Sequence 32931, A
C 474	14	12.5	1764	8	US-10-750-185-11663	Sequence 31663, A
C 475	14	12.5	1764	8	US-10-750-623-51663	Sequence 51663, A
C 476	14	12.5	1792	6	US-09-925-065A-696706	Sequence 696706, A
C 477	14	12.5	1795	8	US-10-750-185-53375	Sequence 53375, A
C 478	14	12.5	1795	8	US-10-750-623-53375	Sequence 53375, A
C 479	14	12.5	1795	11	US-11-086-568A-20264	Sequence 20264, A
C 480	14	12.5	1820	6	US-09-925-065A-722747	Sequence 722747, A
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C 483	14	12.5	1824	6	US-09-925-065A-51381	Sequence 51381, A
C 484	14	12.5	1824	9	US-10-301-480-152618	Sequence 152618, A
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C 488	14	12.5	1824	10	US-10-301-480-1666028	Sequence 1666028, A
C 489	14	12.5	2020	8	US-10-750-185-28506	Sequence 28506, A
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C 493	14	12.5	2070	8	US-10-750-185-30580	Sequence 30580, A
C 494	14	12.5	2070	8	US-10-750-623-30580	Sequence 30580, A
C 495	14	12.5	2094	8	US-10-750-185-49794	Sequence 49794, A
C 496	14	12.5	2094	8	US-10-750-623-49794	Sequence 49794, A
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C 502	14	12.5	2510	6	US-09-925-065A-707161	Sequence 707161, A
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C 542	14	12.5	611587	14	US-11-117-187-209	Sequence 209, App	C 615	13	11.6	25	14	US-11-121-849-133396	Sequence 133396,
C 543	14	12.5	1080000	8	US-10-928-446A-1	Sequence 1, App1	C 616	13	11.6	25	14	US-11-121-849-385634	Sequence 385634,
C 544	14	12.5	1080000	8	US-10-928-446A-181	Sequence 181, App	C 617	13	11.6	25	14	US-11-121-849-385633	Sequence 385633,
C 545	14	12.5	1080000	8	US-10-928-446A-183	Sequence 183, App	C 618	13	11.6	25	14	US-11-121-849-392150	Sequence 392150,
C 546	14	12.5	1080000	8	US-10-928-446A-185	Sequence 185, App	C 619	13	11.6	25	14	US-11-121-849-392151	Sequence 392151,
C 547	14	12.5	1080000	8	US-10-928-446A-187	Sequence 187, App	C 620	13	11.6	25	14	US-11-121-849-421571	Sequence 421571,
C 548	14	12.5	1080000	8	US-10-928-446A-189	Sequence 189, App	C 621	13	11.6	25	14	US-11-121-849-422594	Sequence 422594,
C 549	14	12.5	1080000	8	US-10-928-446A-191	Sequence 191, App	C 622	13	11.6	25	14	US-11-121-849-438574	Sequence 438574,
C 550	14	12.5	1080000	8	US-10-928-446A-193	Sequence 193, App	C 623	13	11.6	25	14	US-11-136-527-216850	Sequence 216850,
C 551	14	12.5	1080000	8	US-10-928-446A-195	Sequence 195, App	C 624	13	11.6	25	14	US-11-136-527-216858	Sequence 216858,
C 552	14	12.5	1080000	8	US-10-928-446A-197	Sequence 197, App	C 625	13	11.6	25	14	US-11-136-527-216866	Sequence 216866,
C 553	14	12.5	1080000	8	US-10-928-446A-199	Sequence 199, App	C 626	13	11.6	25	14	US-11-136-527-231279	Sequence 231279,
C 554	14	12.5	1080000	8	US-10-928-446A-201	Sequence 201, App	C 627	13	11.6	25	14	US-11-136-527-284243	Sequence 284243,
C 555	14	12.5	1691140	14	US-11-091-018-1	Sequence 1, App1	C 628	13	11.6	25	14	US-11-136-527-284251	Sequence 284251,
C 556	13	11.6	18	8	US-10-310-914A-1301993	Sequence 1301993,	C 629	13	11.6	25	14	US-11-136-527-335135	Sequence 335135,
C 557	13	11.6	19	12	US-11-101-244-112311	Sequence 112311,	C 630	13	11.6	27	8	US-10-310-914A-569190	Sequence 569190,
C 558	13	11.6	19	12	US-11-101-244-112411	Sequence 112411,	C 631	13	11.6	28	8	US-10-310-914A-569191	Sequence 569191,
C 559	13	11.6	19	12	US-11-101-244-258576	Sequence 258576,	C 632	13	11.6	29	8	US-10-310-914A-871178	Sequence 871178,
C 560	13	11.6	19	12	US-11-101-244-506521	Sequence 506521,	C 633	13	11.6	50	14	US-11-175-859-19840	Sequence 19840, App
C 561	13	11.6	19	12	US-11-101-244-924120	Sequence 924120,	C 634	13	11.6	63	8	US-10-310-914A-18678	Sequence 18678, A
C 562	13	11.6	19	12	US-11-101-244-924136	Sequence 924136,	C 635	13	11.6	72	8	US-10-310-914A-3536	Sequence 3536, App
C 563	13	11.6	19	12	US-11-101-244-959617	Sequence 959617,	C 636	13	11.6	114	14	US-11-124-367A-200	Sequence 200, App
C 564	13	11.6	19	12	US-11-101-244-1157686	Sequence 1157686,	C 637	13	11.6	190	8	US-10-467-657-5739	Sequence 5739, App
C 565	13	11.6	19	12	US-11-101-244-1236121	Sequence 1236121,	C 638	13	11.6	200	14	US-11-098-686-3833	Sequence 3833, App
C 566	13	11.6	19	12	US-11-101-244-1255596	Sequence 1255596,	C 639	13	11.6	200	14	US-11-098-686-4252	Sequence 4252, App
C 567	13	11.6	19	12	US-11-101-244-1317801	Sequence 1317801,	C 640	13	11.6	201	8	US-10-995-561-27553	Sequence 27553, App
C 568	13	11.6	19	12	US-11-101-244-1317826	Sequence 1317826,	C 641	13	11.6	201	8	US-10-995-561-31637	Sequence 31637, A
C 569	13	11.6	19	12	US-11-101-244-1397337	Sequence 1397337,	C 642	13	11.6	201	8	US-10-995-561-16167	Sequence 16167, A
C 570	13	11.6	19	12	US-11-101-244-1460711	Sequence 1460711,	C 643	13	11.6	201	8	US-10-995-561-193683	Sequence 193683, A
C 571	13	11.6	19	12	US-11-101-244-1471153	Sequence 1471153,	C 644	13	11.6	201	8	US-10-995-561-170709	Sequence 170709, A
C 572	13	11.6	19	13	US-11-083-784-112311	Sequence 112311,	C 645	13	11.6	201	14	US-11-124-368A-15480	Sequence 15480, A
C 573	13	11.6	19	13	US-11-083-784-112411	Sequence 112411,	C 646	13	11.6	201	14	US-11-124-368A-16194	Sequence 16194, A
C 574	13	11.6	19	13	US-11-083-784-112411	Sequence 112411,	C 647	13	11.6	201	14	US-11-124-368A-16446	Sequence 16446, A
C 575	13	11.6	19	13	US-11-083-784-258576	Sequence 258576,	C 648	13	11.6	201	14	US-11-124-368A-16447	Sequence 16447, A
C 576	13	11.6	19	13	US-11-083-784-506521	Sequence 506521,	C 649	13	11.6	201	14	US-11-124-368A-16448	Sequence 16448, A
C 577	13	11.6	19	13	US-11-083-784-924120	Sequence 924120,	C 650	13	11.6	201	14	US-11-124-367A-11051	Sequence 11051, A
C 578	13	11.6	19	13	US-11-083-784-924136	Sequence 924136,	C 651	13	11.6	201	14	US-11-124-367A-19709	Sequence 19709, A
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C 580	13	11.6	19	13	US-11-083-784-959621	Sequence 959621,	C 653	13	11.6	286	11	US-11-159-667-4	Sequence 667, A
C 581	13	11.6	19	13	US-11-083-784-1157686	Sequence 1157686,	C 654	13	11.6	286	14	US-11-009-873A-373	Sequence 373, App1
C 582	13	11.6	19	13	US-11-083-784-1236121	Sequence 1236121,	C 655	13	11.6	288	14	US-11-009-873A-373	Sequence 373, App
C 583	13	11.6	19	13	US-11-083-784-1255596	Sequence 1255596,	C 656	13	11.6	288	14	US-11-009-873A-373	Sequence 373, App
C 584	13	11.6	19	13	US-11-083-784-1317801	Sequence 1317801,	C 657	13	11.6	294	6	US-09-925-065A-192558	Sequence 192558,
C 585	13	11.6	19	13	US-11-083-784-1317826	Sequence 1317826,	C 658	13	11.6	298	10	US-10-301-480-282087	Sequence 282087,
C 586	13	11.6	19	13	US-11-083-784-1397337	Sequence 1397337,	C 659	13	11.6	298	10	US-10-301-480-895496	Sequence 895496,
C 587	13	11.6	19	13	US-11-083-784-1460711	Sequence 1460711,	C 660	13	11.6	325	6	US-09-925-065A-630371	Sequence 630371,
C 588	13	11.6	19	13	US-11-083-784-1471153	Sequence 1471153,	C 661	13	11.6	332	14	US-11-234-786-131	Sequence 131, App
C 589	13	11.6	20	9	US-10-310-914A-637112	Sequence 637112,	C 662	13	11.6	357	8	US-10-467-657-415	Sequence 415, App
C 590	13	11.6	20	9	US-10-831-286A-411	Sequence 411, App	C 663	13	11.6	364	6	US-09-925-065A-914220	Sequence 914220,
C 591	13	11.6	20	9	US-10-831-286A-1371	Sequence 1371, App	C 664	13	11.6	374	6	US-09-925-065A-364999	Sequence 364999,
C 592	13	11.6	21	8	US-10-831-286A-35090	Sequence 35090, A	C 665	13	11.6	374	9	US-10-301-480-1238	Sequence 4238, App
C 593	13	11.6	21	8	US-10-989-597-12	Sequence 12, App1	C 666	13	11.6	374	9	US-10-301-480-617647	Sequence 617647,
C 594	13	11.6	21	8	US-10-310-914A-990606	Sequence 990606,	C 667	13	11.6	375	14	US-11-043-752-975	Sequence 752, App
C 595	13	11.6	21	8	US-10-310-914A-990607	Sequence 990607,	C 668	13	11.6	379	6	US-09-925-065A-839770	Sequence 839770,
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C 599	13	11.6	23	8	US-10-310-914A-337035	Sequence 337035,	C 672	13	11.6	381	10	US-10-301-480-826988	Sequence 826988,
C 600	13	11.6	23	8	US-10-310-914A-990609	Sequence 990609,	C 673	13	11.6	381	10	US-10-301-480-840396	Sequence 840396,
C 601	13	11.6	23	8	US-10-310-914A-990792	Sequence 990792,	C 674	13	11.6	381	10	US-10-301-480-840397	Sequence 840397,
C 602	13	11.6	23	8	US-10-310-914A-1066677	Sequence 1066677,	C 675	13	11.6	382	6	US-09-925-065A-130499	Sequence 130499,



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C 677	13	11.6	393	6	US-09-925-065A-154166	Sequence 154166,	750	13	11.6	471	10	US-10-301-480-967536	Sequence 967536,
C 678	13	11.6	393	6	US-09-925-065A-154167	Sequence 154167,	751	13	11.6	471	10	US-10-301-480-967537	Sequence 967537,
C 679	13	11.6	400	10	US-10-301-480-247713	Sequence 247713,	752	13	11.6	471	10	US-10-301-480-967538	Sequence 967538,
C 680	13	11.6	400	10	US-10-301-480-247714	Sequence 247714,	C 753	13	11.6	472	6	US-09-925-065A-654574	Sequence 654574,
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C 682	13	11.6	400	10	US-10-301-480-861123	Sequence 861123,	C 755	13	11.6	474	6	US-09-925-065A-615332	Sequence 615332,
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687	13	11.6	409	10	US-10-301-480-893772	Sequence 893772,	C 760	13	11.6	478	10	US-10-301-480-1135650	Sequence 1135650,
C 688	13	11.6	410	6	US-09-925-065A-106689	Sequence 106689,	C 761	13	11.6	478	10	US-10-301-480-958949	Sequence 958949,
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C 693	13	11.6	411	6	US-09-925-065A-332075	Sequence 232075,	C 766	13	11.6	480	6	US-09-925-065A-898327	Sequence 898327,
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704	13	11.6	418	10	US-10-301-480-1005099	Sequence 1005099,	C 777	13	11.6	491	6	US-09-925-065A-607906	Sequence 607906,
705	13	11.6	421	10	US-10-301-480-404674	Sequence 404674,	C 778	13	11.6	491	6	US-09-925-065A-607907	Sequence 607907,
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C 708	13	11.6	424	6	US-09-925-065A-630621	Sequence 630621,	C 781	13	11.6	492	6	US-09-925-065A-815285	Sequence 815285,
C 709	13	11.6	425	6	US-09-925-065A-316741	Sequence 316741,	782	13	11.6	492	6	US-09-925-065A-831628	Sequence 831628,
C 710	13	11.6	425	6	US-09-925-065A-535411	Sequence 535411,	783	13	11.6	493	6	US-09-925-065A-530464	Sequence 530464,
C 711	13	11.6	425	6	US-09-925-065A-535412	Sequence 535412,	C 784	13	11.6	494	6	US-09-925-065A-743344	Sequence 743344,
C 712	13	11.6	425	6	US-09-925-065A-535413	Sequence 535413,	785	13	11.6	494	6	US-09-925-065A-743344	Sequence 743344,
C 713	13	11.6	425	6	US-09-925-065A-535414	Sequence 535414,	C 786	13	11.6	496	9	US-10-301-480-209851	Sequence 209851,
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C 715	13	11.6	429	6	US-09-925-065A-330620	Sequence 330620,	C 788	13	11.6	496	10	US-10-301-480-823260	Sequence 823260,
C 716	13	11.6	430	6	US-09-925-065A-190669	Sequence 190669,	C 789	13	11.6	500	6	US-09-925-065A-798303	Sequence 798303,
C 717	13	11.6	435	6	US-09-925-065A-106760	Sequence 106760,	C 790	13	11.6	500	6	US-09-925-065A-981366	Sequence 981366,
C 718	13	11.6	435	9	US-10-932-182A-82139	Sequence 82139, A	C 791	13	11.6	503	9	US-10-301-480-50056	Sequence 50056,
719	13	11.6	435	9	US-10-932-182A-82139	Sequence 82139, A	C 792	13	11.6	503	10	US-10-301-480-663465	Sequence 663465,
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C 722	13	11.6	442	6	US-09-925-065A-429880	Sequence 429880,	C 795	13	11.6	506	10	US-10-301-480-513866	Sequence 513866,
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C 724	13	11.6	442	10	US-10-301-480-820122	Sequence 820122,	797	13	11.6	507	11	US-11-077-813A-14	Sequence 14, App1
C 725	13	11.6	453	6	US-09-925-065A-429058	Sequence 429058,	C 798	13	11.6	508	6	US-09-925-065A-455650	Sequence 455650,
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C 740	13	11.6	470	6	US-09-925-065A-192466	Sequence 192466,	813	13	11.6	514	6	US-09-925-065A-119377	Sequence 119377,
C 741	13	11.6	470	6	US-09-925-065A-192467	Sequence 192467,	C 814	13	11.6	518	6	US-09-925-065A-445497	Sequence 445497,
C 742	13	11.6	470	6	US-09-925-065A-192468	Sequence 192468,	C 815	13	11.6	519	6	US-09-925-065A-497920	Sequence 497920,
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## ALIGNMENTS

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; GENERAL INFORMATION:
; APPLICANT: Monia, Brett P.
; APPLICANT: Szwkowski, Andrew M.
; APPLICANT: Bhanot, Sanjay
; TITLE OF INVENTION: ENHANCED ANTISENSE OLIGONUCLEOTIDES
; FILE REFERENCE: CORE051US
; CURRENT APPLICATION NUMBER: US/11/231,243
; CURRENT FILING DATE: 2005-09-19
; PRIOR APPLICATION NUMBER: 60/611,100
; PRIOR FILING DATE: 2004-09-17
; PRIOR APPLICATION NUMBER: 60/663,442
; PRIOR FILING DATE: 2005-03-18
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; SEQ ID NO 111
; LENGTH: 31737
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; LOCATION: (26994)...(27191)
; OTHER INFORMATION: n = A,T,C or G
US-11-231-243-111
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; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
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; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932,182A
; CURRENT FILING DATE: 2004-09-02
; NUMBER OF SEQ ID NOS: 197023
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US-10-932-182A-89126
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Best Local Similarity 100.0%; Pred. No. 25;
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; Sequence 89126, Application US/10932182A
; Publication No. US20060046253A1
; GENERAL INFORMATION:
; APPLICANT: NAKAO, YOSHIHIRO
; APPLICANT: NAKAMURA, NORIHISA
; APPLICANT: KODAMA, YUKIKO
; APPLICANT: FUJIMURA, TOMOKO
; APPLICANT: ASHIKARI, TOSHIHIKO
; TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
; FILE REFERENCE: 030685-043
; CURRENT APPLICATION NUMBER: US/10/932.182A
; CURRENT FILING DATE: 2004-09-02
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; TYPE: DNA
; ORGANISM: Saccharomyces pastorianus
US-10-932-182A-89126
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; APPLICANT: Tanya Makeev
; TITLE OF INVENTION: Methods of Genetic Analysis of Yeast
; FILE REFERENCE: 3699
; CURRENT APPLICATION NUMBER: US/10/934.048A
; CURRENT FILING DATE: 2004-09-03
; NUMBER OF SEQ ID NOS: 120855
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; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301.480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
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```

```
Query Match          14.3%; Score 16; DB 9; Length 425;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      57 CCGTAAAGAGGTCTT 72
Db      30 CCGTAAAGAGGTCTT 45
```

```
RESULT 7
US-10-301-480-616424
; Sequence 616424, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301.480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 616424
; LENGTH: 425
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-616424
```

```
Query Match          14.3%; Score 16; DB 10; Length 425;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      57 CCGTAAAGAGGTCTT 72
Db      30 CCGTAAAGAGGTCTT 45
```

```
RESULT 8
US-10-301-480-1889/C
; Sequence 1889, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301.480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1889
; LENGTH: 450
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1889
```

```
Query Match          14.3%; Score 16; DB 9; Length 450;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



OY 57 CCGTAAGAAGTCTCT 72  
|||||  
Db 426 CCGTAAGAAGTCTCT 411

RESULT 9  
US-10-301-480-615298/c  
; Sequence 615298, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 126818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 615298  
; LENGTH: 450  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-615298

Query Match 14.3%; Score 16; DB 10; Length 450;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 57 CCGTAAGAAGTCTCT 72  
|||||  
Db 426 CCGTAAGAAGTCTCT 411

RESULT 10  
US-09-925-065A-619252/c  
; Sequence 619252, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 619252  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-619252

Query Match 14.3%; Score 16; DB 6; Length 577;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 331 TGATATATTGGTTTAC 316

RESULT 11  
US-09-925-065A-619253/c  
; Sequence 619253, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 619253  
; LENGTH: 577  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-619253

Query Match 14.3%; Score 16; DB 6; Length 577;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGATATATTGGTTTAC 32  
|||||  
Db 331 TGATATATTGGTTTAC 316

RESULT 12  
US-09-925-065A-682241  
; Sequence 682241, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 682241  
; LENGTH: 623  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-682241

Query Match 14.3%; Score 16; DB 6; Length 623;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



OY 15 AATGATATATTGGTTT 30  
|||||  
Db 581 AATGATATATTGGTTT 596

RESULT 13  
US-09-925-065A-104147/C  
; Sequence 104147, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925, 065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 104147  
; LENGTH: 624  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-104147

Query Match 14.3%; Score 16; DB 6; Length 624;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 AATGATATATTGGTTT 31  
|||||  
Db 395 AATGATATATTGGTTT 380

RESULT 14  
US-10-301-480-204321/C  
; Sequence 204321, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 204321  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-204321

Query Match 14.3%; Score 16; DB 9; Length 634;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 16 AATGATATATTGGTTT 31  
|||||

Db 405 AATGATATATTGGTTT 390

RESULT 15  
US-10-301-480-817730/C  
; Sequence 817730, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 817730  
; LENGTH: 634  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-817730

Query Match 14.3%; Score 16; DB 10; Length 634;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 AATGATATATTGGTTT 31  
|||||  
Db 405 AATGATATATTGGTTT 390

RESULT 16  
US-10-301-480-53371/C  
; Sequence 53371, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 53371  
; LENGTH: 642  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-53371

Query Match 14.3%; Score 16; DB 9; Length 642;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AATGATATATTGGTTT 30  
|||||  
Db 503 AATGATATATTGGTTT 488

RESULT 17  
US-10-301-480-53372/C  
; Sequence 53372, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.



```

; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53372
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-53372

Query Match      14.3%; Score 16; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 AATGATATATTGTTT 30
Db      503 AATGATATATTGTTT 488

RESULT 18
US-10-301-480-53373/c
; Sequence 53373, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53373
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-53373

Query Match      14.3%; Score 16; DB 9; Length 642;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 AATGATATATTGTTT 30
Db      503 AATGATATATTGTTT 488

RESULT 19
US-10-301-480-666780/c
; Sequence 666780, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
```

```

; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666780
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-666780

Query Match      14.3%; Score 16; DB 10; Length 642;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 AATGATATATTGTTT 30
Db      503 AATGATATATTGTTT 488

RESULT 20
US-10-301-480-666781/c
; Sequence 666781, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666781
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-666781

Query Match      14.3%; Score 16; DB 10; Length 642;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      15 AATGATATATTGTTT 30
Db      503 AATGATATATTGTTT 488

RESULT 21
US-10-301-480-666782/c
; Sequence 666782, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 666782
; LENGTH: 642
; TYPE: DNA
; ORGANISM: Homo sapien
; US-10-301-480-666782

Query Match      14.3%; Score 16; DB 10; Length 642;
```



Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATTGCTT 30  
Db 503 AATGATATATTGCTT 488

## RESULT 22

US-09-925-065A-952833  
; Sequence 952833, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 2001-05-09  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 952833  
; LENGTH: 910  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-952833

Query Match 14.3%; Score 16; DB 6; Length 910;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 97 GTTAAAGAGCTGCTG 112  
Db 851 GTTAAAGAGCTGCTG 866

## RESULT 23

US-10-301-480-185389/c  
; Sequence 185389, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 185389  
; LENGTH: 1152  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-185389

Query Match 14.3%; Score 16; DB 9; Length 1152;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
Db 1144 GGTAGTTAAAGAGCT 1129

## RESULT 24

US-09-925-065A-84147/c  
; Sequence 84147, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84147  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-84147

Query Match 14.3%; Score 16; DB 6; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
Db 1147 GGTAGTTAAAGAGCT 1132

## RESULT 25

US-09-925-065A-84148/c  
; Sequence 84148, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 84148  
; LENGTH: 1155  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-84148

Query Match 14.3%; Score 16; DB 6; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
|||||  
Db 1147 GGTAGTTAAAGAGCT 1132

## RESULT 26

US-09-925-065A-84149/c  
; Sequence 84149, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84149  
LENGTH: 1155  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-84149

Query Match 14.3%; Score 16; DB 6; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
|||||  
Db 1147 GGTAGTTAAAGAGCT 1132

RESULT 27  
US-09-925-065A-84150/c  
; Sequence 84150, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 84150  
LENGTH: 1155  
TYPE: DNA  
ORGANISM: Homo sapiens

US-09-925-065A-84150

Query Match 14.3%; Score 16; DB 6; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
|||||  
Db 1147 GGTAGTTAAAGAGCT 1132

## RESULT 28

US-10-301-480-185387/c  
; Sequence 185387, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
FILE REFERENCE: 108827.137  
CURRENT APPLICATION NUMBER: US/10/301,480  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 10/215,598  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,695  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 1226818  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 185387  
LENGTH: 1155  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-301-480-185387

Query Match 14.3%; Score 16; DB 9; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
|||||  
Db 1147 GGTAGTTAAAGAGCT 1132

RESULT 29  
US-10-301-480-185388/c  
; Sequence 185388, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
FILE REFERENCE: 108827.137  
CURRENT APPLICATION NUMBER: US/10/301,480  
PRIOR FILING DATE: 2002-11-21  
PRIOR APPLICATION NUMBER: US 10/215,598  
PRIOR FILING DATE: 2002-08-09  
PRIOR APPLICATION NUMBER: US 60/311,695  
PRIOR FILING DATE: 2001-08-10  
NUMBER OF SEQ ID NOS: 1226818  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 185388  
LENGTH: 1155  
TYPE: DNA  
ORGANISM: Homo sapien  
US-10-301-480-185388

Query Match 14.3%; Score 16; DB 9; Length 1155;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 93 GGTAGTTAAAGAGCT 108  
|||||  
Db 1147 GGTAGTTAAAGAGCT 1132



```
RESULT 30
US-10-301-480-185390/c
; Sequence 185390, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185390
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-185390

Query Match      14.3%; Score 16; DB 9; Length 1155;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 GGTAGTTAAAGAGCT 108
Db      1147 GGTAGTTAAAGAGCT 1132

RESULT 31
US-10-301-480-798796/c
; Sequence 798796, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798796
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-798796

Query Match      14.3%; Score 16; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 GGTAGTTAAAGAGCT 108
Db      1147 GGTAGTTAAAGAGCT 1132

RESULT 32
US-10-301-480-798797/c
; Sequence 798797, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
```

```
; TITLE OF INVENTION: in the Human Genome
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798797
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-798797

Query Match      14.3%; Score 16; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 GGTAGTTAAAGAGCT 108
Db      1147 GGTAGTTAAAGAGCT 1132

RESULT 33
US-10-301-480-798798/c
; Sequence 798798, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 798798
; LENGTH: 1155
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-798798

Query Match      14.3%; Score 16; DB 10; Length 1155;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      93 GGTAGTTAAAGAGCT 108
Db      1147 GGTAGTTAAAGAGCT 1132

RESULT 34
US-10-301-480-798799/c
; Sequence 798799, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; CURRENT FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
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Job time : 471.422 secs

## RESULT 39

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US-10-750-185-40273/c
; Sequence 40273, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40273
; LENGTH: 2512
; TYPE: DNA
; ORGANISM: Bovine 19866880718724
US-10-750-185-40273
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## Query Match

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Best Local Similarity 14.3%; Score 16; DB 8; Length 2512;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 15 AATGATATATTGTTT 30
|||
```

```
Db 1380 AATGATATATTGTTT 1365
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## RESULT 40

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US-10-750-623-40273/c
; Sequence 40273, Application US/10750623
; Publication No. US20050287531A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM1100-1
; CURRENT APPLICATION NUMBER: US/10/750,623
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40273
; LENGTH: 2512
; TYPE: DNA
; ORGANISM: Bovine 19866880718724
US-10-750-623-40273
```

## Query Match

```
Best Local Similarity 14.3%; Score 16; DB 8; Length 2512;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 15 AATGATATATTGTTT 30
|||
```

```
Db 1380 AATGATATATTGTTT 1365
```

Search completed: April 12, 2006, 07:06:54



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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 1542.09 Seconds  
(without alignments)  
3398.084 Million cell updates/sec

Title: US-10-712-654-25

Perfect score: 112

Sequence: 1 ggtacatctgcgcgaatgat.....ggtagttcaagagctcgtcgtg 112

Scoring table:

OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_est3:\*  
4: gb\_est4:\*  
5: gb\_est5:\*  
6: gb\_est6:\*  
7: gb\_est7:\*  
8: gb\_est8:\*  
9: gb\_est9:\*  
10: gb\_est10:\*  
11: gb\_est11:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	19	17.0	457	6	CD860340 TE_002C14
3	18	16.1	350	1	AU233831 AU233831
4	18	16.1	354	1	AU278232 AU278232
5	18	16.1	408	7	CF890289 TCTR-1092
6	18	16.1	452	6	CA673959 w1bu2.DK0
7	18	16.1	455	2	BF599851 BP250012B
8	18	16.1	509	2	BF044692 BP250010A
9	18	16.1	518	10	CM294029 104_774.1
10	18	16.1	512	6	CB438817 687711.ME
11	18	16.1	529	7	CO877190 Bovenen_05
12	18	16.1	539	2	BF039887 BP250025A
13	18	16.1	539	2	BF039887 BP250025A
14	18	16.1	544	2	BF044189 BP250012B
15	18	16.1	549	7	CO551383 LYEST9862
16	18	16.1	551	7	CO884223 Bovenen_12
17	18	16.1	576	10	CM294028 104_774.1
18	18	16.1	591	1	AV984026 AV984026
19	18	16.1	595	6	CB439180 688791.MA
20	18	16.1	597	8	CV977041 UMC-bc1_0
21	18	16.1	602	6	CA696004 w1mk8.DK0
22	18	16.1	617	3	BJ310536 BJ310536

23	18	16.1	630	3	BJ217178 BJ217178
24	18	16.1	639	1	AV997156 AV997156
25	18	16.1	640	2	BR427379 PSR8369-B
26	18	16.1	655	6	CD905731 G468_102L
27	18	16.1	658	5	BM346197 BM346197
28	18	16.1	668	5	BM252739 BM252739
29	18	16.1	672	5	BM034334 BM034334
30	18	16.1	686	1	AV983799 AV983799
31	18	16.1	697	6	CD872302 CD872302
32	18	16.1	698	1	AL612522 AL612522
33	18	16.1	723	5	BM313478 BM313478
34	18	16.1	731	6	CD872303 CD872303
35	18	16.1	731	7	CK767599 CK767599
36	18	16.1	748	10	CL766270 CL766270
37	18	16.1	752	5	BM043930 BM043930
38	18	16.1	752	11	CNS07PNC CNS07PNC
39	18	16.1	825	10	DU070491 DU070491
40	18	16.1	825	8	CV770532 CV770532
41	18	16.1	880	10	CZ218116 CZ218116
42	18	16.1	880	10	DU088089 DU088089
43	18	16.1	899	10	DU088089 DU088089
44	18	16.1	943	7	CR852984 CR852984
45	18	16.1	987	10	CZ966936 CZ966936
46	18	16.1	1090	7	CK162840 CK162840
47	18	16.1	1311	10	CL960647 CL960647
48	17	15.2	197	10	CM292968 CM292968
49	17	15.2	212	5	BU890805 BU890805
50	17	15.2	234	5	BU099090 BU099090
51	17	15.2	256	9	CE021074 CE021074
52	17	15.2	321	7	CK530025 CK530025
53	17	15.2	328	3	BP942313 BP942313
54	17	15.2	343	10	AG979832 AG979832
55	17	15.2	362	5	BQ528900 BQ528900
56	17	15.2	391	9	BZ894063 BZ894063
57	17	15.2	414	5	BQ577507 BQ577507
58	17	15.2	428	6	CF009359 CF009359
59	17	15.2	437	6	CF009787 CF009787
60	17	15.2	438	7	CN774734 CN774734
61	17	15.2	452	2	CB467361 CB467361
62	17	15.2	452	7	CN771062 CN771062
63	17	15.2	458	5	BQ485752 BQ485752
64	17	15.2	458	5	BU097586 BU097586
65	17	15.2	462	6	CF011165 CF011165
66	17	15.2	464	6	CF011477 CF011477
67	17	15.2	471	2	BG467340 BG467340
68	17	15.2	477	6	CF009387 CF009387
69	17	15.2	478	1	AW562658 AW562658
70	17	15.2	480	1	A1584841 A1584841
71	17	15.2	483	6	CR244807 CR244807
72	17	15.2	483	10	CG680398 CG680398
73	17	15.2	485	5	BQ577412 BQ577412
74	17	15.2	486	2	BE232436 BE232436
75	17	15.2	486	3	BM374821 BM374821
76	17	15.2	491	5	BQ486231 BQ486231
77	17	15.2	491	6	CD274069 CD274069
78	17	15.2	497	10	AG966539 AG966539
79	17	15.2	498	5	BQ577748 BQ577748
80	17	15.2	498	6	CF010963 CF010963
81	17	15.2	501	2	BF602434 BF602434
82	17	15.2	502	1	AW355993 AW355993
83	17	15.2	502	3	BM317011 BM317011
84	17	15.2	509	5	BQ486423 BQ486423
85	17	15.2	520	6	CF010957 CF010957
86	17	15.2	520	6	CF010957 CF010957
87	17	15.2	521	6	CF010797 CF010797
88	17	15.2	526	1	AM668797 AM668797
89	17	15.2	526	10	CG915967 CG915967
90	17	15.2	528	2	BF728387 BF728387
91	17	15.2	531	3	BQ091404 BQ091404
92	17	15.2	531	6	CF010901 CF010901
93	17	15.2	533	1	AM618525 AM618525
94	17	15.2	533	6	CF011000 CF011000
95	17	15.2	535	5	BQ450316 BQ450316

BJ217178 BJ217178	AV997156 AV997156	BR427379 PSR8369-B	CD905731 G468_102L	BM346197 BM346197	BM252739 BM252739	BM034334 BM034334	AV983799 AV983799	CD872302 AZO2_120F	AL612522 TENGO332	BM313478 BM313478	CD872303 AZO2_120F	CK767599 968165.MA	CL766270 OR_BBA013	BM043930 BM043930	BH184801 026_M_05-	AL621752 T3 end of	DU070491 138260 TO	CV770532 FGAS06492	CZ218116 AINA-aaf3	DU088089 32515 Tom	CR852984 CR852984	CZ966936 166028 TO	CK162840 FGAS01544	CL960647 OeIFCC004	CM292968 104_773_1	BU890805 P041H11 P	BU099090 3524_1_24	CE021074 r1gr-g88-	CK530025 r1gr-g88-	BP942313 BP942313	AG979832 Drosophila	BQ528900 3524_1_42	BZ894063 UP_366-21	BQ577507 3524_1_38	CF009359 QBU1501.P	CF009787 QBU1501.P	CN774734 lae73d03.	CB467361 00963 1ea	CN771062 lae73d03.	BQ485752 3524_1_18	BU097586 3524_1_51	CF011165 QBU1501.P	CF011477 QBU1501.P	BG467340 00962 1ea	CF009387 QBU1501.P	AW562658 660068F09	A1584841 fb92a09.Y	CR244807 3530_1_7	CG680398 ZMMBDB032	BQ577412 3524_1_29	BE232436 137448.MA	BM374821 EBMA05.SQ	BM486231 3524_1_25	CD274069 T143B0177	AG966539 Drosophila	BQ577748 3524_1_41	CF010963 QBU1501.P	BF602434 267666.MA	AW355993 707018A02	BM317011 f778f09.Y	BQ486423 3524_1_31	CF010957 QBU1501.P	CF010797 QBU1501.P	AM668797 111426.MA	CG915967 ZMMBDB038	BF728387 1000061G0	BO091404 kul6h09.Y	CF010901 QBU1501.P	AM618525 EST320511	CF011000 QBU1501.P	BQ450316 faa78d09.
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C 97	17	15.2	538	6	CF010909	QB44h09.p	C 170	17	15.2	797	9	BM390365	BM390365 AG-ND-126
98	17	15.2	539	6	CF009920	QB274e04.	C 171	17	15.2	800	5	BM155865	BM155865
99	17	15.2	540	5	BQ486533	3524_1.34	C 172	17	15.2	804	6	CB943426	CB943426
100	17	15.2	541	2	BF370082	RCS-FN002	C 173	17	15.2	810	6	CB943632	CB943632
101	17	15.2	541	5	BQ528937	3524_1.43	C 174	17	15.2	816	10	AG395178	AG395178
C 102	17	15.2	546	6	CF009028	CF009028 QB17c10.	C 175	17	15.2	818	10	AG395215	AG395215
C 103	17	15.2	546	5	A07889028	HS 3250.A	C 176	17	15.2	836	9	B2533925	B2533925
C 104	17	15.2	548	5	BQ486112	3524_1.1	C 177	17	15.2	842	10	C2358447	C2358447
C 105	17	15.2	549	6	CB525772	CD525772 kw25h01.y	C 178	17	15.2	842	10	C2358447	C2358447
C 106	17	15.2	550	6	BQ621316	BQ621316 3524_1.48	C 179	17	15.2	843	5	BM953614	BM953614
C 107	17	15.2	550	9	BZ787713	PURFAR85TD	C 180	17	15.2	846	6	DN280616	DN280616
C 108	17	15.2	551	6	CF010614	CF010614 QB3A06.p	C 181	17	15.2	846	10	CG960310	CG960310
C 109	17	15.2	555	2	BE232130	BE232130 137064.MA	C 182	17	15.2	857	9	B2533917	B2533917
C 110	17	15.2	555	10	CG762202	CG762202 ZMMBB034	C 183	17	15.2	880	10	CG162730	CG162730
C 111	17	15.2	558	9	AZ440432	AZ440432 IM0231D03	C 184	17	15.2	880	10	CG162730	CG162730
C 112	17	15.2	562	1	AV870843	AV870843	C 185	17	15.2	881	2	BP248077	BP248077
C 113	17	15.2	565	6	CA827304	CA827304 1114012G0	C 186	17	15.2	907	10	CG203841	CG203841
C 114	17	15.2	571	5	BQ485417	BQ485417 3524_1.14	C 187	17	15.2	908	10	CG963610	CG963610
C 115	17	15.2	575	11	CR898038	CR898038 Sue_groE	C 188	17	15.2	911	10	CG184768	CG184768
C 116	17	15.2	576	2	BF191981	BF191981 243024.MA	C 189	17	15.2	911	10	CG184768	CG184768
C 117	17	15.2	577	6	CF010625	CF010625 QB3b01.p	C 190	17	15.2	937	10	CC013825	CC013825
C 118	17	15.2	578	5	BQ485825	BQ485825 3524_1.20	C 191	17	15.2	943	9	AZ138162	AZ138162
C 119	17	15.2	579	6	CB859928	CB859928 H112A14w	C 192	17	15.2	945	9	CC284683	CC284683
C 120	17	15.2	585	2	BF191985	BF191985 243030.MA	C 193	17	15.2	973	9	CG127440	CG127440
C 121	17	15.2	590	6	CF011510	CF011510 QB3A01.x	C 194	17	15.2	991	10	BM554449	BM554449
C 122	17	15.2	591	5	BQ578180	BQ578180 3524_1.56	C 195	17	15.2	994	3	BM554449	BM554449
C 123	17	15.2	592	5	BQ866719	BQ866719 5070A02.p	C 196	17	15.2	996	9	CC393743	CC393743
C 124	17	15.2	594	5	BQ617655	BQ617655 faa66d06.	C 197	17	15.2	999	11	CNS04CRX	CNS04CRX
C 125	17	15.2	595	5	BQ485579	BQ485579 3524_1.16	C 198	17	15.2	1014	4	AY109812	AY109812
C 126	17	15.2	600	9	BH876196	BH876196 hr29F03.g	C 199	17	15.2	1046	10	CG162729	CG162729
C 127	17	15.2	602	10	CG821105	CG821105 SOYET43TV	C 200	17	15.2	1128	9	CC263849	CC263849
C 128	17	15.2	603	5	BU097644	BU097644 3524_1.19	C 201	17	15.2	1219	9	CG263849	CG263849
C 129	17	15.2	605	1	AM400362	AM400362 707062A04	C 202	17	15.2	1390	4	AK079204	AK079204
C 130	17	15.2	606	3	BJ088767	BJ088767	C 203	17	15.2	2093	4	AK079204	AK079204
C 131	17	15.2	607	3	BM316836	BM316836 fw78F09.x	C 204	17	15.2	3762	10	CL958174	CL958174
C 132	17	15.2	607	9	AO289686	AO289686 nbxb0020G	C 205	17	15.2	162	1	AA256492	AA256492
C 133	17	15.2	613	7	CK698912	CK698912 ZF101-P00	C 206	17	15.2	176	10	CG306649	CG306649
C 134	17	15.2	614	1	AV916180	AV916180	C 207	17	15.2	249	8	DN509682	DN509682
C 135	17	15.2	619	5	BQ783799	BQ783799 faa66d06.	C 208	17	15.2	289	9	BH069491	BH069491
C 136	17	15.2	622	8	CK598090	CK598090 CT020019B	C 209	17	15.2	297	1	AA296804	AA296804
C 137	17	15.2	622	9	CE125060	CE125060 C1gr-g88-	C 210	17	15.2	300	1	AB123974	AB123974
C 138	17	15.2	625	5	BQ485947	BQ485947 3524_1.9	C 211	17	15.2	302	1	BB123974	BB123974
C 139	17	15.2	626	1	AM656062	AM656062 660061A10	C 212	17	15.2	323	3	AA881035	AA881035
C 140	17	15.2	636	9	AZ991104	AZ991104 2M0275D11	C 213	17	15.2	347	6	CD031037	CD031037
C 141	17	15.2	640	11	DE026787	DE026787 Branch108	C 214	17	15.2	352	7	CNS84146	CNS84146
C 142	17	15.2	644	10	CM652177	CM652177 OG_BBA000	C 215	17	15.2	361	7	CN931897	CN931897
C 143	17	15.2	646	9	BH771087	BH771087 Gm_S1UD00	C 216	17	15.2	373	6	CA615046	CA615046
C 144	17	15.2	647	9	BH876195	BH876195 hr29F03.b	C 217	17	15.2	383	10	C2686565	C2686565
C 145	17	15.2	649	9	BZ701878	BZ701878 PUCDB78TD	C 218	17	15.2	384	7	CG148635	CG148635
C 146	17	15.2	649	10	EX230320	EX230320 Dario_rer	C 219	17	15.2	384	7	CK553793	CK553793
C 147	17	15.2	650	1	AV863903	AV863903	C 220	17	15.2	387	1	AA255526	AA255526
C 148	17	15.2	654	6	CF011166	CF011166 QBU6F06.x	C 221	17	15.2	392	9	CA843516	CA843516
C 149	17	15.2	655	6	CF442550	CF442550 EST678895	C 222	17	15.2	394	7	CN931622	CN931622
C 150	17	15.2	665	10	CM691131	CM691131 OG_BBA005	C 223	17	15.2	395	2	BF087726	BF087726
C 151	17	15.2	668	1	BB110969	BB110969	C 224	17	15.2	397	1	AM788993	AM788993
C 152	17	15.2	687	5	BU548688	BU548688 CM880015B	C 225	17	15.2	403	3	BM528241	BM528241
C 153	17	15.2	688	7	CNS54622	CNS54622 cae31C06.	C 226	17	15.2	416	8	RA1621	RA1621
C 154	17	15.2	693	10	CM861947	CM861947 she2h81-5	C 227	17	15.2	422	9	AZ200639	AZ200639
C 155	17	15.2	698	2	BB225525	BB225525	C 228	17	15.2	428	1	AI915810	AI915810
C 156	17	15.2	698	3	BI934721	BI934721 EST554610	C 229	17	15.2	431	5	BM563461	BM563461
C 157	17	15.2	711	9	CC999065	CC999065 ZUAEG04TV	C 230	17	15.2	435	1	AM237855	AM237855
C 158	17	15.2	732	5	BM413433	BM413433	C 231	17	15.2	435	9	AO864011	AO864011
C 159	17	15.2	746	10	CM667107	CM667107 OG_BBA002	C 232	17	15.2	440	10	CM035257	CM035257
C 160	17	15.2	750	5	BM391132	BM391132	C 233	17	15.2	442	5	BY249381	BY249381
C 161	17	15.2	751	9	BZ616441	BZ616441 1959C07.b	C 234	17	15.2	442	9	AO886773	AO886773
C 162	17	15.2	752	9	AZ341872	AZ341872 IM0074M05	C 235	17	15.2	448	1	AM195653	AM195653
C 163	17	15.2	755	9	CC647606	CC647606 OGUG88TH	C 236	17	15.2	464	2	BF696753	BF696753
C 164	17	15.2	760	10	CG816016	CG816016 SOYER81TV	C 237	17	15.2	468	2	BB491117	BB491117
C 165	17	15.2	778	8	DN124300	DN124300 1125185.M	C 238	17	15.2	472	6	CA403231	CA403231
C 166	17	15.2	781	8	CM663398	CM663398 OG_BBA001	C 239	17	15.2	478	6	CA743907	CA743907
C 167	17	15.2	781	8	DN124642	DN124642 1125569.M	C 240	17	15.2	480	7	CK644947	CK644947
C 168	17	15.2	782	5	BM399183	BM399183	C 241	17	15.2	482	6	CD067258	CD067258

CK124049	BS182410	BM390365	AG-ND-126	BM155865	BM155865	CB943426	AGBNC09A1	CA435332	BE04009A1	AG395178	Mus muscu	CG9642515	MBE159TF	BE533923	OGAKB21TC	B2989911	PUG1X17TB	CG258447	ZMMBF0099	BM953614	BM953614	DN280616	1161743.M	CG960310	ATAA-aab0	CG537703	PURGO72TB	BE533917	OGAKB21TC	CG162730	PUPFV15TD	BP248077	60185935	CG346137	OGAF68TV	CG203841	PURFC2TB	CG963610	MBLFP20TF	CG186630	PUBBA77B	CG184768	PUCG55TD	CC013825	PUDHL25TD	AZ138162	SP_0175.A	CC284683	CH261-37N	CG127440	PUIHF33TB	BM554449	AGENCOURT	CC393743	PURSE91TD	AL288433	Tetereodon	AY109812	Zea_mays	CG162729	PUPFV15TB	CG270669	CH261-181	CC263849	CH261-49L	AX041223	Mus muscu	AX079204	Mus muscu	CL958174	OB1FCC000	AA256492	zr18F09.B	CG630649	OSTY46132	DN509682	HL02016B2	BH069491	RPCT-24-2	AA296804	EST112369	AA296804	AJ473147	AJ473147	BB123974	BB123974	AA881035	vx35e07.r	CD031037	mgmE004X1	CNS84146	USDA-FP.1	CN931897	000428A7B	CA615046	wr1.PK151	CG686565	OA_BBA015	AA255526	zr18b02.8	AA255526	nbxb0020K	CN931622	000427A7B	BF087726	IL3-H7061	AM788993	CO0854-F	BM528241	sal156A07.	RA1621	Y104908.r1	AZ200639	RPCT-23-1	AI915810	wg94C05.x	AI915810	wg94C05.x	BX563461	BX563461	BM563461	IL3-ET01.x	BF696753	IL3-ET01.x	BE491117	uw02N06.Y	CF403231	CSCCS003B	CA743907	wr118.pK0	CK644947	81.04.A3.	CD067258	MA1-0049T
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242	16	14.3	494	2	BG660720	BG660720	TGSTRZyal	c 315	16	14.3	630	9	BH389714	BH389714	AG-ND-135
c 243	16	14.3	496	10	CM085407	CM085407	104_428_1	316	16	14.3	631	9	AO661096	AO661096	Shreaded D
c 244	16	14.3	496	10	CM070658	CM070658	ATAA-aaB5	317	16	14.3	631	7	CN818257	CN818257	HR04470_E
245	16	14.3	499	3	BW738695	BW738695	K-EST0006	318	16	14.3	631	2	EG036594	EG036594	602326383
c 246	16	14.3	500	7	CN814814	CN814814	HR04502_G	c 319	16	14.3	637	6	CB008163	CB008163	VC054C09
c 247	16	14.3	503	7	AA329932	AA329932	EST33606	c 320	16	14.3	637	8	DR161663	DR161663	RTEP1_13-
248	16	14.3	510	10	CM897219	CM897219	RPCI42_13	c 321	16	14.3	638	8	DR161745	DR161745	RTEP1_13-
c 249	16	14.3	512	9	B2932496	B2932496	CH240_51A	c 322	16	14.3	639	8	CM673613	CM673613	UCRCS10_2
c 250	16	14.3	513	1	AA586148	AA586148	28797_Lam	c 323	16	14.3	639	10	CM371810	CM371810	febb001f0
c 251	16	14.3	517	1	A1435926	A1435926	CH80B02_X	c 324	16	14.3	640	6	CA167839	CA167839	SCEBS104
c 252	16	14.3	518	1	A1590271	A1590271	tnA8e01.x	c 325	16	14.3	641	7	CN819288	CN819288	HR04452_C
c 253	16	14.3	520	1	A1367587	A1367587	qg30a09.x	c 326	16	14.3	643	10	CM237363	CM237363	104_693_1
254	16	14.3	523	6	CF355895	CF355895	lab75a08.	c 327	16	14.3	644	11	DE031774	DE031774	Branch108
255	16	14.3	523	9	A2967344	A2967344	2M0238D14	c 328	16	14.3	646	10	CM419047	CM419047	febb001f1
c 256	16	14.3	524	9	B2629377	B2629377	ih49e04.9	c 329	16	14.3	647	9	B2415264	B2415264	1f53a08.g
c 257	16	14.3	530	10	CM100298	CM100298	104_467_1	c 330	16	14.3	648	7	CF834993	CF834993	UCRCS02_0
c 258	16	14.3	533	2	BE676538	BE676538	7f31f12.x	c 331	16	14.3	651	8	CK669748	CK669748	UCRCP01_0
c 259	16	14.3	534	11	TA76A08Q	TA76A08Q	AL459703_T_brucel	c 332	16	14.3	652	11	CR923004	CR923004	Sus_bctof
c 260	16	14.3	536	7	CR554994	CR554994	DKFZP468A	c 333	16	14.3	654	1	AL850698	AL850698	AL850698
c 261	16	14.3	537	10	CE682608	CE682608	tlgr-988-	c 334	16	14.3	658	10	CL799523	CL799523	OR_CBA001
c 262	16	14.3	540	7	CN818828	CN818828	HR04460_A	c 335	16	14.3	660	10	CM269236	CM269236	104_740_1
263	16	14.3	540	11	TA309B12Q	TA309B12Q	AL489015_T_brucel	c 336	16	14.3	661	10	CN820636	CN820636	104_693_1
c 264	16	14.3	543	1	A1670847	A1670847	wa04h10.x	c 337	16	14.3	664	7	CN820636	CN820636	104_693_1
c 265	16	14.3	550	10	CL720779	CL720779	OR_BBA004	c 338	16	14.3	665	1	AV382453	AV382453	AV382453
c 266	16	14.3	550	11	DE013429	DE013429	Branch108	c 339	16	14.3	665	10	CM371809	CM371809	BP130439
267	16	14.3	552	3	B1700836	B1700836	sag51f10.	c 340	16	14.3	666	3	BP130439	BP130439	BP130439
c 268	16	14.3	553	6	CD116210	CD116210	ME1-0039T	c 341	16	14.3	671	7	CN423691	CN423691	170006008
c 269	16	14.3	554	7	CN423679	CN423679	170006001	c 342	16	14.3	676	6	CF178772	CF178772	808282_MA
c 270	16	14.3	554	7	CV404297	CV404297	RCO-EN002	c 343	16	14.3	676	10	CM061114	CM061114	104_304_1
c 271	16	14.3	555	11	TA325B06Q	TA325B06Q	AL491567_T_brucel	c 344	16	14.3	683	7	CN184460	CN184460	170005939
272	16	14.3	559	7	CN818919	CN818919	HR04473_A	c 345	16	14.3	684	7	CN423674	CN423674	170005939
c 273	16	14.3	560	7	CO831610	CO831610	LM_GBS_01	c 346	16	14.3	685	10	C2576894	C2576894	OA_BBA017
274	16	14.3	560	7	CO854496	CO854496	LM_SH5_00	c 347	16	14.3	688	9	AQ330042	AQ330042	nbXB0046M
c 275	16	14.3	562	9	A2467192	A2467192	IM0278U19	c 348	16	14.3	691	9	BH459286	BH459286	BOG0U53TF
c 276	16	14.3	568	9	B2940618	B2940618	CH240_108	c 349	16	14.3	691	9	CE135512	CE135512	tlgr-988-
c 277	16	14.3	569	6	CA142275	CA142275	SCMCRT208	c 350	16	14.3	693	6	CA207229	CA207229	SCEBS1C10
c 278	16	14.3	569	8	CV910674	CV910674	PE016P9_m	c 351	16	14.3	693	10	AG158877	AG158877	Pan_troQ1
c 279	16	14.3	570	6	CD471715	CD471715	LeukoS6_4	c 352	16	14.3	697	3	BM626046	BM626046	170006874
280	16	14.3	571	6	CD471600	CD471600	LeukoS6_4	c 353	16	14.3	697	3	CT711916	CT711916	OGVAD54TC
281	16	14.3	572	5	BX567701	BX567701	BX567701	c 354	16	14.3	697	10	CM397154	CM397154	febb001f0
c 282	16	14.3	572	10	CM771156	CM771156	OG_BBA003	c 355	16	14.3	702	9	CE133509	CE133509	tlgr-988-
c 283	16	14.3	574	10	BH761857	BH761857	BMBAC325F	c 356	16	14.3	704	2	B1117804	B1117804	602866821
c 284	16	14.3	576	7	CO830897	CO830897	LM_GBS_01	c 357	16	14.3	704	9	BH927604	BH927604	od161e08.
c 285	16	14.3	577	11	CR214403	CR214403	RCMward_8	c 358	16	14.3	704	9	BZ021536	BZ021536	od161e12.
c 286	16	14.3	578	9	AZ605950	AZ605950	IM0427003	c 359	16	14.3	706	10	CM223301	CM223301	104_659_1
c 287	16	14.3	585	10	C2793058	C2793058	OC_Ba016	c 360	16	14.3	711	2	CE694832	CE694832	tlgr-988-
c 288	16	14.3	587	9	CC772484	CC772484	CH240_8U1	c 361	16	14.3	713	10	BE783363	BE783363	601471836
c 289	16	14.3	588	6	CM192475	CM192475	104_614_1	c 362	16	14.3	713	9	AO941212	AO941212	Sheared_D
c 290	16	14.3	589	6	CA343052	CA343052	673067_NC	c 363	16	14.3	716	10	CM031241	CM031241	259_1
c 291	16	14.3	589	7	CV010289	CV010289	zf101-3m8	c 364	16	14.3	720	11	CG398453	CG398453	CG922821
292	16	14.3	592	6	CD082882	CD082882	MA3-9999U	c 365	16	14.3	720	11	CG922821	CG922821	Sus_bctof
293	16	14.3	592	7	CN818052	CN818052	HR04472_C	c 366	16	14.3	725	6	CF178446	CF178446	807514_MA
c 294	16	14.3	594	10	CM072422	CM072422	104_325_1	c 367	16	14.3	728	9	BH529063	BH529063	BOHAB27TF
c 295	16	14.3	599	2	BE884568	BE884568	601506265	c 368	16	14.3	731	9	BZ388904	BZ388904	EINCY53TR
296	16	14.3	606	1	AM965459	AM965459	EST377427	c 369	16	14.3	734	9	CE079505	CE079505	tlgr-988-
297	16	14.3	606	7	CN423688	CN423688	170005999	c 370	16	14.3	735	7	CK936663	CK936663	CG100451
298	16	14.3	608	1	AM999785	AM999785	MRO-BN007	c 371	16	14.3	740	10	CL151404	CL151404	104_334_1
299	16	14.3	609	9	AQ946626	AQ946626	Sheared_D	c 372	16	14.3	741	9	AQ050246	AQ050246	nbXB0003C
300	16	14.3	610	7	CN817450	CN817450	HR04466_A	c 373	16	14.3	741	9	AQ033089	AQ033089	nbXB00460
c 301	16	14.3	611	1	AU168000	AU168000	AU168000	c 374	16	14.3	742	7	CN763722	CN763722	ID0AA4DE
c 302	16	14.3	612	9	B2780840	B2780840	1120h05.g	c 375	16	14.3	743	3	BM674954	BM674954	UI-E-ETO-
c 303	16	14.3	613	6	CB915700	CB915700	VND102A06	c 376	16	14.3	744	10	CL163030	CL163030	104_355_1
c 304	16	14.3	613	10	CE532842	CE532842	tlgr-988-	c 377	16	14.3	744	10	CG160159	CG160159	P1EH77TD
c 305	16	14.3	614	1	A1468646	A1468646	th83h08.x	c 378	16	14.3	746	7	CN755667	CN755667	ID0AA16C
c 306	16	14.3	616	5	BU353244	BU353244	603526007	c 379	16	14.3	746	9	BH738389	BH738389	BOMNO46TR
307	16	14.3	616	6	CD306663	CD306663	StcPb691.	c 380	16	14.3	751	9	BZ330910	BZ330910	hw03b01.g
c 308	16	14.3	619	3	AQ164239	AQ164239	HS_2207_B	c 381	16	14.3	755	7	CF829957	CF829957	UCRCR01_0
c 309	16	14.3	619	3	B1693618	B1693618	BtE93618	c 382	16	14.3	756	7	CM671521	CM671521	OGVAV35TV
310	16	14.3	622	5	BQ485611	BQ485611	3524_1_16	c 383	16	14.3	760	7	CN755575	CN755575	ID0AA16B
311	16	14.3	624	10	CM512556	CM512556	115_1_105	c 384	16	14.3	760	10	CL445893	CL445893	ZMBB0046
312	16	14.3	625	6	CD307997	CD307997	StcPb691.	c 385	16	14.3	762	9	B2403066	B2403066	OGAAB89TH
313	16	14.3	626	1	AA739514	AA739514	279_PtIFG	c 386	16	14.3	763	10	C2728522	C2728522	OC_Ba005
314	16	14.3	630	6	CF395553	CF395553	RTDS2_12_	c 387	16	14.3	764	2	B1182328	B1182328	UNL-P-FN-



388	16	14.3	764	9	A0858877	A0858877	nbbp0003H	461	16	14.3	891	10	CG165677	CG165677	PUIHJ070TB
389	16	14.3	766	3	BQ220676	BQ220676	AGENCOURT	462	16	14.3	893	6	CD381690	CD381690	PTM06859
390	16	14.3	766	10	CL830158	CL830158	OR_CBA005	463	16	14.3	899	9	CG685288	CG685288	OGJPS20TH
391	16	14.3	768	9	B2489426	B2489426	BOND48TF	464	16	14.3	901	5	BQ946620	BQ946620	AGENCOURT
392	16	14.3	768	10	CG144924	CG144924	PURCO95TD	465	16	14.3	905	10	CG086895	CG086895	PURKSH1TD
393	16	14.3	771	6	CA273287	CA273287	SCORET3CO	466	16	14.3	908	10	CG298992	CG298992	259054 TO
394	16	14.3	771	8	CX073200	CX073200	UCRCS08_3	467	16	14.3	909	3	B1335198	B1335198	60298071
395	16	14.3	771	10	DU076507	DU076507	88127 Tom	468	16	14.3	911	8	DN571070	DN571070	92507761
396	16	14.3	771	10	CG284687	CG284687	OGMLX03TH	469	16	14.3	912	9	CC357427	CC357427	PURHFB6TB
397	16	14.3	772	2	BF867774	BF867774	963093H06	470	16	14.3	917	10	CL474349	CL474349	SATL_218
398	16	14.3	772	9	B2403065	B2403065	OGAB89TF	471	16	14.3	918	8	DR466804	DR466804	WS00939_B
399	16	14.3	774	7	CL828554	CL828554	OR_CBA004	472	16	14.3	918	9	CC373114	CC373114	PURHE08TB
400	16	14.3	774	10	CG182855	CG182855	OR_CBA004	473	16	14.3	922	9	CC781348	CC781348	CC781348_ZMWBBCO44
401	16	14.3	777	7	CG817641	CG817641	HRO4463_B	474	16	14.3	930	11	CGNS06VR	CGNS06VR	AL417589_T7 end of
402	16	14.3	777	10	CG034500	CG034500	PURFS89TD	475	16	14.3	931	7	CK936450	CK936450	CGF100438
403	16	14.3	778	10	CG029133	CG029133	104_256_1	476	16	14.3	939	8	DR591187	DR591187	WS00830_B
404	16	14.3	780	9	BF219322	BF219322	601883193	477	16	14.3	943	10	CG266711	CG266711	CG306882_OG3B063TH
405	16	14.3	780	9	CC342681	CC342681	OGIBU54TV	478	16	14.3	945	10	CG306882	CG306882	CG263897_WS02023_B
406	16	14.3	781	10	AG133973	AG133973	Mus_muscu	479	16	14.3	946	7	CV263897	CV263897	BU150013_AGENCOURT
407	16	14.3	781	10	CG202763	CG202763	PURBZ93TD	480	16	14.3	951	5	BU150013	BU150013	DU017817_317297 TO
408	16	14.3	787	8	CX788369	CX788369	HESC3_97	481	16	14.3	955	10	DU017817	DU017817	CL238779_ZMWB058
409	16	14.3	787	8	AO688663	AO688663	MDX0078G	482	16	14.3	967	10	CL238779	CL238779	CZ983658_197611 TO
410	16	14.3	789	11	CR923167	CR923167	Sub_acrofe	483	16	14.3	982	10	CZ983658	CZ983658	BZ754027_PUREG92TD
411	16	14.3	797	8	CV840919	CV840919	ID0AD14D	484	16	14.3	983	9	BZ754027	BZ754027	CL121099_1881_-79P1
412	16	14.3	798	10	CZ850499	CZ850499	OC_BA023	485	16	14.3	1001	10	CG092394	CG092394	CG092394_PUJCN18TD
413	16	14.3	798	9	BX155674	BX155674	Dantlo_rer	486	16	14.3	1009	1	AM155143	AM155143	AN155143_mg1e002C
414	16	14.3	799	9	BZ069351	BZ069351	IKg81f12.	487	16	14.3	1021	10	BM471908	BM471908	BM471908_AGENCOURT
415	16	14.3	800	10	CG144923	CG144923	PURCO95TB	488	16	14.3	1024	3	BM471908	BM471908	BZ158239_CH320-433
416	16	14.3	801	9	BHS33564	BHS33564	BOH8219TF	489	16	14.3	1027	9	BZ158239	BZ158239	BX424216
417	16	14.3	806	2	BF65066	BF65066	602119667	490	16	14.3	1035	5	BX424216	BX424216	AL335861_Tetracodon
418	16	14.3	806	6	CA311306	CA311306	UI-CF-FNO	491	16	14.3	1048	11	CNS05G58	CNS05G58	AG5559140_Mus_muscu
419	16	14.3	808	2	BF797261	BF797261	602257766	492	16	14.3	1064	10	CNS0205E	CNS0205E	AL175163_Tetracodon
420	16	14.3	808	6	CD642994	CD642994	AGENCOURT	493	16	14.3	1064	10	CL085258	CL085258	CL085258_1881_-4M15
421	16	14.3	809	5	CL831581	CL831581	OR_CBA005	494	16	14.3	1096	5	BQ884602	BQ884602	BQ884602_AGENCOURT
422	16	14.3	812	5	BUB54693	BUB54693	AGENCOURT	495	16	14.3	1243	5	BQ884602	BQ884602	AG561611_Mus_muscu
423	16	14.3	812	9	CC346346	CC346346	OGQA018TV	496	16	14.3	1306	10	AG561611	AG561611	AG582044_Mus_muscu
424	16	14.3	814	2	BP966028	BP966028	602277326	497	16	14.3	1459	9	CC309661	CC309661	CL977381_OstFCC022
425	16	14.3	818	2	BC444464	BC444464	GA_Ba002	498	16	14.3	1485	10	AG582044	AG582044	BC015150_Homo sapi
426	16	14.3	820	10	CM800641	CM800641	WICDBLOX	499	16	14.3	2157	10	CL977381	CL977381	BC015150_Homo sapi
427	16	14.3	821	9	BZ434695	BZ434695	BONCW72TF	500	16	14.3	4459	4	BC015150	BC015150	AL968505
428	16	14.3	822	9	BZ529002	BZ529002	OGAG131TC	501	16	14.3	942	1	AL968505	AL968505	CK553035_rbw1A0_01
429	16	14.3	823	7	CN760270	CN760270	ID0AAA27D	502	16	14.3	166	10	CG512466	CG512466	CG512466_OSTF5408
430	16	14.3	824	7	CK239983	CK239983	AGENCOURT	503	16	14.3	168	10	BX982718	BX982718	BS982718_Reverse
431	16	14.3	827	7	CN758358	CN758358	ID0AAA22A	504	16	14.3	170	1	AV925852	AV925852	AV925852_AV925852
432	16	14.3	827	8	CX073199	CX073199	UCRCS08_3	505	16	14.3	189	9	AL9271125	AL9271125	AL9271125_ArabiD10p8
433	16	14.3	834	9	CO454946	CO454946	M2CCL1020	506	16	14.3	189	9	AL9271125	AL9271125	CN801058_D18P0394
434	16	14.3	836	9	CC582638	CC582638	CH240_378	507	16	14.3	194	7	CN801058	CN801058	BS534197_ArabiD10p8
435	16	14.3	840	9	BH561732	BH561732	B0GZNI0TR	508	16	14.3	196	10	BS534197	BS534197	CD535867
436	16	14.3	840	10	DU072940	DU072940	60664 Tom	509	16	14.3	198	6	CD535867	CD535867	H06420
437	16	14.3	844	10	CG264118	CG264118	OG2AR30TH	510	16	14.3	203	8	H06420	H06420	AV282032_AV282032
438	16	14.3	846	9	BH426853	BH426853	BOH1T87TR	511	16	14.3	209	1	AV282032	AV282032	BM857359_BM857359
439	16	14.3	846	9	CC342669	CC342669	OGIBU54TF	512	16	14.3	221	5	BM857359	BM857359	DR083774_CAS7013B0
440	16	14.3	847	2	BC368818	BC368818	HVSMF1002	513	16	14.3	221	8	DR083774	DR083774	CG590406_OSTF43807
441	16	14.3	850	10	CG448893	CG448893	OGSEAO4TV	514	16	14.3	224	10	CG590406	CG590406	CKR75624_ZF101-P00
442	16	14.3	851	10	DU033893	DU033893	15836 Tom	515	16	14.3	224	7	CKR75624	CKR75624	CO787719_NT002B_AO
443	16	14.3	861	10	CL282608	CL282608	ZMWB062	516	16	14.3	227	10	AV282032	AV282032	AV282032_AV282032
444	16	14.3	862	2	B1257330	B1257330	602967286	517	16	14.3	227	7	CO787719	CO787719	AV280376_AV280376
445	16	14.3	862	7	CN758380	CN758380	ID0AAA22A	518	16	14.3	232	3	B1576952	B1576952	B1576952_RH33648_5
446	16	14.3	863	8	DR759740	DR759740	HESC4_107	519	16	14.3	244	10	BB554910	BB554910	BS54910_BBS54910
447	16	14.3	865	10	DU038705	DU038705	22000 Tom	520	16	14.3	244	10	BB554910	BB554910	BS54910_BBS54910
448	16	14.3	868	5	BU183581	BU183581	AGENCOURT	521	16	14.3	247	1	AV272899	AV272899	AV272899_AV272899
449	16	14.3	872	10	CG308165	CG308165	OGOF747TH	522	16	14.3	248	10	AV253894	AV253894	AV253894_AV253894
450	16	14.3	874	5	BU193833	BU193833	AGENCOURT	523	16	14.3	248	1	AV253894	AV253894	AV253894_AV253894
451	16	14.3	876	8	DR593094	DR593094	WS00836_B	524	16	14.3	248	10	BB554910	BB554910	BS54910_BBS54910
452	16	14.3	877	9	CC474840	CC474840	CH240_300	525	16	14.3	248	10	BB554910	BB554910	BS54910_BBS54910
453	16	14.3	878	10	DU015115	DU015115	292621 TO	526	16	14.3	247	1	AV272899	AV272899	AV272899_AV272899
454	16	14.3	880	7	CV268221	CV268221	WS0204_B2	527	16	14.3	247	10	CG149760	CG149760	CG149760_OA_BBA006
455	16	14.3	881	10	DU090346	DU090346	318932 TO	528	16	14.3	251	9	CC151291	CC151291	CC151291_NDL_54G15
456	16	14.3	884	8	DR556077	DR556077	WS0327_C2	529	16	14.3	252	1	AA594293	AA594293	AA594293_n191902_8
457	16	14.3	886	8	DR576449	DR576449	WS00743_C	530	16	14.3	252	7	CN833568	CN833568	CN833568_4117580_B
458	16	14.3	886	10	CG334480	CG334480	PURFM14TD	531	16	14.3	255	1	AV770452	AV770452	AV770452_AV770452
459	16	14.3	889	10	CG308174	CG308174	OGOF747TV	532	16	14.3	255	1	AV770452	AV770452	AV770452_AV770452
460	16	14.3	889	10	CG308174	CG308174	OGOF747TV	533	16	14.3	255	1	AV770452	AV770452	AV770452_AV770452



534	15	13.4	255	5	BM876636	BM876636	607	15	13.4	348	10	CG949379	CG949379
535	15	13.4	256	7	CV198479	CV198479	608	15	13.4	349	11	AA457848	AA457848
536	15	13.4	259	8	DN929500	DN929500	609	15	13.4	350	11	CR298128	CR298128
537	15	13.4	262	5	BU980147	BU980147	610	15	13.4	351	11	AA786281	AA786281
538	15	13.4	263	9	BH506632	BH506632	611	15	13.4	352	8	DR174407	DR174407
539	15	13.4	265	1	AV262488	AV262488	612	15	13.4	353	1	AA052852	AA052852
540	15	13.4	266	6	CB965546	CB965546	613	15	13.4	354	10	BX511869	BX511869
541	15	13.4	270	10	CG489655	CG489655	614	15	13.4	355	9	AZ175280	AZ175280
542	15	13.4	272	9	BI4514	BI4514	615	15	13.4	356	1	A1324001	A1324001
543	15	13.4	272	10	AG911207	AG911207	616	15	13.4	358	1	A1083053	A1083053
544	15	13.4	273	1	AA713446	AA713446	617	15	13.4	358	9	AZ219078	AZ219078
545	15	13.4	273	6	CA57910	CA57910	618	15	13.4	359	3	BQ011559	BQ011559
546	15	13.4	273	8	DN332959	DN332959	619	15	13.4	360	1	AB610746	AB610746
547	15	13.4	274	1	AM619646	AM619646	620	15	13.4	362	1	A1363706	A1363706
548	15	13.4	277	6	CA574487	CA574487	621	15	13.4	363	9	CC888488	CC888488
549	15	13.4	278	6	CA575748	CA575748	622	15	13.4	364	1	A1552257	A1552257
550	15	13.4	278	6	CD453158	CD453158	623	15	13.4	365	1	AA602787	AA602787
551	15	13.4	284	1	AV930600	AV930600	624	15	13.4	365	8	HH94013	HH94013
552	15	13.4	284	6	CF590944	CF590944	625	15	13.4	368	8	L44374	L44374
553	15	13.4	284	8	DN178930	DN178930	626	15	13.4	368	9	AQ639468	AQ639468
554	15	13.4	285	9	AQ385817	AQ385817	627	15	13.4	375	1	A1210591	A1210591
555	15	13.4	288	2	BF198193	BF198193	628	15	13.4	376	9	BH809568	BH809568
556	15	13.4	290	1	AA304476	AA304476	629	15	13.4	377	6	CD392956	CD392956
557	15	13.4	291	1	AA759999	AA759999	630	15	13.4	377	7	CO318531	CO318531
558	15	13.4	294	1	AT093760	AT093760	631	15	13.4	379	2	BE592205	BE592205
559	15	13.4	295	7	CV342284	CV342284	632	15	13.4	379	9	AQ637854	AQ637854
560	15	13.4	298	1	AV205154	AV205154	633	15	13.4	380	1	A1326545	A1326545
561	15	13.4	300	1	AL960575	AL960575	634	15	13.4	382	9	AQ095319	AQ095319
562	15	13.4	300	5	AU098537	AU098537	635	15	13.4	384	1	A1101592	A1101592
563	15	13.4	300	5	C31660	C31660	636	15	13.4	385	1	AU108417	AU108417
564	15	13.4	300	6	CD802061	CD802061	637	15	13.4	385	10	CG858833	CG858833
565	15	13.4	300	8	CM104916	CM104916	638	15	13.4	386	2	BF438981	BF438981
566	15	13.4	301	10	AG267834	AG267834	639	15	13.4	386	9	CE224070	CE224070
567	15	13.4	303	5	BK629451	BK629451	640	15	13.4	387	1	AU304182	AU304182
568	15	13.4	305	8	R38893	R38893	641	15	13.4	388	9	CC932975	CC932975
569	15	13.4	307	2	BE200905	BE200905	642	15	13.4	390	10	CE484056	CE484056
570	15	13.4	307	6	CB665284	CB665284	643	15	13.4	391	8	D22775	D22775
571	15	13.4	307	7	CR475501	CR475501	644	15	13.4	391	8	DR083168	DR083168
572	15	13.4	307	10	CM483172	CM483172	645	15	13.4	392	6	CB640935	CB640935
573	15	13.4	310	6	CF514869	CF514869	646	15	13.4	393	9	AQ292717	AQ292717
574	15	13.4	310	9	AQ386486	AQ386486	647	15	13.4	395	7	CV461913	CV461913
575	15	13.4	312	1	AA877974	AA877974	648	15	13.4	398	5	C96907	C96907
576	15	13.4	313	1	AT634289	AT634289	649	15	13.4	398	6	CA388884	CA388884
577	15	13.4	313	5	C29118	C29118	650	15	13.4	401	1	AA601640	AA601640
578	15	13.4	314	9	BE292596	BE292596	651	15	13.4	404	10	C2795596	C2795596
579	15	13.4	316	10	CE580028	CE580028	652	15	13.4	405	2	BG834330	BG834330
580	15	13.4	317	1	BB134896	BB134896	653	15	13.4	405	10	CZ495896	CZ495896
581	15	13.4	318	8	DN240344	DN240344	654	15	13.4	406	3	BI798331	BI798331
582	15	13.4	319	6	CA284778	CA284778	655	15	13.4	406	5	BY534423	BY534423
583	15	13.4	319	6	CB005117	CB005117	656	15	13.4	408	2	BG005887	BG005887
584	15	13.4	319	8	DR083459	DR083459	657	15	13.4	410	3	BP793360	BP793360
585	15	13.4	320	7	CO280384	CO280384	658	15	13.4	410	4	AY440769	AY440769
586	15	13.4	321	2	BG184413	BG184413	659	15	13.4	410	8	W95586	W95586
587	15	13.4	324	1	AU058191	AU058191	660	15	13.4	411	8	AV741165	AV741165
588	15	13.4	325	1	AT173095	AT173095	661	15	13.4	411	8	DN898522	DN898522
589	15	13.4	325	9	CE248934	CE248934	662	15	13.4	412	1	AA299897	AA299897
590	15	13.4	325	10	AL761184	AL761184	663	15	13.4	412	10	CM375158	CM375158
591	15	13.4	326	1	AA634392	AA634392	664	15	13.4	415	5	BY534766	BY534766
592	15	13.4	328	3	BJ464017	BJ464017	665	15	13.4	421	1	A1862086	A1862086
593	15	13.4	331	5	BK637759	BK637759	666	15	13.4	423	6	CD455200	CD455200
594	15	13.4	331	6	CD860433	CD860433	667	15	13.4	424	1	AA663914	AA663914
595	15	13.4	332	1	AA411832	AA411832	668	15	13.4	424	7	CN902484	CN902484
596	15	13.4	333	5	BQ377915	BQ377915	669	15	13.4	425	1	AA108977	AA108977
597	15	13.4	333	5	BM885581	BM885581	670	15	13.4	425	9	B2287977	B2287977
598	15	13.4	336	9	CN903355	CN903355	671	15	13.4	426	5	BX528132	BX528132
599	15	13.4	339	1	AJ661241	AJ661241	672	15	13.4	426	8	W09299	W09299
600	15	13.4	340	1	AA962698	AA962698	673	15	13.4	428	1	AA787821	AA787821
601	15	13.4	340	9	BH840438	BH840438	674	15	13.4	429	3	EM425446	EM425446
602	15	13.4	341	6	CA432888	CA432888	675	15	13.4	431	1	A1323747	A1323747
603	15	13.4	341	6	AJ731846	AJ731846	676	15	13.4	432	7	BN796876	BN796876
604	15	13.4	344	1	AA428652	AA428652	677	15	13.4	433	5	CN309537	CN309537
605	15	13.4	344	1	AZ790645	AZ790645	678	15	13.4	434	1	A1279482	A1279482
606	15	13.4	347	9	AQ727791	AQ727791	679	15	13.4	434	9	AQ727791	AQ727791
					BM876636	BM876636						CG949379	CG949379
					CV198479	CV198479						AA457848	AA457848
					DN929500	DN929500						CR298128	CR298128
					BU980147	BU980147						AA786281	AA786281
					BH506632	BH506632						DR174407	DR174407
					AV262488	AV262488						AA052852	AA052852
					CB965546	CB965546						BX511869	BX511869
					CG489655	CG489655						AZ175280	AZ175280
					BI4514	BI4514						A1324001	A1324001
					AG911207	AG911207						A1083053	A1083053
					AA713446	AA713446						A2219078	A2219078
					CA57910	CA57910						BQ011559	BQ011559
					DN332959	DN332959						AB610746	AB610746
					AM619646	AM619646						A1363706	A1363706
					CA574487	CA574487						CC888488	CC888488
					CA57448	CA57448						A1552257	A1552257
					CD453158	CD453158						AA602787	AA602787
					AV930600	AV930600						HH94013	HH94013
					CF590944	CF590944						L44374	L44374
					DN178930	DN178930						AQ639468	AQ639468
					AQ385817	AQ385817						A1210591	A1210591
					BF198193	BF198193						BH809568	BH809568
					AA304476	AA304476						CD392956	CD392956
					AA759999	AA759999						CO318531	CO318531
					AT093760	AT093760						BE592205	BE592205
					CV342284	CV342284						AQ637854	AQ637854
					AV205154	AV205154						A1326545	A1326545
					AL960575	AL960575						AQ095319	AQ095319
					AU098537	AU098537						A1101592	A1101592
					C31660	C31660							



C 680	15	13.4	434	9	AQ148442 HS_2229_B	753	15	13.4	476	5	BUB836751
C 681	15	13.4	435	1	AI088389 qbl1.c01_x	754	15	13.4	477	2	BG894076
C 682	15	13.4	436	7	CN133939 OX1_19_F0	755	15	13.4	477	3	BI323824
C 683	15	13.4	437	1	AA539474 LDI7622.5	756	15	13.4	477	6	CB098587
C 684	15	13.4	437	6	BU174046 BU174046	757	15	13.4	477	9	AZ581357
C 685	15	13.4	437	3	CA724721 wd83f.Dk0	758	15	13.4	477	9	AQ686709
C 686	15	13.4	438	10	BX896912 BX896912	759	15	13.4	478	6	CA766951
C 687	15	13.4	440	6	CA433482 CA13-H-CO0-	760	15	13.4	479	3	BI476170
C 688	15	13.4	441	3	BP909978 BP909978	761	15	13.4	480	1	AJ464278
C 689	15	13.4	441	3	AI327447 ma63d01.y	762	15	13.4	480	1	AJ466237
C 690	15	13.4	442	1	AA336688 zvs9b02.8	763	15	13.4	480	1	AV629632
C 691	15	13.4	442	1	CO266474 EK146528.	764	15	13.4	480	9	AQ177164
C 692	15	13.4	443	5	BU228329 603230509	765	15	13.4	480	10	C2574256
C 693	15	13.4	444	1	AA963834 UI-R-CO-g	766	15	13.4	481	1	CF431304
C 694	15	13.4	444	9	BZ942612 CH240_93H	767	15	13.4	482	6	AZ170063
C 695	15	13.4	445	1	AI449165 m89sh02.x	768	15	13.4	482	9	AE210565
C 696	15	13.4	445	10	CZ178123 M1Aa-26D0	769	15	13.4	483	1	AA802362
C 697	15	13.4	446	1	AM131037 xe68h09.x	770	15	13.4	483	1	BH107880
C 698	15	13.4	447	2	BF443905 261570_MA	771	15	13.4	483	10	AG267706
C 699	15	13.4	447	5	BU889781 P025E03_P	772	15	13.4	483	11	DE001374
C 700	15	13.4	447	7	CV273946 MS01712-B	773	15	13.4	484	1	AM209324
C 701	15	13.4	448	1	AA508956 MBARCM1.F0	774	15	13.4	484	9	AQ431056
C 702	15	13.4	448	7	CO643546 USDA-FP_1	775	15	13.4	485	1	AJ731847
C 703	15	13.4	449	10	CE373190 LiGr-G58-	776	15	13.4	488	1	AQ866351
C 704	15	13.4	449	1	AU223028 AU223028	777	15	13.4	489	1	AI519464
C 705	15	13.4	449	7	CKE60969 LP19975.5	778	15	13.4	489	7	CV284337
C 706	15	13.4	450	1	AU101961 AU101961	779	15	13.4	490	2	BI137911
C 707	15	13.4	451	1	AA470643 ne12d02.8	780	15	13.4	491	3	BI236170
C 708	15	13.4	451	2	BI711389 IPI_60_B0	781	15	13.4	491	3	BI819457
C 709	15	13.4	451	5	BW887280 BW887280	782	15	13.4	491	8	CA106784
C 710	15	13.4	451	6	CA724651 wd83f.Dk0	783	15	13.4	493	8	DN851913
C 711	15	13.4	451	6	CM510754 C0c678.F0	784	15	13.4	493	2	DN851913
C 712	15	13.4	452	2	BG543649 E1258 CH1	785	15	13.4	494	1	AV396880
C 713	15	13.4	453	9	BZ517294 i64g406.g	786	15	13.4	494	5	BO449423
C 714	15	13.4	453	10	BX223318 Danilo_rer	787	15	13.4	494	7	CO324757
C 715	15	13.4	454	3	BP932270 BP932270	788	15	13.4	494	9	AQ200693
C 716	15	13.4	455	7	CO420227 GGEZHC100	789	15	13.4	495	6	CD217686
C 717	15	13.4	456	1	AI417274 t976h07.x	790	15	13.4	496	2	BI136943
C 718	15	13.4	457	10	AG928834 Drosoph11	791	15	13.4	496	9	BH449112
C 719	15	13.4	458	6	CA573604 K0603B04-	792	15	13.4	496	11	FR0007526
C 720	15	13.4	458	6	CA575227 K0627D10-	793	15	13.4	497	1	Al672778
C 721	15	13.4	459	2	BF661834 UI-R-C2-m	794	15	13.4	498	2	BE677709
C 722	15	13.4	460	3	BI483831 RE66781.1	795	15	13.4	498	6	CF934395
C 723	15	13.4	460	11	DE130256 Oryzias_1	796	15	13.4	499	2	BG700353
C 724	15	13.4	461	8	BG308890 f195b05.x	797	15	13.4	500	1	AM557711
C 725	15	13.4	461	8	W69200 z4d4f01.81	798	15	13.4	500	3	BJ465125
C 726	15	13.4	461	10	CM487123 f8bD001f2	799	15	13.4	500	3	BP187081
C 727	15	13.4	461	10	CM510412 C0c678.F0	800	15	13.4	501	3	BP189336
C 728	15	13.4	461	10	AG270054 Cyanid108	801	15	13.4	501	2	BF623897
C 729	15	13.4	462	5	BX275870 BX275870	802	15	13.4	501	3	BI563898
C 730	15	13.4	462	8	CX104330 BI077N10	803	15	13.4	501	8	R38203
C 731	15	13.4	463	6	CB688220 OSUNEA00E	804	15	13.4	501	9	CE084242
C 732	15	13.4	465	1	AI095527 qD23c07.x	805	15	13.4	502	5	BX275871
C 733	15	13.4	466	1	BI357901 RE44524.5	806	15	13.4	502	7	CF983358
C 734	15	13.4	466	9	BZ406224 OGACJ047C	807	15	13.4	502	9	BH776064
C 735	15	13.4	467	1	AV630376 AV630376	808	15	13.4	504	2	BF548433
C 736	15	13.4	467	7	CO154210 EN03722.5	809	15	13.4	504	3	BI355892
C 737	15	13.4	467	9	AQ147558 HS_3065_B	810	15	13.4	504	10	C2829015
C 738	15	13.4	468	1	AI493194 q288906.x	811	15	13.4	505	5	BX265699
C 739	15	13.4	468	10	CU111626 282241_LB	812	15	13.4	505	7	CR581236
C 740	15	13.4	469	3	BF777561 NXS1_070	813	15	13.4	506	1	AJ743968
C 741	15	13.4	469	3	BI582729 RH21026.5	814	15	13.4	506	6	CA574681
C 742	15	13.4	469	3	AQ726691 HS_5415_F	815	15	13.4	506	6	CB686115
C 743	15	13.4	472	2	BE284693 601098106	816	15	13.4	508	3	BM707500
C 744	15	13.4	473	6	CA693317 w1m96.PK0	817	15	13.4	508	3	BM930435
C 745	15	13.4	473	6	CF291240 14RO0T-0	818	15	13.4	508	6	CA576346
C 746	15	13.4	474	1	AF269169 AF269169	819	15	13.4	509	5	BU628871
C 747	15	13.4	474	1	AA235382 z770a12.x	820	15	13.4	509	5	BX265700
C 748	15	13.4	474	1	BH077094 RPCT-24-2	821	15	13.4	509	6	CA573413
C 749	15	13.4	475	7	CO266284 EK145860.	822	15	13.4	509	7	CV500211
C 750	15	13.4	476	2	BF656311 FMI_44_H0	823	15	13.4	510	1	AA062968
C 751	15	13.4	476	2	BE302162 DB82C03.x	824	15	13.4	510	5	BW844752
C 752	15	13.4	476	3	BI351860 GM16434.5	825	15	13.4	511	7	CN577128

BUB836751	T090E02_P
BG934076	Kcl17h03.y
BI323824	Kt45c05.y
CB098587	kus5d03.y
AZ581357	IM0370N03
AQ686709	nbx00072P
CA766951	AF53-Rd1
BI476170	fp53c05.y
AJ464278	AJ464278
AJ466237	AJ466237
AV629632	AV629632
AQ177164	HS_3070_B
CF574256	OC_BBa015
W69304	z4d4f01.r1
CP431304	NIT1_5_G0
AZ170063	SP_O15_A
AA802362	GM01261.5
AG267706	Cyanid108
DE001374	Branch108
AQ431056	u007e08.y
HS_5087_A	
AJ731847	AJ731847
AQ866351	nbde00027H
AI519464	LD3970.5
CV284337	lKs51f02.
BI137911	F095P52Y
BI236170	RE33187.5
BI819457	J008F10_O
CA106784	BI128H07
BI137746	F092P87Y
DN851913	4147566_B
AV396880	AV396880
BO449423	faa47a12.
CO324757	EK194748.
AQ200693	RPCL11-61
CD217686	PcP1n.Dk0
BI136943	F077P24Y
BH449112	BOHNY18TR
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Al672778	Al672778
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CF934395	JMT--03-K
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AM557711	L0285C09-
BJ465125	BJ465125
BP187081	BP187081
BP189336	BP189336
BF623897	HV8MBa000
BI563898	RH34633.5
R38203	yc93h06.g1
CE084242	LiGr-G58-
BX275871	BX275871
CF983358	mak19a03.
BH776064	fzmb013f0
BF548433	UI-R-CO-h
BI355892	GM32805.5
C2829015	OC_Ba021
BX265699	BX265699
CR581236	CR581236
AJ743968	AJ743968
CA574681	K0619F07-
CB686115	Bn019_P31
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BM930435	UI-F-EJ1-
CA576346	K0643D11-
BU628871	UI-H-FLO-
BX265700	BX265700
CA573413	K0600F07-
CV500211	64650.1_M
AA062968	z689e10.8
BW844752	BW844752
tf57a05.x	



C 826	15	13.4	512	1	AT533878	AT533878	SD05851.5	C 899	15	13.4	549	1	AA539137	AA539137	LD17226.5
C 827	15	13.4	512	7	CE911823	CE911823	AT0621G06-	C 900	15	13.4	549	7	CV205986	CV205986	ESR865596
C 828	15	13.4	513	7	BO447256	BO447256	UT-H-EU1-	C 901	15	13.4	550	7	BU615743	BU615743	BD15743
C 829	15	13.4	513	5	BU743120	BU743120	UT-E-EU1-	C 902	15	13.4	550	7	CN488598	CN488598	MD12026m
C 830	15	13.4	513	9	AQ435869	AQ435869	HS_5063_A	C 903	15	13.4	550	8	DT051055	DT051055	COT_EH_C1
C 831	15	13.4	514	1	AA817347	AA817347	LD32602.5	C 904	15	13.4	551	1	AI511898	AI511898	LD43463.5
C 832	15	13.4	514	2	BI172812	BI172812	RE15493.5	C 905	15	13.4	551	2	BG047825	BG047825	OVL_28_CO
C 833	15	13.4	514	9	AQ182769	AQ182769	HS_3115_A	C 906	15	13.4	551	3	BO166481	BO166481	UT-E-EU1-
C 834	15	13.4	515	1	AA264751	AA264751	LD084545_5	C 907	15	13.4	551	9	AZ592718	AZ592718	IM0403P17
C 835	15	13.4	515	1	CC160832	CC160832	IG11e05.b	C 908	15	13.4	552	6	CA576566	CA576566	K0633H07-
C 836	15	13.4	516	2	BF819609	BF819609	IL0-RT001	C 909	15	13.4	552	6	CD233324	CD233324	SS1_13_E0
C 837	15	13.4	516	2	BG300348	BG300348	HVMEB0010	C 910	15	13.4	553	2	BI265520	BI265520	NF093C07I
C 838	15	13.4	516	6	CA761006	CA761006	RO6000010	C 911	15	13.4	553	2	BF078572	BF078572	228944_MA
C 839	15	13.4	516	11	DE125182	DE125182	Oxy2ias_1	C 912	15	13.4	553	6	CA573573	CA573573	K0602G02-
C 840	15	13.4	517	6	AI405679	AI405679	GH35781.5	C 913	15	13.4	553	6	CA576443	CA576443	K0644H02-
C 841	15	13.4	517	6	CD206885	CD206885	HS1_25_A0	C 914	15	13.4	554	3	BI538352	BI538352	428895_MA
C 842	15	13.4	519	9	BH144448	BH144448	TDEGL18TH	C 915	15	13.4	554	6	CF789273	CF789273	866529_MA
C 843	15	13.4	519	9	BH694751	BH694751	BOMCL63TF	C 916	15	13.4	554	10	CM177266	CM177266	104_590_1
C 844	15	13.4	520	6	CA573968	CA573968	K0608C10-	C 917	15	13.4	554	10	CE444990	CE444990	LI9T-g88-
C 845	15	13.4	520	9	BH204004	BH204004	Sm1-60N8.	C 918	15	13.4	555	1	AV628294	AV628294	AV628294
C 846	15	13.4	521	1	AV631041	AV631041	AV631041	C 919	15	13.4	555	10	CL750338	CL750338	OR_BB011
C 847	15	13.4	522	8	DR478945	DR478945	WS02815.C	C 920	15	13.4	556	1	AA801478	AA801478	HL02368.5
C 848	15	13.4	522	8	DR484596	DR484596	WS02815.C	C 921	15	13.4	556	3	BP239981	BP239981	BP239981
C 849	15	13.4	522	11	CR861956	CR861956	Sus_sctroF	C 922	15	13.4	557	5	BU779288	BU779288	SJBERWD05
C 850	15	13.4	524	6	CA573705	CA573705	K0604E10-	C 923	15	13.4	557	2	BG048147	BG048147	OVL_28_CO
C 851	15	13.4	524	6	CA573849	CA573849	K0606P05-	C 924	15	13.4	557	6	CA576544	CA576544	K0646D02-
C 852	15	13.4	524	6	CA575199	CA575199	K0641D02-	C 925	15	13.4	557	6	CD430319	CD430319	ETH1_18-D
C 853	15	13.4	524	6	BH515716	BH515716	BOGFZ76TR	C 926	15	13.4	557	9	AQ061550	AQ061550	CIT-HSP-2
C 854	15	13.4	525	1	AV630155	AV630155	AV630155	C 927	15	13.4	558	1	A1729099	A1729099	BNLGH1126
C 855	15	13.4	526	3	BI588240	BI588240	RH29381.5	C 928	15	13.4	558	2	BI168781	BI168781	RE09645.5
C 856	15	13.4	526	3	BI949802	BI949802	HVMEB1001	C 929	15	13.4	558	5	BM216222	BM216222	BM216222
C 857	15	13.4	526	8	DN559446	DN559446	E10-D03-T	C 930	15	13.4	558	5	BM845480	BM845480	BM845480
C 858	15	13.4	526	8	DN559446	DN559446	F058P66Y	C 931	15	13.4	559	1	AW916615	AW916615	ES7347919
C 859	15	13.4	527	10	BI135804	BI135804	Drosophy1	C 932	15	13.4	560	5	BU805833	BU805833	haa23a02.
C 860	15	13.4	528	10	AG976085	AG976085	Phlo_rer	C 933	15	13.4	560	6	CA952609	CA952609	IG14e02.x
C 861	15	13.4	528	10	BX165383	BX165383	Phlo_rer	C 934	15	13.4	560	7	CO075263	CO075263	GR_Ba3525
C 862	15	13.4	529	6	CA701466	CA701466	Wm2C_Pk0	C 935	15	13.4	561	2	BG642449	BG642449	EST735925
C 863	15	13.4	531	1	BE549918	BE549918	7b43a12.x	C 936	15	13.4	561	6	CA576473	CA576473	K0645C08-
C 864	15	13.4	532	1	AV699220	AV699220	AV699220	C 937	15	13.4	561	9	CE189772	CE189772	LI9T-g88-
C 865	15	13.4	532	6	CD223959	CD223959	CCCL_31_B	C 938	15	13.4	562	10	CZ427318	CZ427318	103021_R
C 866	15	13.4	533	6	CD320322	CD320322	StcPu538.	C 939	15	13.4	563	1	AJ436536	AJ436536	AJ436536
C 867	15	13.4	534	1	A1694675	A1694675	Wea1f09.x	C 940	15	13.4	563	1	AM020707	AM020707	AM020707
C 868	15	13.4	534	1	A1943245	A1943245	fc87e06.x	C 941	15	13.4	563	1	AM020972	AM020972	AM020972
C 869	15	13.4	534	1	AW747153	AW747153	WS1_66_G0	C 942	15	13.4	563	3	BI797453	BI797453	H077E04_E
C 870	15	13.4	534	2	BI135807	BI135807	F058P71Y	C 943	15	13.4	563	6	CF368818	CF368818	853525_MA
C 871	15	13.4	535	1	AV944386	AV944386	AV944386	C 944	15	13.4	564	3	BP334719	BP334719	BP334719
C 872	15	13.4	535	5	BU721417	BU721417	SJM2BKF07	C 945	15	13.4	565	6	CA236339	CA236339	CA236339
C 873	15	13.4	535	10	CNS000K3	CNS000K3	Arabidops	C 946	15	13.4	565	10	CZ152517	CZ152517	F0659P10Y
C 874	15	13.4	536	3	BU466324	BU466324	BU466324	C 947	15	13.4	566	2	BI136500	BI136500	F0659P10Y
C 875	15	13.4	536	9	AQ233954	AQ233954	HS_2053_A	C 948	15	13.4	566	5	BM874273	BM874273	BM874273
C 876	15	13.4	537	2	BI139858	BI139858	IP1_46_D1	C 949	15	13.4	566	7	CNI131943	CNI131943	OX1_3_E02
C 877	15	13.4	537	3	BI796344	BI796344	H043H03_E	C 950	15	13.4	566	9	AZ250027	AZ250027	PCGT-23-5
C 878	15	13.4	537	7	CNI28108	CNI28108	RHOH1_27	C 951	15	13.4	567	2	BE856651	BE856651	7f65H01.x
C 879	15	13.4	537	7	BH562174	BH562174	BOGHV5TF	C 952	15	13.4	568	3	BO016656	BO016656	UI-H-DT1-
C 880	15	13.4	538	7	CV219747	CV219747	EST879457	C 953	15	13.4	568	9	AZ444566	AZ444566	IM0239M17
C 881	15	13.4	539	1	AL829991	AL829991	AL829991	C 954	15	13.4	568	10	CM012663	CM012663	ZMMBLC000
C 882	15	13.4	539	1	AA439440	AA439440	LD14016.5	C 955	15	13.4	569	3	BI593320	BI593320	RH11329.5
C 883	15	13.4	539	9	AZ142872	AZ142872	SP_0006_B	C 956	15	13.4	569	7	CK301000	CK301000	UI-E-EU1-
C 884	15	13.4	540	10	CE464060	CE464060	LI9T-g88-	C 957	15	13.4	569	7	CK766390	CK766390	Pam01_14m
C 885	15	13.4	541	9	BZ903845	BZ903845	CH240_25E	C 958	15	13.4	570	9	BH583312	BH583312	BOGXH6TR
C 886	15	13.4	543	6	CB397067	CB397067	OSTR18G1	C 959	15	13.4	572	6	CF234867	CF234867	Pr4JXT001
C 887	15	13.4	543	6	CB397106	CB397106	OSTR18G1	C 960	15	13.4	572	6	CF323256	CF323256	HDN-03-F
C 888	15	13.4	544	3	BI354068	BI354068	GM26171.5	C 961	15	13.4	572	9	BZ715403	BZ715403	PUDAC54TD
C 889	15	13.4	544	7	CNI42625	CNI42625	WOOND1_11	C 962	15	13.4	573	1	AI457031	AI457031	LD37243.5
C 890	15	13.4	545	2	BE236006	BE236006	143662_MA	C 963	15	13.4	573	3	BU591860	BU591860	BU591860
C 891	15	13.4	545	2	BI376190	BI376190	RE61253.5	C 964	15	13.4	573	5	BU069573	BU069573	Im02F06.Y
C 892	15	13.4	546	1	AI061829	AI061829	GH02945.5	C 965	15	13.4	574	6	CF431266	CF431266	NIT1_5_A0
C 893	15	13.4	546	1	AI055202	AI055202	AU55202	C 966	15	13.4	574	5	CA015846	CA015846	AV952283
C 894	15	13.4	546	1	BZ958044	BZ958044	P94007008	C 967	15	13.4	574	5	CA015846	CA015846	HV11004u
C 895	15	13.4	547	2	BG884701	BG884701	ED833c09.	C 968	15	13.4	574	6	CD429862	CD429862	ETH1_16_H
C 896	15	13.4	547	7	CV201737	CV201737	EST861447	C 969	15	13.4	575	2	BI235850	BI235850	RE31794.5
C 897	15	13.4	547	9	AZ563008	AZ563008	RPC1-23-2	C 970	15	13.4	575	6	CA388882	CA388882	ce03e11.x
C 898	15	13.4	548	5	CA005247	CA005247	HU11K12u	C 971	15	13.4	575	7	CF911757	CF911757	A0620F06-



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c 972 15 13.4 575 10 C2245526
973 15 13.4 576 1 A392821
974 15 13.4 576 5 B0784774
975 15 13.4 576 6 B0784774
976 15 13.4 576 6 CA721842
977 15 13.4 576 6 CF484117
978 15 13.4 577 6 BH424531
979 15 13.4 577 6 CF427380
980 15 13.4 578 3 BJ189220
981 15 13.4 578 5 C98236
982 15 13.4 579 6 A0596498
983 15 13.4 579 6 CD462795
984 15 13.4 579 7 C0106362
985 15 13.4 579 7 CN309532
986 15 13.4 581 3 BP207334
987 15 13.4 582 3 BM512538
988 15 13.4 582 3 BP324054
989 15 13.4 582 7 CK052885
990 15 13.4 582 7 CV684084
991 15 13.4 582 10 C2115964
992 15 13.4 583 3 BP316861
993 15 13.4 583 6 CD632404
994 15 13.4 583 9 A2109970
995 15 13.4 583 9 BH723723
996 15 13.4 584 2 BG274888
997 15 13.4 586 2 BM707490
998 15 13.4 586 5 CD702773
999 15 13.4 586 7 CK905618
1000 15 13.4 586 9 A2953910

```

## ALIGNMENTS

```

RESULT 1
LOCUS DR421506/c
DEFINITION CCHS7B08 Coprinus cinereus heat-shocked mycelia cDNAs Coprinopsis
cineres cDNA, mRNA sequence.
ACCESSION DR421506
VERSION DR421506.1 GI:68323522
KEYWORDS EST.
SOURCE Coprinopsis cinerea (Coprinus cinereus)
ORGANISM Coprinopsis cinerea
Bukariyota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
Agaricales; Pezizyrellaceae; Coprinopsis.
1 (bases 1 to 582)
Carlson,M.D., Barr,C., Murphy,B., Wilke,S.K., Gathman,A.C.,
Lilly,W.W. and Puklia,P.J.
Expressed sequence tags from Coprinus cinereus (Coprinopsis
cineres) cDNAs, spring 2005
Unpublished (2005)
CONTACT: Gathman AC
Biology Department
Southeast Missouri State University
1 University Plaza, Cape Girardeau, MO 63701, USA
Tel: 5736512361
Fax: 573 651 2382
Email: agathman@semo.edu.
Location/Qualifiers
1..582
/organism="Coprinopsis cinerea"
/mol_type="mRNA"
/strain="Okayama7#130"
/db_xref="taxon:5346"
/dev_stage="vegetative monokaryotic mycelium"
/lab_host="E. coli XL10-Gold"
/clone_lib="Coprinus cinereus heat-shocked mycelia cDNAs"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Mycelia grown for three days at 37 degrees on
minimal medium, then transferred to pre-warmed minimal
media and incubated at 42 degrees for one hour before
harvesting."

```

## ORIGIN

```

Query Match 18.8%; Score 21; DB 8; Length 582;
Best Local Similarity 100.0%; Pred. No. 0.44;
Matches 21; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
QY 40 GAGCAACCGATTAGCCCGT 60
|||||
469 GAGCAACCGATTAGCCCGT 449

```

## RESULT 2

```

CD860340/c
LOCUS CD860340/c
DEFINITION TE.002C14F011204 TE Pisum sativum cDNA clone TE002C14, mRNA
sequence.
ACCESSION CD860340
VERSION CD860340.1 GI:32544156
KEYWORDS EST.
SOURCE Pisum sativum (pea)
ORGANISM Pisum sativum
Bukariyota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Viciaeae;
Pisum.
1 (bases 1 to 457)
Genopiante.
Unpublished (2003)
CONTACT: Genopiante
Genopiante
93, rue Henri Rochefort 91025 EVRY CEDEX France
Tel: 33 1 69 47 54 00
Fax: 33 1 69 47 54 10
This sequence has been generated in the framework of the french
plant genomics programme 'Genopiante' (http://www.genopiante.com
and http://genopiante-info.inbio.gen.fr).
Location/Qualifiers
1..457
/organism="Pisum sativum"
/mol_type="mRNA"
/cultivar="Terese"
/db_xref="taxon:3888"
/clone="TE002C14"
/issue_type="stipule"
/clone_lib="TE"

```

## REFERENCE

```

AUTHORS Genopiante, a major partnership french program in plant genomics
TITLE Unpublished (2003)
JOURNAL CONTACT: Genopiante
COMMENT

```

## FEATURES

```

source
1..457
/organism="Pisum sativum"
/mol_type="mRNA"
/cultivar="Terese"
/db_xref="taxon:3888"
/clone="TE002C14"
/issue_type="stipule"
/clone_lib="TE"

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## ORIGIN

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Query Match 17.0%; Score 19; DB 6; Length 457;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 19; Conservative 0; Mismatches 0; Gaps 0;
Indels 0;
QY 59 GTAAAGAGGTCCTAATAT 77
|||||
204 GTAAAGAGGTCCTAATAT 186

```

## Db

```

RESULT 3
LOCUS AU233831
DEFINITION AU233831 Bovine placenta cDNA Bos taurus cDNA clone Cln61 3', mRNA
sequence.
ACCESSION AU233831
VERSION AU233831.1 GI:15719049
KEYWORDS EST.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
Bukariyota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovora; Bovidae; Bovinae; Bos.
1 (bases 1 to 350)
Gohma,H., Lejukole,H.Y., Taniguchi,Y., Yamada,T., Akagi,S.,
Yasue,H. and Sasaki,Y.

```

## FEATURES

```

source
1..582
/organism="Coprinopsis cinerea"
/mol_type="mRNA"
/strain="Okayama7#130"
/db_xref="taxon:5346"
/dev_stage="vegetative monokaryotic mycelium"
/lab_host="E. coli XL10-Gold"
/clone_lib="Coprinus cinereus heat-shocked mycelia cDNAs"
/notes="Vector: pBluescript II SK+; Site_1: EcoRI; Site_2:
XhoI; Mycelia grown for three days at 37 degrees on
minimal medium, then transferred to pre-warmed minimal
media and incubated at 42 degrees for one hour before
harvesting."

```



TITLE Analysis of expressed sequence tags from a cDNA library of bovine placenta

JOURNAL Unpublished (2001)

COMMENT Contact: Takahisa Yamada  
Graduate School of Agriculture  
Kyoto University  
Sakyo-ku, Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-6323  
Fax: 81-75-753-6340  
Email: tyamada@kans.kyoto-u.ac.jp  
This clone was obtained from a 3' end cDNA library.

FEATURES  
Source  
1. .350  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="Cln361"  
/issue\_type="placenta"  
/clone\_id="Bovine placenta cDNA"

ORIGIN

Query Match 16.1%; Score 18; DB 1; Length 350;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGGTTTAC 32  
|||||  
23 AATGATATATTGGTTTAC 40

RESULT 4  
LOCUS AU278232 354 bp mRNA linear EST 02-JUL-2002  
DEFINITION AU278232 Cloned bovine placenta cDNA Bos taurus cDNA clone  
ACCESSION AU278232  
VERSION AU278232.1 GI:21681542  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 354)  
Oishi, M., Yamada, T., Goma, H., Lejukole, H.Y., Taniguchi, Y. and Sasaki, Y.  
EST analysis of cloned bovine fetus and placenta  
Unpublished (2002)  
Contact: Masahito Oishi  
Graduate School of Agriculture  
Kyoto University  
Sakyo-ku Kitashirakawa, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-6331  
Fax: 81-75-753-6340  
Email: oishi@kans.kyoto-u.ac.jp.

FEATURES  
Source  
1. .354  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="placenta0275"  
/dev\_stage="60 embryonic day"  
/clone\_id="Cloned bovine placenta cDNA"

ORIGIN

Query Match 16.1%; Score 18; DB 1; Length 354;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGGTTTAC 32  
|||||  
23 AATGATATATTGGTTTAC 311

RESULT 5  
LOCUS CF890289/c 408 bp mRNA linear EST 04-MAR-2004  
DEFINITION TcTR-1092 Trypanosoma cruzi cDNA clone 09h2 5', mRNA sequence.  
ACCESSION CF890289  
VERSION CF890289.1 GI:44920172  
KEYWORDS EST.  
SOURCE Trypanosoma cruzi  
ORGANISM Trypanosoma cruzi  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma; Schizotrypanum.  
1 (bases 1 to 408)  
Agüero, F., Ben Abdellah, K., Tekiel, V., Sanchez, D.O. and Gonzalez, A.  
Generation and analysis of expressed sequence tags from Trypanosoma cruzi trypanastigote and amastigote cDNA libraries  
Mol. Biochem. Parasitol. 136 (2), 221-225 (2004)  
15478800  
Contact: Sanchez DO  
Genomics and Bioinformatics  
Instituto de Investigaciones Biologicas  
Av. Gral Paz S/N, INTI, Edificio 24, B 1650 KNA, San Martin, Buenos Aires, Argentina  
Tel: (54-11) 4580/7255/7  
Fax: (54-11) 4752-9639  
Email: dsanchez@ib.unsam.edu.ar  
Sequences were basecalled with phred and vector was masked with crossmatch (see <http://www.phrap.org>). Sequences were then trimmed from both ends to remove low quality bases and masked vector.  
Plate: 09 row: h column: 2  
Seq primer: T7.

FEATURES  
Source  
1. .408  
/organism="Trypanosoma cruzi"  
/mol\_type="mRNA"  
/db\_xref="taxon:5693"  
/clone="09h2"  
/dev\_stage="trypanastigote"  
/clone\_id="TcTR"

ORIGIN

Query Match 16.1%; Score 18; DB 7; Length 408;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 76 ATCGGTGACGACGACGAG 93  
|||||  
Db 202 ATCGGTGACGACGACGAG 185

RESULT 6  
LOCUS CA673959 452 bp mRNA linear EST 24-NOV-2002  
DEFINITION wlsu2.pk020.p22 wlsu2 Triticum aestivum cDNA clone wlsu2.pk020.p22  
ACCESSION CA673959  
VERSION CA673959.1 GI:25253216

(5'-ACGGAATTCGT-3') were ligated to the cDNA. The resulting cDNA mixture was then digested with NotI and EcoRI restriction enzymes, subjected to size fractionation on SizeSep400 Spun Columns (Pharmacia) to select fragments longer than 400 bp, and cloned into the dephosphorylated NotI/EcoRI sites of the vector."



KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poaceae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 452)  
AUTHORS Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
Mao, G., Caraher, N. and Hanafey, M.K.  
TITLE Dupont Wheat cDNA Sequence  
JOURNAL Unpublished (2002)  
COMMENT Contact: Scott V. Tingey  
Crop Genetics  
E. I. Dupont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2602  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.  
Location/Qualifiers  
1..452  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Stephens"  
/db\_xref="taxon:4565"  
/clone="wlsu2.pk020.p22"  
/issue\_type="leaf"  
/clone\_lib="wlsu2"  
/note="Vector: pGEM-T Easy; Site 1: SCOR1; Site 2: Xho1;  
wheat (Triticum aestivum L.) w1k8 cDNAs substracted with  
w1m0 cDNAs"

ORIGIN  
Query Match 16.1%; Score 18; DB 6; Length 452;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 78 CGGTAGCAACGCGAGGT 95  
|||||  
39 CGGTAGCAACGCGAGGT 56

RESULT 7  
BF599851 455 bp mRNA linear EST 25-APR-2001  
LOCUS BF599851  
DEFINITION 264184 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.  
ACCESSION BF599851  
VERSION BF599851.1 GI:11696747  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 455)  
AUTHORS Smith, T.P.L., Grose, W.M., Freking, B.A., Roberts, A.J., Stone, R.T.,  
Caas, E., Wray, J.E., White, J., Cho, J., Fahrenkrug, S.C.,  
Bennett, G.L., Heaton, M.P., Laegreid, W.W., Rohrer, G.A.,  
Chitko-McKown, C.G., Perce, G., Holt, I., Karamycheva, S., Liang, F.,  
Quackenbush, J. and Keefe, J.W.  
TITLE Sequence evaluation of four pooled-tissue normalized bovine cDNA  
libraries and construction of a gene index for cattle  
JOURNAL Genome Res. 11 (4), 626-630 (2001)  
PUBMED 11282978  
COMMENT Contact: Smith TPL  
USDA, ARS, US Meat Animal Research Center  
PO Box 166, Clay Center, NE 68933-0166, USA  
Tel: 402 762 4366  
Fax: 402 762 4390  
Email: smith@mail.marc.usda.gov  
Single pass sequencing. Bases called and alt trimmed with phred  
v0.980904.e. Vector identified by cross\_match with the -minscore 18  
and -mismatch 12 options.

PCR primers  
FORWARD: AGGAACAGCTATGACCAT  
BACKWARD: GTTTCCAGTCACGACG  
Plate: 35 row: K column: 13  
Seq primer: ATTATGGTACACATATAG.  
Location/Qualifiers  
1..455  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_lib="MARC 3BOV"  
/note="Vector: pCMV SPORT6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from marrow, alveolar  
macrophage, ovary, fetal semitendinosus muscle, and fetal  
longissimus muscle."

ORIGIN  
Query Match 16.1%; Score 18; DB 2; Length 455;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 AATGATATATGTTTAC 32  
|||||  
294 AATGATATATGTTTAC 311

RESULT 8  
BF044692/c 509 bp mRNA linear EST 10-OCT-2000  
LOCUS BF044692/c  
DEFINITION BP250010A20B2 Soares normalized bovine placenta Bos taurus cDNA  
ACCESSION BP250010A20B2  
VERSION BF044692  
KEYWORDS BF044692.1 GI:10761747  
SOURCE EST.  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.  
REFERENCE 1 (bases 1 to 509)  
AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and  
Larson, J.H.  
TITLE Bovine ESTs  
JOURNAL Unpublished (2000)  
COMMENT Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Funding for cattle EST sequencing was provided by the USDA National  
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534  
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED  
from Washington University Genome Center. Vector trimm g:  
Cross match from Washington University Genome Center PHRAP suite.  
This sequence is vector free and at least 200 bp in length.  
PCR primers  
FORWARD: TAAATGACCTACTATAGCG  
BACKWARD: ATTACCTCCTACTAAG  
Insert length: 509 Std Error: 0.00  
Plate: BP250010A20 row: B column: 2  
Seq primer: AGCGATTAACAATTTCACACAGCA  
High quality sequence prop: 509.  
Location/Qualifiers  
1..509  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="BP250010A20B2"



/sex="female"  
 /lab host="DH10B"  
 /clone\_lib="Soares normalized bovine placenta"  
 /note="Organ: Placenta; Vector: pTV3pac; Site 1: EcoRI;  
 Site 2: NotI; The cDNA library was contributed by the  
 Soares laboratory and it was constructed and normalized  
 as described by Bonaldo, M.F., Lennon, G. and Soares,  
 M.B. (1996), Genome Research 6(9): 791-806. "

## ORIGIN

Query Match 16.1%; Score 18; DB 2; Length 509;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATGTTTAC 32  
 |||  
 Db 323 AATGATATATGTTTAC 306

RESULT 9 512 bp DNA linear GSS 31-OCT-2004  
 LOCUS CM294029 104 774 11414970 148 35603 067 Sorghum methylation filtered library  
 DEFINITION (libid: 104) Sorghum bicolor genomic clone 11414970, genomic survey  
 sequence.  
 ACCESSION CM294029  
 VERSION CM294029.1 GI:55010217  
 KEYWORDS GSS.  
 ORGANISM Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 512)  
 Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
 Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
 McKenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korfi,I.F.,  
 Rabinowicz,P.D., Lakey,N., McCombie,W.R., Teddeloh,J.A. and  
 Martienssen,R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154  
 Contact: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 6979  
 Email: jbedell@oriongenomics.com  
 Plate: 774 row: n column: 18  
 Seq primer: SMfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 512.  
 Location/Qualifiers  
 1..512  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone\_lib="11414970"  
 /clone\_lib="Sorghum methylation filtered library (libid:  
 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBCSK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."

## ORIGIN

Query Match 16.1%; Score 18; DB 10; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGATATATGTTTACT 33  
 |||  
 Db 482 ATGATATATGTTTACT 499

RESULT 10 518 bp mRNA linear EST 25-MAR-2003  
 LOCUS CB438817 687711 MARC 6BOV Bos taurus cDNA 5', mRNA sequence.  
 DEFINITION CB438817  
 ACCESSION CB438817 GI:29223207  
 VERSION CB438817.1  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 518)  
 Smith,T.P.L., Roberts,A.J., Echeerikamp,S.B., Chitko-McKown,C.G.,  
 Wray,J.E. and Keefe,J.W.  
 A second set of bovine ESTs from pooled-tissue normalized libraries  
 Unpublished (2003)  
 Contact: Smith TPL  
 USDA, ARS, US Meat Animal Research Center  
 PO Box 166, Clay Center, NE 68933-0166, USA  
 Tel: 402 762 4366  
 Fax: 402 762 4390  
 Email: smtlh@mail.marc.usda.gov  
 Single pass sequencing. Bases called with phred v0.020425.c and  
 trimmed with the aid of the trim\_alt option. Vector identified with  
 cross match v0.990329.  
 Plate: FOY8044 row: L column: 4  
 Seq primer: GTAATACGACTCACTATAGG.  
 Location/Qualifiers  
 1..518  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9913"  
 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 6BOV"  
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
 library made with RNA pooled from multiple tissues  
 including liver, lung, hypothalamus, pituitary, and  
 placenta/endometrium."

## FEATURES

source  
 1..518  
 /organism="Bos taurus"  
 /mol\_type="mRNA"  
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 /tissue\_type="pooled"  
 /lab\_host="DH10B"  
 /clone\_lib="MARC 6BOV"  
 /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;  
 library made with RNA pooled from multiple tissues  
 including liver, lung, hypothalamus, pituitary, and  
 placenta/endometrium."

## ORIGIN

Query Match 16.1%; Score 18; DB 6; Length 518;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATGTTTAC 32  
 |||  
 Db 395 AATGATATATGTTTAC 412

RESULT 11 529 bp mRNA linear EST 01-SEP-2004  
 LOCUS CO877190/c 80877190 529 bp mRNA linear EST 01-SEP-2004  
 DEFINITION B2PDP05611556Q 3', mRNA sequence.  
 ACCESSION CO877190  
 VERSION CO877190.1 GI:51807106  
 KEYWORDS EST.  
 SOURCE Bos taurus (cow)  
 ORGANISM Bos taurus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
 Pecora; Bovidae; Bovinae; Bos.  
 1 (bases 1 to 529)  
 Hennig,S., Janitz,M., Herwig,R. and Williams,J.  
 Generation, annotation, evolutionary analysis and database  
 integration of 14969 cattle EST clusters

Query Match 16.1%; Score 18; DB 10; Length 512;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



JOURNAL  
COMMENT

Unpublished (2004)  
Contact: Hennig S  
Laboratory 123, dept. Lehnach  
Max-Planck-Institut fuer Molekulare Genetik  
Innster.63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hennig@molgen.mpg.de  
The library was characterised by oligonucleotide fingerprinting (ONFP) to reduce sequencing redundancy. According to the ONFP procedure, clones that display the same hybridisation matrix with a battery of 200 8mer oligonucleotides are grouped into clusters. One clone per ONFP cluster was selected for sequencing. cDNA clones and filters are distributed via Deutsches Ressourcenzentrum fuer Genomforschung GmbH (http://www.rzpd.de).  
PCR Primers  
FORWARD: 5' CCCGAGCTTACACTTATGCTCCGCGTCG 3' (M13RSP) 5'-seq  
BACKWARD: 5' GCTATTACGCGAGTGGGAAAGGGGATGTG 3' (M13FSP) 3'-seq  
Seq primer: 5' GCTATTACGCGAGTGGGAAAGGGGATGTG 3' (M13FSP).

## FEATURES

## Source

Location/Qualifiers  
1..529  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="RZPDp1056r1556Q"  
/sex="female"  
/tissue\_type="brain tissue"  
/dev\_stage="adult brain"  
/clone\_lib="normal cattle brain"  
/note="Organ: brain; Vector: pSPori1; Site 1: NotI;  
Site 2: SalI; Random primed and directionally cloned in  
pSport1 vector using NotI  
5'-pGACTAGTCTTAGATCGAGCGCCGCC (715-3' and SalI 5'-  
TCGACCCAGCGCTCCG-3' adapters (Gibco BRL)"

## ORIGIN

Query Match 16.1%; Score 18; DB 7; Length 529;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTTAC 32  
|||||  
344 AATGATATATTGTTTAC 327

RESULT 12  
BF039887 539 bp mRNA linear EST 10-OCT-2000  
LOCUS BP250025A10H7 Soares normalized bovine placenta Bos taurus cDNA  
DEFINITION clone BP250025A10H7 5', mRNA sequence.  
ACCESSION BF039887  
VERSION BF039887.1 GI:10756879  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 539)  
Lewin,H.A., Soares,M.B., Rebeltz,M., Pardinas,J., Liu,L. and  
Larson,J.H.  
Bovine ESTs  
Unpublished (2000)  
Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Funding for cattle EST sequencing was provided by the USDA National  
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534

FEATURES  
source

to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED  
from Washington University Genome Center. Vector Trimmi g:  
Cross match from Washington University Genome Center PHRAP suite.  
This sequence is vector free and at least 200 bp in length.  
PCR Primers  
FORWARD: TTAATGACACTCCTATAGGG  
BACKWARD: ATTAACTCCTACTAAG  
Insert Length: 539 Std Error: 0.00  
Plate: BP250025A10 row: H column: 7  
Seq primer: AGCGATACATTTTCACACGGA  
High quality sequence stop: 539.  
Location/Qualifiers  
1..539  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="BP250025A10H7"  
/sex="female"  
/lab\_host="DH10B"  
/clone\_lib="Soares normalized bovine placenta"  
/note="Organ: placenta; Vector: pT73Pac; Site 1: EcoRI;  
Site 2: NotI; The cDNA library was contributed by the  
Soares Laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. "

## ORIGIN

Query Match 16.1%; Score 18; DB 2; Length 539;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTTAC 32  
|||||  
416 AATGATATATTGTTTAC 433

RESULT 13  
BF045364 539 bp mRNA linear EST 10-OCT-2000  
LOCUS BP250025A20H6 Soares normalized bovine placenta Bos taurus cDNA  
DEFINITION clone BP250025A20H6 5', mRNA sequence.  
ACCESSION BF045364  
VERSION BF045364.1 GI:10762419  
KEYWORDS EST.  
SOURCE Bos taurus (cow)  
ORGANISM Bos taurus  
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Pecora; Bovidae; Bovinae; Bos.  
1 (bases 1 to 539)  
Lewin,H.A., Soares,M.B., Rebeltz,M., Pardinas,J., Liu,L. and  
Larson,J.H.  
Bovine ESTs  
Unpublished (2000)  
Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Funding for cattle EST sequencing was provided by the USDA National  
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534  
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED  
from Washington University Genome Center. Vector Trimmi g:  
Cross match from Washington University Genome Center PHRAP suite.  
This sequence is vector free and at least 200 bp in length.  
PCR Primers  
FORWARD: TTAATGACACTCCTATAGGG  
BACKWARD: ATTAACTCCTACTAAG  
Insert Length: 539 Std Error: 0.00  
Plate: BP250025A20 row: H column: 6



Seq primer: AGCGATACATTTTCACACAGA  
High quality sequence stop: 539.

FEATURES  
SOURCE  
Location/Qualifiers  
1..539  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="BP250025A20H6"  
/sex="female"  
/lab\_host="DH10B"  
/clone\_1lb="Soares normalized bovine placenta"  
/note="Organ: Placenta; Vector: p773pac; Site 1: EcoRI;  
Site 2: NotI; The cDNA library was contributed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN  
Query Match 16.1%; Score 18; DB 2; Length 539;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 15 AATGATATATTGTTTAC 32  
|||||  
416 AATGATATATTGTTTAC 433

Db

RESULT 14  
BF044189/c 544 bp mRNA linear EST 10-OCT-2000  
LOCUS BP250012B20G Soares normalized bovine placenta Bos taurus cDNA  
DEFINITION  
clone BP250012B20G 5', mRNA sequence.  
ACCESSION  
BF044189 GI:10761244  
VERSION  
BF044189.1  
KEYWORDS  
EST.  
SOURCE  
Bos taurus (cow)  
ORGANISM  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovidae; Bos.  
REFERENCE  
1 (bases 1 to 544)  
Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and  
Larson,J.H.  
Bovine ESTs  
TITLE  
Unpublished (2000)  
JOURNAL  
COMMENT  
Contact: Lewin, H. A.  
W. M. Keck Center for Comparative and Functional Genomics  
University of Illinois at Urbana-Champaign  
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL  
61801, USA  
Tel: 217 333 5998  
Fax: 217 244 5617  
Email: h-lewin@uiuc.edu  
Funding for cattle EST sequencing was provided by the USDA National  
Research Initiative, Animal Genome Resource Grant AG 99-3205-0534  
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED  
from Washington University Genome Center. Vector titriml g:  
Cross match from Washington University Genome Center PHRAP suite.  
This sequence is vector free and at least 200 bp in length.  
PCR primers  
FORWARD: TAATACGACTCAGCTATGAGG  
BACKWARD: ATTAACCTCAGCTAAG  
Insert Length: 544 Std Error: 0.00  
Plate: BP250012B20 row: G column: 9  
Seq primer: AGCGATACATTTTCACACAGA  
High quality sequence stop: 544.  
Location/Qualifiers  
1..544  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="BP250012B20G9"  
/sex="female"

/lab\_host="DH10B"  
/clone\_1lb="Soares normalized bovine placenta"  
/note="Organ: placenta; Vector: p773pac; Site 1: EcoRI;  
Site 2: NotI; The cDNA library was contributed by the  
Soares laboratory and it was constructed and normalized  
as described by Bonaldo, M.F., Lennon, G. and Soares,  
M.B. (1996), Genome Research 6(9): 791-806. "

ORIGIN  
Query Match 16.1%; Score 18; DB 2; Length 544;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 15 AATGATATATTGTTTAC 32  
|||||  
323 AATGATATATTGTTTAC 306

Db

RESULT 15  
COS51383/c 549 bp mRNA linear EST 01-SEP-2004  
LOCUS LYEST9862 Sea lamprey lyEST Petromyzon marinus cDNA, mRNA sequence.  
DEFINITION  
COS51383  
ACCESSION  
COS51383.1 GI:51799709  
VERSION  
COS51383.1  
KEYWORDS  
EST.  
SOURCE  
Petromyzon marinus (sea lamprey)  
ORGANISM  
Petromyzon marinus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;  
Petromyzontiformes; Petromyzontidae; Petromyzon.  
REFERENCE  
1 (bases 1 to 549)  
Pancer,Z., Mayer,W.E., Klein,J. and Cooper,M.D.  
Prototypic T-cell receptor and CD4-like coreceptor expressed in  
lymphocytes of the agnathan sea lamprey  
Proc. Natl. Acad. Sci. U.S.A. 101 (36), 13273-13278 (2004)  
JOURNAL  
PUBMED  
COMMENT  
Contact: Pancer, Zeev  
Division of Developmental and Clinical Immunology  
The University of Alabama at Birmingham  
378 Wallace Tumor Institute, 1530 Third Avenue, South, Birmingham,  
AL 35294-3300  
Tel: 205-975-5812  
Fax: 205-975-7218  
Email: zpancer@uab.edu.  
Location/Qualifiers  
1..549  
/organism="Petromyzon marinus"  
/mol\_type="mRNA"  
/db\_xref="taxon:7757"  
/cell\_type="lymphocyte"  
/dev\_stage="unstimulated larvae"  
/clone\_1lb="Sea lamprey lyEST"  
/note="Vector: Lambda ZAP Express; lymphocyte mRNA ESTs  
from unstimulated larvae. All are from arrayed colonies  
from a directionally cloned cDNA library in Lambda ZAP  
Express (Stratagene). All are single pass 5' sequences."

FEATURES  
SOURCE  
Location/Qualifiers  
1..549  
/organism="Petromyzon marinus"  
/mol\_type="mRNA"  
/db\_xref="taxon:7757"  
/cell\_type="lymphocyte"  
/dev\_stage="unstimulated larvae"  
/clone\_1lb="Sea lamprey lyEST"  
/note="Vector: Lambda ZAP Express; lymphocyte mRNA ESTs  
from unstimulated larvae. All are from arrayed colonies  
from a directionally cloned cDNA library in Lambda ZAP  
Express (Stratagene). All are single pass 5' sequences."

ORIGIN  
Query Match 16.1%; Score 18; DB 7; Length 549;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 77 TCGGTGAGCAACGAGG 94  
|||||  
334 TCGGTGAGCAACGAGG 317

Db

RESULT 16  
CO884223 551 bp mRNA linear EST 01-SEP-2004  
LOCUS BovGen\_12548 normal cattle brain Bos taurus cDNA clone  
DEFINITION  
R2PDP1056P2220Q 5', mRNA sequence.  
ACCESSION  
CO884223  
VERSION  
CO884223.1 GI:51814171



KEYWORDS  
SOURCE EST.  
ORGANISM Bos taurus (cow)  
Bos taurus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;  
Bovidae; Bovinae; Bos.

REFERENCE  
AUTHORS 1 (bases 1 to 551)  
Hennig, S., Janitz, M., Herwig, R. and Williams, J.  
TITLE Generation, annotation, evolutionary analysis and database  
integration of 14969 cattle EST clusters  
JOURNAL Unpublished (2004)  
COMMENT Contact: Hennig S  
laboratory 123, dept. lehrbach  
Max-Planck-Institut fuer Molekulare Genetik  
Innestr.63-73, D-14195 Berlin, Germany  
Tel: +49 30 8413 1612  
Fax: +49 30 8413 1380  
Email: hennig@molgen.mpg.de

FEATURES  
source The library was characterised by oligonucleotide fingerprinting  
(ONFP) to reduce sequencing redundancy. According to the ONFP  
procedure, clones that display the same hybridisation matrix with a  
battery of 200 8mer oligonucleotides are grouped into clusters. One  
clone per ONFP cluster was selected for sequencing. cDNA clones and  
filers are distributed via Deutsches Ressourcenzentrum fuer  
Genomforschung GmbH (<http://www.rzpd.de>).  
PCR Primers  
FORWARD: 5' CCCGAGCTTACCTTATGCTTCCGGCTG 3' (M13RSP) 5'-seq  
BACKWARD: 5' GCTATTAGCCGACGCTGGGAAAGGAGGATGTG 3' (M13FSP) 3'-seq  
Seq primer: 5'-CCGGTCCGGAATTCCTCGGT-3' (M13RSP).  
Location/Qualifiers  
1..551  
/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/clone="RZPD1056P2220Q"  
/sex="female"  
/tissue\_type="brain tissue"  
/dev\_stage="adult brain"  
/clone\_1lb="normal cattle brain"  
/note="Organ: brain; Vector: pSport1; Site\_1: NotI;  
Site\_2: SalI; Random primed and directionally cloned in  
pSport1 vector using NotI  
(5'-GGACTAGTCTTAGACGACGCGCGCCGCC (T)15-3' and SalI 5'-  
TCGACCCACGCTCGG-3' adapters (Gibco BRL)."

ORIGIN  
Query Match 16.1%; Score 18; DB 7; Length 551;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATTGTTTAC 32  
|||||  
Db 210 AATGATATATTGTTTAC 227

RESULT 17  
CM294028/c 576 bp DNA linear GSS 31-OCT-2004  
LOCUS 104 774 1141970 116 35599 067 Sorghum methylation filtered library  
DEFINITION (LibID: 104) Sorghum bicolor genomic clone 1141970, genomic survey  
sequence.  
ACCESSION CM294028  
VERSION CM294028.1 GI:55010216  
KEYWORDS GSS.  
SOURCE Sorghum bicolor  
ORGANISM Sorghum bicolor (sorghum)  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 576)  
Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korf, I.P.,

TITLE Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
Martensen, R.A.  
JOURNAL Sorghum genome sequencing by methylation filtration  
PUBMED PLoS Biol. 3 (1), e13 (2005)  
COMMENT 15660154  
Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 774 row: n column: 18  
Seq primer: T3 Reverse  
Class: methylation filtered  
High quality sequence stop: 576.  
Location/Qualifiers  
source 1..576  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultiivar="ATx623"  
/db\_xref="taxon:4558"  
/clone="11414970"  
/clone\_1lb="Sorghum methylation filtered library (LibID:  
104)";  
/note="Organ: leaf; Vector: pBCK(-); Site\_1: HincII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBCK(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

ORIGIN  
Query Match 16.1%; Score 18; DB 10; Length 576;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 ATGATATATTGTTTACT 33  
|||||  
Db 243 ATGATATATTGTTTACT 226

RESULT 18  
AV984026 591 bp mRNA linear EST 14-MAR-2002  
LOCUS AV984026 Nori Satoh unpublished cDNA library, egg cDNA  
DEFINITION Intestinalis cDNA clone c1eg28008 5', mRNA sequence.  
ACCESSION AV984026  
VERSION AV984026.1 GI:19473107  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Cloniidae; Ciona.  
1 (bases 1 to 591)  
Satoh, N., Satou, Y., Kohara, Y. and Shin-I, T.  
TITLE Expressed genes in Ciona intestinalis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-Ku, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@scidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1..591  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="c1eg28008"  
/tissue\_type="whole animal"  
/dev\_stage="egg"  
/clone\_1lb="Nori Satoh unpublished cDNA library, egg"

FEATURES  
source



```

ORIGIN
  Query Match      16.1%; Score 18; DB 1; Length 591;
  Best Local Similarity 100.0%; Pred. No. 26;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  72 TAAATATCGTGACGACG 89
  |||
  73 TAAATATCGTGACGACG 90

RESULT 19
CB439180/c      595 bp  mRNA  linear  EST 25-MAR-2003
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Bos taurus (cow)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
  Pecora; Bovidae; Bovinae; Bos.
  1 (bases 1 to 595)
  Smith,T.P.L., Roberts,A.J., Scherrenkamp,S.E., Chitko-Mckown,C.G.,
  Wray,J.E. and Keefe,J.W.
  A second set of bovine ESTs from pooled-tissue normalized libraries
  Unpublished (2003)
  Contact: Smith TPL
  USDA, ARS, US Meat Animal Research Center
  PO Box 166, Clay Center, NE 68933-0166, USA
  Tel: 402 762 4366
  Fax: 402 762 4390
  Email: smtlt@mail.marc.usda.gov
  Single pass sequencing. Bases called with phred v0.020425.c and
  trimmed with the aid of the trim_alt option. Vector identified with
  plate: POY8044 row: 1. column: 4
  Seq primer: TAGAAGCAGACGTGACG.
  Location/Qualifiers
    1..595
    /organism="Bos taurus"
    /mol_type="mRNA"
    /db_xref="taxon:9913"
    /tissue_type="pooled"
    /lab_host="DH10B"
    /clone_lib="MARC 6BOV"
    /note="Vector: pCDNA3.1; Site 1: EcoRI; Site 2: NotI;
    library made with RNA pooled from multiple tissues
    including liver, lung, hypothalamus, pituitary, and
    placenta/endoritrium."

FEATURES
  source
    1..595

ORIGIN
  Query Match      16.1%; Score 18; DB 6; Length 595;
  Best Local Similarity 100.0%; Pred. No. 26;
  Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
  15 AATGATATATTGGTTTAC 32
  |||
  334 AATGATATATTGGTTTAC 317

RESULT 20
CV977041/c      597 bp  mRNA  linear  EST 12-MAY-2005
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
  Bos taurus (cow)
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

```

```

REFERENCE
AUTHORS
  Prather,R.S., Antoniou,E., Garverick,H.A., Green,J.A., Lucy,M.C.,
  Roberts,R.M., Smith,M.F. and Youngquist,R.S.
  USDA Grant NRI-2002-03476: Bovine ESTs: Focus on Female
  Reproduction
  Unpublished (2002)
  Contact: DNA Core Facility (Bovine Project)
  Animal Science - RS Prather
  University of Missouri-Columbia
  M616 Medical Sciences Bldg., Columbia, MO 65212, USA
  Tel: (573)882-0428
  Fax: (573)884-5552
  Email: bovine@net.missouri.edu
  POLYA=yes.

TITLE
  JOURNAL
  COMMENT

FEATURES
  source
    1..597
    /organism="Bos taurus"
    /mol_type="mRNA"
    /db_xref="taxon:9913"
    /clone_lib="pcl"
    /note="Funding: The production of ESTs submitted in this
    project was funded by USDA Grant MRI-2002-03476 entitled
    'Bovine ESTs: Focus on Female Reproduction' to RS
    Prather(Primary Investigator), E Antoniou, HA Garverick,
    JA Green, MC Lucy, RM Roberts, MF Smith and RS Youngquist.
    Genetic Source: Heifers for the project were purchased
    from Circle A Ranch, Iberia, MO
    (http://www.circlearanch.com/home.html). These heifers,
    while not registered have known Angus pedigree going back
    at least 4 generations. Samples collected: The samples
    consisted of the following: germinal vesicle-stage
    oocytes; in vitro derived embryos (2-cell, morula,
    blastocyst and nuclear transfer blastocyst); in vivo
    blastocysts and conceptuses (days 8, 14, 16 and 35); ovarian
    corpora lutea (days 3, 5, 8, 14, 16, 18 and 35); ovarian
    follicles (days 0, non-recruited, recruited, early
    selected and preovulatory); oviduct (days 0, 3 and 5);
    endometrium (days 5, 8, 14, 16, 18 and 35); and
    placenta/embryo from day 35 conceptuses. Expanded
    descriptions of how the tissues were collected can be
    found at the following URL:
    http://genome.mrc.missouri.edu/Bovine/Methods.html.
    Library construction (Standard Protocol): All procedures
    have been described in detail elsewhere (Soares et al.,
    1994; Bonaldo et al., 1996; Jiang et al., 2001). Total
    cellular RNA from each sample was isolated by using
    STRAT-60 reagent (Tel-Test, Friendswood, TX) and the
    poly(A)+ RNA was obtained by two rounds of purification
    with the Oligotex mRNA isolation kit (Qiagen) according to
    the manufacturer's instructions. The libraries were
    constructed essentially as described by the manufacturer's
    instructions provided with the SuperScript Plasmid System
    (Invitrogen, cat. no. 18248-013). Briefly, 10mg of
    poly(A)+ RNA was annealed at c37 degrees with 10mg of
    NotI-tag-d18 oligonucleotide (GGCTCGCGCGC-cag-T18)
    and reverse transcribed at c37 degrees with SuperScript II
    (Invitrogen) reverse transcriptase (Jiang et al., 2001).
    The 'tag' represents a tissue/stage-specific ten-base
    sequence identifier
    (http://genome.owa.edu/pubsoft/software.html) present in
    the oligonucleotide used to prime first-strand synthesis.
    Second strand synthesis was performed with T4 DNA
    polymerase in the presence of DNA ligase and RNase H.
    After second strand synthesis, the double-stranded cDNAs
    were ligated to SalI adapters (Invitrogen-life
    Technologies) and digested with NotI. The cDNAs were size
    selected by passage through cDNA size fractionation
    columns (Invitrogen-life technologies). The cDNAs derived
    from each developmental stage of a particular tissue were
    mixed on an equimolar basis and ligated directionally into
    the NotI and SalI sites of the pCMV-SPORT6 vector

```



(Invitrogen). After ligation of the inserts, the plasmids were electroporated into DH10B bacteria. Library construction (PCR Protocol): The amount of mRNA that was recovered from oocytes and embryos was quite limiting and was not sufficient for library production with the standard protocol. Therefore, PCR-based protocol was utilized for producing libraries from sources in which the amount of extracted mRNA was small (oocytes and embryos). Poly-A RNA was isolated by using the MicroPoly(A) Pure kit from Ambion (cat. # 1918). The mRNA was reverse transcribed with a NotI-tag-dT18 oligonucleotide and a SMART oligonucleotide (Clontech) modified to contain a SalI site to generate full-length cDNA with a sequence complementary to the SMART oligonucleotide. Sequences within the SMART and dt oligonucleotides were used as primers to amplify the cDNAs by PCR with plu turbo polymerase (Stratagene). The resulting PCR products were purified, digested with NotI and SalI and size fractionated by using Chroma Spin-1000 columns (Clontech). Purified cDNA from each PCR reaction was quantitated and mixed on an equimolar basis for ligation into the pCMV-SPORT6 vector. Preliminary Library Characterization: Randomly chosen clones from each library were analyzed by restriction digestion to determine average insert size (96 clones) and by sequencing (~4 96-well plates) to confirm library quality (e.g. the presence of short polyA+ tails, genomic DNA contamination (must be <1%), ribosomal RNA clones (must be <1%), etc.) and to provide a sequence database representing the predominant clones in each library. The clones were sequenced at the University of Missouri-Columbia DNA Core Facility. After production of the libraries, equal numbers of recombinants from each library were pooled to produce a single mixed library (mega-library) for more extensive sequencing.

Bioinformatics work was performed by GK Springer's bioinformatics group in Computer Science at the University of Missouri-Columbia. Clone Requests: Requests for clones should be made to the Director of the University of Missouri DNA Core Facility at: bovine@net.missouri.edu. Bonaldo MF, Lennon G, Soares MB. Normalization and Subtraction: Two approaches to facilitate gene discovery. Genome Res, 1996; 6:791-806. Jiang H, Bivens NJ, Ries JE, Whitworth KM, Green JA, Forrester LJ, Springer GK, Didion BA, Mathiasagan N, Prether RS, Lucy MC (2001) Constructing cDNA libraries with fewer clones that contain long poly(dA) tails. Biotechniques 31:38-42. Soares MB, MF Bonaldo, P Jeleno, L Su, L Lawton, A Efstratiadis. 1994. Construction and characterization of a normalized cDNA library. Proc Natl Acad Sci, 91:9228-9232.

TAG TISSUE=Day 14 CL from a pregnant animal  
TAG\_SEQ=Not found"

## ORIGIN

Query Match 16.1%; Score 18; DB 8; Length 597;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 AATGATATATTGGTTTAC 32  
|||||  
Db 328 AATGATATATTGGTTTAC 311

RESULT 21  
CA696004/c 602 bp mRNA linear EST 26-NOV-2002  
LOCUS wlmk8.pk0018.c3 wlmk8 Triticum aestivum cDNA clone wlmk8.pk0018.c3  
DEFINITION 5' end, mRNA sequence.  
ACCESSION CA696004  
VERSION CA696004.1 GI:25417790  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE  
1 (bases 1 to 602)  
Tingey, S.V., Powell, W., Wolters, P., Dolan, M., Hainey, C., Yuan, Z.,  
Miao, G., Caraher, N. and Hanafey, M.K.  
TITLE  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Scott V. Tingey  
Crop Genetics  
E. I. Dupont de Nemours and Company  
1 Innovation Way, P.O. Box 6104, Newark, DE 19714-6104, USA  
Tel: 302-631-2607  
Fax: 302-631-2607  
Email: Scott.V.Tingey@USA.dupont.com  
Seq primer: M13.

## FEATURES

## source

Location/Qualifiers  
1..602  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Stephens"  
/db\_xref="taxon:4565"  
/clone="wlmk8.pk0018.c3"  
/issue\_type="leaf"  
/clone\_id="wlmk8"  
/note="Vector: pBluescript SK+; Site\_1: EcoRI; Site\_2:  
XhoI; Wheat (Triticum aestivum L.) seedlings 8 hr after  
inoculation w/ E. graminis and  
6-Iodo-3-propyl-2-propyl-4(3H)-quinazolinone"

## ORIGIN

Query Match 16.1%; Score 18; DB 6; Length 602;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGATATATTGGTTTACT 33  
|||||  
Db 179 ATGATATATTGGTTTACT 162

RESULT 22  
B3J10536/c 617 bp mRNA linear EST 09-APR-2002  
LOCUS B3J10536 Y. Ogihara unpublished cDNA library, wh\_yd Triticum  
DEFINITION B3J10536 Y. Ogihara unpublished cDNA library, wh\_yd Triticum  
aestivum cDNA clone wh\_yd7112 3', mRNA sequence.  
ACCESSION B3J10536  
VERSION B3J10536.1 GI:20118155  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 617)  
Ogihara, Y. and Murai, K.  
TITLE  
JOURNAL  
Unpublished (2002)  
COMMENT  
Contact: Tadasi Shin-i  
Center For Genetic Resource Information  
National Institute of Genetics  
1111 Yata, Mishima, Shizuoka 411-8540, Japan  
Tel: 81-559-81-6856  
Fax: 81-559-81-6855  
Email: tshin@genes.nig.ac.jp.  
Location/Qualifiers  
1..617  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultivar="Chinese Spring"  
/db\_xref="taxon:4565"  
/clone="wh\_yd7112"  
/issue\_type="spikelet at late flowering"  
/dev\_stage="Flekes" scale 6"  
/clone\_id="Y. Ogihara unpublished cDNA library, wh\_yd"

## FEATURES

## source



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ORIGIN
Query Match      16.1%; Score 18; DB 3; Length 617;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      78 CGGTGAGCAACGACGGGT 95
      |||||
Db      429 CGGTGAGCAACGACGGGT 412

RESULT 23
Bj217178/c      630 bp      mRNA      linear      EST 04-APR-2002
LOCUS           Bj217178 Y. Ogihara unpublished cDNA library, wh Triticum aestivum
DEFINITION      cDNA clone wh15108 3', mRNA sequence.
ACCESSION       Bj217178
VERSION         Bj217178.1 GI:19957051
KEYWORDS
SOURCE          Triticum aestivum (bread wheat)
ORGANISM        Triticum aestivum
AUTHORS         Ogihara,Y. and Murai,K.
TITLE           Expressed genes in Triticum aestivum
JOURNAL         Unpublished (2002)
COMMENT         Contact: Tadasu Shin-i
                  National Institute of Genetics
                  1111 Yata, Mishima, Shizuoka 411-8540, Japan
                  Tel: 81-559-81-6856
                  Fax: 81-559-81-6855
                  Email: tshin@genes.nig.ac.jp.
FEATURES
  source
    1..630
    /organism="Triticum aestivum"
    /mol_type="mRNA"
    /culturvar="Chinese Spring"
    /db_xref="taxon:4565"
    /clone="wh15108"
    /tissue_type="spike at meiosis"
    /dev_stage="feeder" scale 9"
    /clone_id="Y. Ogihara unpublished cDNA library, wh"
ORIGIN
Query Match      16.1%; Score 18; DB 3; Length 630;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      78 CGGTGAGCAACGACGGGT 95
      |||||
Db      448 CGGTGAGCAACGACGGGT 431

RESULT 24
AV997156      639 bp      mRNA      linear      EST 15-MAR-2002
LOCUS           AV997156 Nori Satoh unpublished cDNA library, tailbud embryo Clona
DEFINITION      AV997156 Nori Satoh unpublished cDNA library, tailbud embryo Clona
ACCESSION       AV997156
VERSION         AV997156.1 GI:19488490
KEYWORDS
SOURCE          Clona intestinalis
ORGANISM        Clona intestinalis
AUTHORS         Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;
                  Phlebobranchia; Clonidae; Clona.
TITLE           1 (bases 1 to 639)
JOURNAL         Satoh,N., Satoou,Y., Kohara,Y. and Shin-i,T.
COMMENT         Expressed genes in Clona intestinalis
                  Unpublished (2000)
                  Contact: Nori Satoh

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Kyoto University
Sakyo-Ku, Kyoto 606-8502, Japan
Tel: 81-75-753-4081
Fax: 81-75-705-1113
Email: satoh@ascidian.zool.kyoto-u.ac.jp.
FEATURES
  source
    1..639
    /organism="Clona intestinalis"
    /mol_type="mRNA"
    /db_xref="taxon:7719"
    /clone="ctb19112"
    /tissue_type="whole animal"
    /dev_stage="tailbud embryo"
    /clone_id="Nori Satoh unpublished cDNA library, tailbud
    embryo"
ORIGIN
Query Match      16.1%; Score 18; DB 1; Length 639;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      72 TAATATCGTGACGACG 89
      |||||
Db      560 TAATATCGTGACGACG 577

RESULT 25
BE427379      640 bp      mRNA      linear      EST 24-JUL-2000
LOCUS           PSR6369-B ITRC PSR wheat Pericarp/Teesta library Triticum aestivum
DEFINITION      PSR6369-B ITRC PSR wheat Pericarp/Teesta library Triticum aestivum
ACCESSION       BE427379
VERSION         BE427379.1 GI:9425222
KEYWORDS
SOURCE          EST.
ORGANISM        Triticum aestivum (bread wheat)
AUTHORS         Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                  Poideae; Triticeae; Triticum.
                  1 (bases 1 to 640)
                  Anderson,O.A., Appels,R., Bailey,P., Blake,T., Close,T.,
                  Cloutier,S., Dubcovsky,J., Feuillet,C., Gale,M., Graner,A.,
                  Gustafson,P., Hermann,R.G., Holton,T., Jacquemin,J.M., Jia,J.,
                  Joudrier,P., Langridge,P., Lazo,G.R., Lin,J.U., McGuire,P.,
                  Ogihara,Y., Pecchioni,N., Qualset,C., Schuch,W., Selvaraj,G.,
                  Shariflou,M., Sorrells,M., Warburton,M. and Wenzel,G.
                  International Triticeae EST Cooperative (ITREC): Production of
                  Expressed Sequence Tags for Species of the Triticeae
                  Unpublished (2000)
                  Contact: Bailey P
                  Cereals Group, John Innes Centre
                  Norfolk, Norwich NR4 7UH UNITED KINGDOM
                  Tel: 44 1603 452571 ext. 2587
                  Fax: 44 1603 502241
                  Email: paul.bailey@brc.ac.uk
                  International Triticeae EST Cooperative (ITREC)
                  http://wheat.pw.usda.gov/genome.
FEATURES
  source
    1..640
    /organism="Triticum aestivum"
    /mol_type="mRNA"
    /culturvar="Novosibirskaya 67"
    /db_xref="taxon:4565"
    /clone="PSR6369-B"
    /tissue_type="pericarp/teesta"
    /dev_stage="3:1 mix 10:20 days post anthesis"
    /clone_id="ITRC PSR wheat Pericarp/Teesta library"
    /note="Vector: Lambda ZAP II (Stratagene)"
ORIGIN
Query Match      16.1%; Score 18; DB 2; Length 640;
Best Local Similarity 100.0%; Pred. No. 26;

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Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 CGGTGAGCAACGACGGGT 95  
|||||

Db 363 CGGTGAGCAACGACGGGT 380

# RESULT 26

CD905731 655 bp mRNA linear EST 14-JUL-2003  
LOCUS G468.102L13P010808 G468 Triticum aestivum cDNA clone G468102L13,  
DEFINITION mRNA sequence.

CD905731

ACCESSION CD905731.1 GI:32680060

VERSION EST.

KEYWORDS Triticum aestivum (bread wheat)

SOURCE Triticum aestivum

ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Poideae; Triticeae; Triticum.

1 (bases 1 to 655)

REFERENCE Genoplatte, a major partnership french program in plant genomics

AUTHORS Genoplatte, (2003)

JOURNAL Unpublished (2003)

COMMENT Contact: Genoplatte

Genoplatte 93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genome programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..655

/organism="Triticum aestivum"

/mol\_type="mRNA"

/cultivar="recital"

/db\_xref="taxon:4565"

/clone="G468102L13"

/tissue\_type="grain (468 degrees per day after

pollination)"

/clone\_1ib="G468"

## ORIGIN

Query Match 16.1%; Score 18; DB 6; Length 655;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 78 CGGTGAGCAACGACGGGT 95  
|||||

Db 298 CGGTGAGCAACGACGGGT 315

# RESULT 27

BM346197 658 bp mRNA linear EST 27-MAY-2004

LOCUS BM346197 Yutaka Satou unpublished cDNA library, embryo whole animal

DEFINITION Ciona intestinalis cDNA clone ciem832ml3 5', mRNA sequence.

BM346197

ACCESSION BM346197.1 GI:47757998

VERSION EST.

KEYWORDS Ciona intestinalis

SOURCE Ciona intestinalis

ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 658)

REFERENCE Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2004)

Unpublished (2004)

CONTACT: Yutaka Satou

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4095

Fax: 81-75-705-1113

Email: [yutaka@ascidian.zool.kyoto-u.ac.jp](mailto:yutaka@ascidian.zool.kyoto-u.ac.jp).

Location/Qualifiers

1..658

/organism="Ciona intestinalis"

/mol\_type="mRNA"

/db\_xref="taxon:7719"

/clone="ciem832ml3"

/tissue\_type="whole animal"

/dev\_stage="embryo"

/clone\_1ib="Yutaka Satou unpublished cDNA library, embryo

whole animal"

## ORIGIN

Query Match 16.1%; Score 18; DB 5; Length 658;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TAATATCGGTGAGCAACG 89  
|||||

Db 273 TAATATCGGTGAGCAACG 290

# RESULT 28

BM252739 668 bp mRNA linear EST 03-JUN-2005

LOCUS BM252739 Nori Satoh unpublished cDNA library, tailbud embryo Ciona

DEFINITION intestinalis cDNA clone c1tb094c10 5', mRNA sequence.

BM252739

ACCESSION BM252739.1 GI:24832657

VERSION EST.

KEYWORDS Ciona intestinalis

SOURCE Ciona intestinalis

ORGANISM Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 668)

REFERENCE Satou, Y., Shin-I, T., Kohara, Y. and Satoh, N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

CONTACT: Nori Satoh

Department of Zoology

Kyoto University

Sakyo-ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: [satoh@ascidian.zool.kyoto-u.ac.jp](mailto:satoh@ascidian.zool.kyoto-u.ac.jp).

Location/Qualifiers

1..668

/organism="Ciona intestinalis"

/mol\_type="mRNA"

/db\_xref="taxon:7719"

/clone="c1tb094c10"

/tissue\_type="whole animal"

/dev\_stage="tailbud embryo"

/clone\_1ib="Nori Satoh unpublished cDNA library, tailbud

embryo"

## ORIGIN

Query Match 16.1%; Score 18; DB 5; Length 668;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 72 TAATATCGGTGAGCAACG 89  
|||||

Db 56 TAATATCGGTGAGCAACG 73

# RESULT 29

BM034334 672 bp mRNA linear EST 13-OCT-2002

LOCUS BM034334 Nori Satoh unpublished cDNA library, blood cells Ciona

DEFINITION intestinalis cDNA clone c1bd025j15 5', mRNA sequence.



ACCESSION BM034334  
VERSION BM034334.1 GI:23950286  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 672)  
AUTHORS Satoh,Y., Satake,M., Azumi,K., Nonaka,M., Shin-i,T., Kohara,Y. and Satoh,N.  
TITLE Expressed genes in Ciona intestinalis (2002)  
JOURNAL Unpublished (2002)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1..672  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="cibd025j15"  
/tissue\_type="blood cells"  
/clone\_lib="Nori Satoh unpublished cDNA library, blood cells"  
ORIGIN  
Query Match 16.1%; Score 18; DB 5; Length 672;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 72 TAATATCGGTGAGCAACG 89  
Db 179 TAATATCGGTGAGCAACG 196  
RESULT 30  
AV982799 686 bp mRNA linear EST 14-MAR-2002  
LOCUS AV982799 Nori Satoh unpublished cDNA library, tailbud embryo Ciona  
DEFINITION intestinalis cDNA clone cib30p1 5', mRNA sequence.  
ACCESSION AV982799  
VERSION AV982799.1 GI:19472086  
KEYWORDS EST.  
SOURCE Ciona intestinalis  
ORGANISM Ciona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Ciona.  
REFERENCE 1 (bases 1 to 686)  
AUTHORS Satoh,N., Satou,Y., Kohara,Y. and Shin-i,T.  
TITLE Expressed genes in Ciona intestinalis  
JOURNAL Unpublished (2000)  
COMMENT Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.  
Location/Qualifiers  
1..686  
/organism="Ciona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="cib30p1"  
/tissue\_type="whole animal"  
/dev\_stage="tailbud embryo"  
/clone\_lib="Nori Satoh unpublished cDNA library, tailbud embryo"  
ORIGIN

Query Match 16.1%; Score 18; DB 1; Length 686;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 72 TAATATCGGTGAGCAACG 89  
Db 562 TAATATCGGTGAGCAACG 579  
RESULT 31  
CD872302 697 bp mRNA linear EST 11-JUL-2003  
LOCUS CD872302  
DEFINITION AZO2.120F05F010209 AZO2 Triticum aestivum cDNA clone AZO2120F05,  
mRNA sequence.  
ACCESSION CD872302  
VERSION CD872302.1 GI:32556118  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
REFERENCE 1 (bases 1 to 697)  
AUTHORS Genopiante.  
TITLE Genopiante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genopiante  
Genopiante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genopiante' (<http://www.genopiante.com>  
and <http://genopiante-info.inbioigen.fr>).  
Location/Qualifiers  
1..697  
/organism="Triticum aestivum"  
/mol\_type="mRNA"  
/cultiivar="recital"  
/db\_xref="taxon:4565"  
/clone="AZO2120F05"  
/tissue\_type="root"  
/clone\_lib="AZO2"  
ORIGIN  
Query Match 16.1%; Score 18; DB 6; Length 697;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 78 CGGTGAGCAACGCGGT 95  
Db 666 CGGTGAGCAACGCGCGGT 683  
RESULT 32  
A1612522/c 698 bp mRNA linear EST 07-JUL-1999  
LOCUS A1612522  
DEFINITION TENG0332 T. Cruzi epimastigote normalised cDNA library Trypanosoma  
cruzi cDNA clone n695.r 5', mRNA sequence.  
ACCESSION A1612522  
VERSION A1612522.1 GI:4621689  
KEYWORDS EST.  
SOURCE Trypanosoma cruzi  
ORGANISM Trypanosoma cruzi  
Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae;  
Trypanosoma; Schizotrypanum.  
REFERENCE 1 (bases 1 to 698)  
AUTHORS Gonzalez Rey,E., Remisz,E., Delgado Garcia,A. and Gonzalez,A.  
TITLE Characterization of ESTs from Trypanosoma cruzi epimastigotes  
JOURNAL Unpublished (1998)  
COMMENT Contact: Delgado Alberto  
Departamento de Biologia Molecular, Lab 303



Instituto de Parasitología Y Biomedicina  
Consejo Superior de Investigaciones Científicas C/ Ventanilla No  
11, E-18001, Granada, Spain  
Tel: 34 958 805058  
Fax: 34 958 203323  
Seq primer: 17

High quality sequence stop: 698.

FEATURES  
Location/Qualifiers

1..698

/organism="Trypanosoma cruzi"

/mol\_type="mRNA"

/strain="Cl - Brenner"

/db\_xref="taxon:5693"

/clone="n695.r"

/cell\_type="epimastigote"

/clone\_1ib="T. cruzi epimastigote normalised cDNA library"

/note="Site 1: EcoRI; Site 2: NotI; cDNA library

constructed with oligo dt primed epimastigote mRNA and

cloned in pUC18D phagemid with modified polylinker"

ORIGIN

Query Match 16.1%; Score 18; DB 1; Length 698;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 76 ATCGTGAGCAACGACG 93

DB 180 ATCGTGAGCAACGACG 163

RESULT 33

LOCUS

BM313478 723 bp mRNA linear EST 11-NOV-2002

DEFINITION BM313478 Nori Satoh unpublished cDNA library, heart Ciona

intestinalis cDNA clone c1nc026h17 5', mRNA sequence.

ACCESSION

BM313478

VERSION

BM313478.1 GI:24894089

KEYWORDS

EST.

SOURCE

Ciona intestinalis

Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;

Phlebobranchia; Clonidae; Ciona.

1 (bases 1 to 723)

REFERENCE

Satoh,Y., Shin-I.,T., Kohara,Y. and Satoh,N.

Expressed genes in Ciona intestinalis (2002c)

Unpublished (2002)

CONTACT: Nori Satoh

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Kyoto University

Sakyo-Ku, Kyoto 606-8502, Japan

Tel: 81-75-753-4081

Fax: 81-75-705-1113

Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers

1..723

/organism="Ciona intestinalis"

/mol\_type="mRNA"

/db\_xref="taxon:7719"

/clone="c1nc026h17"

/tissue\_type="heart"

/clone\_1ib="Nori Satoh unpublished cDNA library, heart"

ORIGIN

Query Match 16.1%; Score 18; DB 5; Length 723;

Best Local Similarity 100.0%; Pred. No. 26;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 72 TATATCGTGAGCAACG 89

DB 495 TATATCGTGAGCAACG 512

RESULT 34

CD872303/c

LOCUS

DEFINITION

CD872303

VERSION

CD872303.1

KEYWORDS

SOURCE

ORGANISM

1..731

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone="AZO2120F05"

/tissue\_type="root"

/clone\_1ib="AZO2"

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Unpublished (2003)

Contact: Genoplatte

Genoplatte

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>

and <http://genoplatte-info.infobiogen.fr>).

Location/Qualifiers

1..731

/organism="Triticum aestivum"

/mol\_type="mRNA"

/db\_xref="taxon:4565"

/clone="AZO2120F05"

/tissue\_type="root"

/clone\_1ib="AZO2"

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

COMMENT

Unpublished (2003)

Contact: Smith TPL

USDA, ARS, US Meat Animal Research Center

PO Box 166, Clay Center, NE 68933-0166, USA

Tel: 402 762 4366

Fax: 402 762 4390

Email: [smith@mail.marc.usda.gov](mailto:smith@mail.marc.usda.gov)

Single pass sequencing. Bases called with phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and

phred v0.020425.c and



trimmed with the aid of the trim\_alt option. Vector identified with cross match v0.990329.

Plate: 40 row: C column: 10  
Seq primer: GTATATGACTGCTATTAGGG.

Location/Qualifiers  
1. .731

/organism="Bos taurus"  
/mol\_type="mRNA"  
/db\_xref="taxon:9913"  
/issue\_type="pooled"  
/lab\_host="DH10B"  
/clone\_id="MARC\_4BOV"  
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;  
library made from pooled tissue from day 20 and day 40  
embryos."

## ORIGIN

Query Match 16.1%; Score 18; DB 7; Length 731;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 AATGATATATGTTTAC 32  
|||||  
Db 328 AATGATATATGTTTAC 311

RESULT 36  
CL766270/c 738 bp DNA linear GSS 27-JUL-2004  
LOCUS OR BBA0137L23.r OR Bba Oryza niyara genomic clone OR\_BBA0137L23 3',  
DEFINITION genomic survey sequence.  
ACCESSION CL766270  
VERSION CL766270.1 GI:50724217  
KEYWORDS GSS.  
SOURCE Oryza niyara  
ORGANISM Oryza niyara  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Erihartoideae; Oryzaceae; Oryza.  
1 (bases 1 to 738)  
Kim, H., Yu, Y., Stum, D., Yost, D., Rao, K., Luo, M., Jetty, R.,  
Kudrna, D., Muller, C., Hatfield, J., Soderlund, C. and Wing, R.  
OMAP Project  
Unpublished (2004)  
Contact: Rod A. Wing  
Arizona Genomics Institute  
University of Arizona  
Forbes Building Room 303, Tucson, AZ 85721-0036, USA  
Tel: 520 626 9595  
Fax: 520 621 1259  
Email: rwing@genome.arizona.edu

PCR Primers  
FORWARD: TAA TAC GAC TCA CTA TAG GG  
BACKWARD: CAC TCA TTA GGC ACC CCA  
Insert length: 161 Std Error: 0.00  
Plate: 0137 row: L column: 23  
Seq primer: CAC TCA TTA GGC ACC CCA  
Class: BAC ends.

Location/Qualifiers

1. .738  
/organism="Oryza niyara"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4536"  
/clone="OR\_BBA0137L23"  
/issue\_type="young leaves"  
/lab\_host="DH10B-T1 phage resistant"  
/clone\_id="OR\_BBA"  
/note="Vector: PABIBAC1; Site\_1: HindIII; Site\_2: HindIII"

## ORIGIN

Query Match 16.1%; Score 18; DB 10; Length 738;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 GATATATGTTTACTGA 35  
|||||  
Db 402 GATATATGTTTACTGA 385

RESULT 37  
BM043930 748 bp mRNA linear EST 19-OCT-2002  
LOCUS BM043930 Nori Satoh unpublished cDNA library, blood cells Clona  
DEFINITION intestinalis cDNA clone cld054b16 5', mRNA sequence.  
ACCESSION BM043930  
VERSION BM043930.1 GI:24144626  
KEYWORDS EST.  
SOURCE Clona intestinalis  
ORGANISM Clona intestinalis  
Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona;  
Phlebobranchia; Clonidae; Clona.  
1 (bases 1 to 748)  
Satoh, Y., Satake, M., Azumi, K., Nonaka, M., Shin-i, T., Kohara, Y. and  
Satoh, N.  
Expressed genes in Clona intestinalis (2002)  
Unpublished (2002)  
Contact: Nori Satoh  
Department of Zoology  
Kyoto University  
Sakyo-ku, Kyoto 606-8502, Japan  
Tel: 81-75-753-4081  
Fax: 81-75-705-1113  
Email: satoh@ascidian.zool.kyoto-u.ac.jp.

Location/Qualifiers  
1. .748  
/organism="Clona intestinalis"  
/mol\_type="mRNA"  
/db\_xref="taxon:7719"  
/clone="cld054b16"  
/issue\_type="blood cells"  
/clone\_id="Nori Satoh unpublished cDNA library, blood  
cells"

## FEATURES

ORIGIN  
Query Match 16.1%; Score 18; DB 5; Length 748;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 72 TAATATCGGTGACCAAG 89  
|||||  
Db 230 TAATATCGGTGACCAAG 247

RESULT 38  
BH184801 752 bp DNA linear GSS 29-OCT-2001  
LOCUS BH184801  
DEFINITION 026 M.05-rev SmbAC1 Schistosoma mansoni genomic clone 026M05 5',  
genomic survey sequence.  
ACCESSION BH184801  
VERSION BH184801.1 GI:16291566  
KEYWORDS GSS.  
SOURCE Schistosoma mansoni  
ORGANISM Schistosoma mansoni  
Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
Strigidae; Schistosomatidae; Schistosomatidae; Schistosoma.  
1 (bases 1 to 752)  
Le Paslier, M.C., Pierce, R.J., Merlin, F., Hiral, H., Wu, W.,  
Williams, D.L., Johnston, D., Loverde, P.T. and Le Paslier, D.  
Construction and characterization of a Schistosoma mansoni  
bacterial artificial chromosome library  
Genomics 65 (2), 87-94 (2000)  
10783255  
Other GSSs: 026 M.05-21  
Contact: Pierre RJ  
INSERM U 167  
Institut Pasteur de Lille



1 rue du Professeur A. Calmette, 59019-Lille, France  
 Tel: (33) (0)3 20877783  
 Fax: (33) (0)3 20877888  
 Email: Raymond.pierce@pasteur-lille.fr  
 CNS sequencing ID=DG0A026AG03BPI Bases 1-198 have 86% identity to  
 S. mansoni EST A1394788.1 from base 233-35. Bases 54-267 have 82%  
 identity to S. mansoni EST A1976273.1 from base 552-339.

Plate: 026 row: M column: 05  
 Seq primer: M13 reverse primer  
 Class: BAC ends  
 High quality sequence stop: 752.

## FEATURES

location/Qualifiers

1..752  
 /organism="Schistosoma mansoni"  
 /mol\_type="genomic DNA"  
 /strain="Puerto-Rican"  
 /db\_xref="taxon:6183"  
 /clone="026M05"  
 /sex="mixed"  
 /dev\_stage="cercariae"  
 /lab\_host="Blomphalaria glabrata"  
 /clone\_lib="SmbAC1"  
 /note="Vector: pBelOBAC 11; Site 1: Hind III; Partially  
 Hind III digested and size-selected S. mansoni cercarial  
 DNA was ligated into Hind III digested pBelOBAC 11 vector  
 and used to transform E. coli DH10B. The complete library  
 contains 23808 clones from 4 independent  
 sizing-ligation-transformations. Average insert size  
 ranges from 70-127 kb and genome coverage is 7.9-fold."

## ORIGIN

Query Match 16.1%; Score 18; DB 9; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGATATATTGGTTTACT 33  
 Db 619 ATGATATATTGGTTTACT 636

RESULT 39  
 CENS07PNO 752 bp DNA linear GSS 30-NOV-2001  
 LOCUS T3 end of clone 026AG03 of library SmbAC1 from strain Puerto-Rican  
 DEFINITION of Schistosoma mansoni, genomic survey sequence.  
 ACCESSION AL621752  
 VERSION AL621752.1 GI:16035894  
 KEYWORDS GSS

## SOURCE

Schistosoma mansoni  
 Schistosoma mansoni  
 Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea;  
 Strigedidae; Schistosomatidae; Schistosoma.

## REFERENCES

1 (bases 1 to 752)  
 Le Paslier M.C., Pierce R.J., Merlin P., Hirai H., Wu W.,  
 Williams D.L., Johnston D., Loyerde P.T. and Le Paslier D.  
 Construction and characterization of a Schistosoma mansoni  
 bacterial artificial chromosome library  
 Genomics 65 (2), 87-94 (2000)

## JOURNAL

## PUBMED

## REFERENCE

## AUTHORS

Genoscope.  
 Direct Submission  
 Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage :  
 BP 191 91006 Evry cedex - FRANCE (E-mail : seqref@genoscope.cns.fr  
 - Web : www.genoscope.cns.fr)  
 Partially Hind III digested and size-selected S. mansoni cercarial  
 DNA was ligated into Hind III digested pBelOBAC 11 vector and used  
 to transform E. coli DH10B. The complete library contains 23808  
 clones from 4 independent sizing-ligation-transformations. Average  
 insert size ranges from 70-127 kb and genome coverage is 7.9-fold.

## FEATURES

location/Qualifiers  
 1..752  
 /organism="Schistosoma mansoni"

/mol\_type="genomic DNA"  
 /strain="Puerto-Rican"  
 /db\_xref="taxon:6183"  
 /clone="026AG03"  
 /clone\_lib="SmbAC1"  
 /note="end : T3"

## ORIGIN

Query Match 16.1%; Score 18; DB 11; Length 752;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 ATGATATATTGGTTTACT 33  
 Db 619 ATGATATATTGGTTTACT 636

RESULT 40  
 DU070491 825 bp DNA linear GSS 12-AUG-2005  
 LOCUS 138260 Tomato HindIII BAC library Lycopersicon esculentum genomic  
 DEFINITION clone LB\_HBA0191N20 3, genomic survey sequence.

ACCESSION DU070491 GI:72506632  
 KEYWORDS GSS.  
 Lycopersicon esculentum (Solanum lycopersicum)  
 ORGANISM Lycopersicon esculentum

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 asterids; lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.  
 1 (bases 1 to 825)  
 Mueller L.A., Bueler R.M., Wang Y., Tanksley S.D., Giovannoni J.J.,  
 Van Eck J. and Stack S.  
 BAC end sequencing from three Solanum lycopersicon libraries  
 Unpublished (2005)

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 Other GSSs: 138261  
 Contact: Lukas Mueller  
 Tanksley Lab, Dept. of Plant Breeding  
 Cornell University  
 251 Emerson Hall, Ithaca, NY 14853, USA  
 Tel: 607-255-6557  
 Fax: 607-255-6683  
 Email: egn-feedback@cornell.edu  
 Insert Length: 68293 Std Error: 0.00  
 Plate: 191 row: N column: 20  
 Seq primer: SP6  
 Class: BAC ends  
 High quality sequence start: 27  
 High quality sequence stop: 520.

## FEATURES

location/Qualifiers  
 1..825  
 /organism="Lycopersicon esculentum"  
 /mol\_type="genomic DNA"  
 /cultivar="Heinz 1706"  
 /db\_xref="taxon:4081"  
 /clone="LB\_HBA0191N20"  
 /lab\_host="E. coli"  
 /clone\_lib="Tomato HindIII BAC library"  
 /note="Vector: pBelOBAC11; Site 1: HindIII"

## ORIGIN

Query Match 16.1%; Score 18; DB 10; Length 825;  
 Best Local Similarity 100.0%; Pred. No. 26;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 60 TAAAGAGGTCCTTAATAT 77  
 Db 224 TAAAGAGGTCCTTAATAT 241

Search completed: April 11, 2006, 21:42:06  
 Job time : 1618.09 secs



GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 344.008 Seconds  
(without alignments)  
9253.359 Million cell updates/sec

Title: US-10-712-654-26

Perfect score: 56

Sequence: 1 gcatccgcgtgtagtctgaa.....ggagcatgagaattacacg 56

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

Genembl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_sy:\*  
12: gb\_un:\*  
13: gb\_vl:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query	Length	ID	Description
1	56	100.0	3244	1	BACCAPABC
2	56	100.0	94829	1	AB011191
3	56	100.0	94830	1	AB017335
4	56	100.0	96231	1	AF188935
5	18	32.1	825	10	BV618443
6	18	32.1	60211	14	AC068685
7	18	32.1	145190	9	AC156285
8	18	32.1	163784	8	CNS07BD1
9	18	32.1	184648	14	AC017102
10	18	32.1	191501	14	AL592113
11	18	32.1	193221	9	AC158673
12	18	32.1	226128	14	AC136487
13	18	32.1	266188	14	AC103296
14	17	30.4	201	6	AX505342
15	17	30.4	527	10	BV240969
16	17	30.4	1997	1	AY696754
17	17	30.4	1999	1	AY696752
18	17	30.4	2202	1	AY696755

19	17	30.4	2231	1	AY696753	AY696753 Shigella
20	17	30.4	2795	2	AF084556	AF084556 Apis mell
21	17	30.4	3362	2	AF315555	AF315555 Caenorhab
22	17	30.4	7881	2	AF315554	AF315554 Caenorhab
23	17	30.4	9096	6	A93560	A93560 Sequence 5
24	17	30.4	9096	6	AR182400	AR182400 Sequence
25	17	30.4	15936	6	A93556	A93556 Sequence 1
26	17	30.4	15936	6	AR182396	AR182396 Sequence
27	17	30.4	15936	2	AF077011	AF077011 Homo sapi
28	17	30.4	20244	2	CEY10666	CEY10666 Caenorhab
29	17	30.4	21072	8	AY497901	AY497901 Homo sapi
30	17	30.4	36976	6	CQ870229	CQ870229 Sequence
31	17	30.4	38810	15	AB028610	AB028610 Arabidops
32	17	30.4	43429	2	CBR644102	CBR644102 Caenorhab
33	17	30.4	49362	8	AL355875	AL355875 Human DNA
34	17	30.4	51828	14	AC108345_3	AC108345_3 Continuation (4 of
35	17	30.4	68550	14	AC118389_5	AC118389_5 Continuation (6 of
36	17	30.4	68589	14	AC087682	AC087682 Homo sapi
37	17	30.4	68689	14	AC161705	AC161705 Bos tauru
38	17	30.4	69049	14	AC101430	AC101430 Mus muscu
39	17	30.4	69966	8	AL391804	AL391804 Human DNA
40	17	30.4	84732	8	AL445677	AL445677 Human DNA
41	17	30.4	89743	9	AC003062	AC003062 Mouse Chr
42	17	30.4	91481	9	AL645530	AL645530 Mouse DNA
43	17	30.4	96089	14	AC142524	AC142524 Rattus no
44	17	30.4	103846	14	AP007608	AP007608 Locust cor
45	17	30.4	110000	1	AB00516_28	AB00516_28 Continuation (29 of
46	17	30.4	110000	14	AC107099_1	AC107099_1 Continuation (2 of
47	17	30.4	110000	14	AC107099_3	AC107099_3 Continuation (4 of
48	17	30.4	110000	14	AC115573	AC115573 Continuation (4 of
49	17	30.4	110000	14	AC113637_2	AC113637_2 Continuation (3 of
50	17	30.4	110000	14	AC114431_0	AC114431_0 Continuation (7 of
51	17	30.4	110000	14	AC114431_6	AC114431_6 Continuation (3 of
52	17	30.4	110000	14	AC117038	AC117038 Rattus no
53	17	30.4	110000	14	AC127447_2	AC127447_2 Continuation (3 of
54	17	30.4	110702	8	BX664704	BX664704 Human DNA
55	17	30.4	120099	8	AC011449	AC011449 Homo sapi
56	17	30.4	127407	14	AC146863	AC146863 Medicago
57	17	30.4	129667	15	AC006629	AC006629 Arabidops
58	17	30.4	137914	14	AC166629	AC166629 Loxodonta
59	17	30.4	141159	14	AP000754	AP000754 Homo sapi
60	17	30.4	147412	9	AC079831	AC079831 Mus muscu
61	17	30.4	150543	14	AC148055	AC148055 Atelerix
62	17	30.4	151707	14	AC151630	AC151630 Didelphis
63	17	30.4	155079	14	AC015603	AC015603 Homo sapi
64	17	30.4	176054	9	AC122214	AC122214 Mus muscu
65	17	30.4	184044	9	AC008020	AC008020 Mus muscu
66	17	30.4	184391	8	AL592043	AL592043 Human DNA
67	17	30.4	184695	14	AL354719	AL354719 Homo sapi
68	17	30.4	191328	14	AC128745	AC128745 Rattus no
69	17	30.4	192177	14	AC141378	AC141378 Rattus no
70	17	30.4	192478	14	AC164657	AC164657 Pan trogl
71	17	30.4	194996	8	AC103858	AC103858 Homo sapi
72	17	30.4	195798	14	AC118890	AC118890 Rattus no
73	17	30.4	197714	14	AC128967	AC128967 Rattus no
74	17	30.4	197891	14	AC109837	AC109837 Rattus no
75	17	30.4	200337	8	AL590608	AL590608 Human DNA
76	17	30.4	200358	14	AC137450	AC137450 Rattus no
77	17	30.4	206315	9	AL806514	AL806514 Mouse DNA
78	17	30.4	207191	14	AC125202	AC125202 Mus muscu
79	17	30.4	215727	14	AL358795	AL358795 Homo sapi
80	17	30.4	215819	14	AC099288	AC099288 Rattus no
81	17	30.4	216129	14	AC097530	AC097530 Pan trogl
82	17	30.4	216330	14	AC098443	AC098443 Rattus no
83	17	30.4	216506	14	AC107127	AC107127 Rattus no
84	17	30.4	222589	14	AC113264	AC113264 Mus muscu
85	17	30.4	224138	9	AC133573	AC133573 Mus muscu
86	17	30.4	224886	14	AC156811	AC156811 Bos tauru
87	17	30.4	224922	14	AC106531	AC106531 Rattus no
88	17	30.4	225666	14	AC106531	AC106531 Rattus no
89	17	30.4	226356	14	AC106919	AC106919 Rattus no
90	17	30.4	227533	14	AC094895	AC094895 Rattus no
91	17	30.4	233565	14	AC094208	AC094208 Rattus no



C 92	17	30.4	235214	14	AC110403	Rattus no	165	16	28.6	869	1	CG1123968	AJ132968
C 93	17	30.4	235453	14	AC131525	Rattus no	166	16	28.6	905	10	BV505745	BV505745
C 94	17	30.4	238134	14	AC115520	Rattus no	167	16	28.6	880	8	CR456864	CR456864
C 95	17	30.4	239461	14	AC094508	Rattus no	168	16	28.6	921	1	ISTNCA	V00623
C 96	17	30.4	239781	14	AC106535	Rattus no	169	16	28.6	930	10	BV520853	BV520853
C 97	17	30.4	240675	14	AC106325	Rattus no	170	16	28.6	945	6	CS029939	CS029939
C 98	17	30.4	242877	14	AC094344	Rattus no	171	16	28.6	945	11	SYNBOCPX	M13493
C 99	17	30.4	243422	14	AC098453	Rattus no	172	16	28.6	974	6	ISTN52	I07552
C 100	17	30.4	245095	14	AC096172	Rattus no	173	16	28.6	1113	6	AO2739	I07552
C 101	17	30.4	250500	14	AC098524	Rattus no	174	16	28.6	1113	6	A14592	AO2739
C 102	17	30.4	253774	9	AC102062	Mus muscu	175	16	28.6	1142	1	ISTN93	A14592
C 103	17	30.4	257675	14	AC094136	Rattus no	176	16	28.6	1162	6	CS016660	V00622
C 104	17	30.4	262794	14	AC119702	Rattus no	177	16	28.6	1162	6	CS016704	CS016660
C 105	17	30.4	265613	14	AC120224	Rattus no	178	16	28.6	1188	6	CO895477	CS016704
C 106	17	30.4	276643	14	AC132782	Rattus no	179	16	28.6	1194	1	A3973195	CO895477
C 107	17	30.4	287702	14	AC119453	Rattus no	180	16	28.6	1221	6	AO2226	A02296
C 108	17	30.4	287702	14	AC119453	Rattus no	181	16	28.6	1221	6	A14593	AO2226
C 109	17	30.4	288710	14	AC119453	Rattus no	182	16	28.6	1247	6	AX060366	A14593
C 110	17	30.4	288813	14	AC153063	Bos tauru	183	16	28.6	1319	6	AY781404	AX060366
C 111	17	30.4	288813	14	AC153063	Bos tauru	184	16	28.6	1349	6	AX300702	AY781404
C 112	17	30.4	298982	14	AC111908	Rattus no	185	16	28.6	1351	11	AY781405	AX300702
C 113	17	30.4	303166	14	AC156978	Bos tauru	186	16	28.6	1392	11	EGSCAT	AY781405
C 114	17	30.4	306550	14	BX248342	Mycobacte	187	16	28.6	1507	11	AY150807	EGSCAT
C 115	17	30.4	342245	14	AC119559	Rattus no	188	16	28.6	1534	6	HLPRRX	AY150807
C 116	17	30.4	342245	14	AC119559	Rattus no	189	16	28.6	1535	6	A11244	HLPRRX
C 117	17	30.4	344682	14	AC096269	Rattus no	190	16	28.6	1542	6	A11241	A11244
C 118	17	30.4	345345	14	AC126167	Rattus no	191	16	28.6	1582	11	AY733065	A11241
C 119	17	30.4	346051	1	BX842580	Mycobacte	192	16	28.6	1626	6	AX364163	AY733065
C 120	17	30.4	346215	14	AC103046	Rattus no	193	16	28.6	1626	6	AX364196	AX364163
C 121	17	30.4	346215	14	AC103046	Rattus no	194	16	28.6	1642	11	AF061788	AX364196
C 122	16	28.6	40	6	AX685572	Sequence	195	16	28.6	1750	6	AR489288	AF061788
C 123	16	28.6	457	6	AR042385	Sequence	196	16	28.6	1774	11	AY822458	AR489288
C 124	16	28.6	133	4	RABPFM19	ML4474	197	16	28.6	1774	11	AY822459	AY822458
C 125	16	28.6	158	6	BD028835	Sequence	198	16	28.6	1774	11	AY822460	AY822459
C 126	16	28.6	158	6	AX893302	Sequence	199	16	28.6	1774	11	AY822461	AY822460
C 127	16	28.6	202	6	AR147341	Sequence	200	16	28.6	1795	11	SYNCCMR	AY822461
C 128	16	28.6	315	6	I07551	Sequence	201	16	28.6	1808	11	AY781408	SYNCCMR
C 129	16	28.6	457	6	AR042385	Sequence	202	16	28.6	1817	11	AY733066	AY781408
C 130	16	28.6	457	6	AR042385	Sequence	203	16	28.6	1822	11	AY733069	AY733066
C 131	16	28.6	457	6	AR153718	Sequence	204	16	28.6	1822	11	AY733069	AY733069
C 132	16	28.6	510	1	AY617066	AY617066	205	16	28.6	1824	6	AR635658	AY617066
C 133	16	28.6	510	1	I14155	Sequence	206	16	28.6	1825	6	AR042908	AR635658
C 134	16	28.6	561	6	AX634117	Sequence	207	16	28.6	1825	6	AR079857	AR042908
C 135	16	28.6	657	6	E05428	Part of seq	208	16	28.6	1846	6	AX703501	AR079857
C 136	16	28.6	658	6	AX348049	Sequence	209	16	28.6	1851	1	ACCTN670L	AX703501
C 137	16	28.6	658	6	AX353916	Sequence	210	16	28.6	1852	8	AB209788	ACCTN670L
C 138	16	28.6	660	6	CQ821302	Sequence	211	16	28.6	1866	6	AO2227	AB209788
C 139	16	28.6	660	6	E15555	Sequence	212	16	28.6	1866	6	AO2295	AO2227
C 140	16	28.6	660	6	E15555	CDNA encodi	213	16	28.6	1866	6	AO2740	AO2295
C 141	16	28.6	660	6	AR282862	Sequence	214	16	28.6	1866	6	A07053	AO2740
C 142	16	28.6	660	6	AX111414	Sequence	215	16	28.6	1866	6	A14594	A07053
C 143	16	28.6	663	6	BD181876	Alveolar	216	16	28.6	1874	1	ACCCACAA	A14594
C 144	16	28.6	663	6	E02706	Sequence	217	16	28.6	1883	6	CQ955895	ACCCACAA
C 145	16	28.6	663	6	I09322	Data sequence	218	16	28.6	1936	15	BT022112	CQ955895
C 146	16	28.6	708	10	BV503149	qkq24b05	219	16	28.6	1938	15	AK176493	BT022112
C 147	16	28.6	723	6	BD181874	Alveolar	220	16	28.6	1998	9	MMPF2RE5	AK176493
C 148	16	28.6	723	6	I07535	Sequence	221	16	28.6	2004	4	AP384053	MMPF2RE5
C 149	16	28.6	723	6	I09320	Sequence	222	16	28.6	2029	11	AY733067	AP384053
C 150	16	28.6	723	6	AR363731	Sequence	223	16	28.6	2031	1	PASPCAT	AY733067
C 151	16	28.6	741	6	AR178141	Sequence	224	16	28.6	2047	8	AK055060	PASPCAT
C 152	16	28.6	741	6	AR178142	Sequence	225	16	28.6	2082	8	CQ715628	AK055060
C 153	16	28.6	755	10	BV552762	Sequence	226	16	28.6	2101	6	CO894627	CQ715628
C 154	16	28.6	760	6	BD187669	Methods f	227	16	28.6	2101	6	CO894627	CO894627
C 155	16	28.6	760	6	BD187692	Methods f	228	16	28.6	2135	15	AK103764	CO894627
C 156	16	28.6	760	6	BD189721	Methods f	229	16	28.6	2147	8	HS2CHIA	AK103764
C 157	16	28.6	768	6	AR178143	Sequence	230	16	28.6	2167	8	HS2CHIA	HS2CHIA
C 158	16	28.6	768	6	AR387347	Sequence	231	16	28.6	2267	8	HSNCHIM	HS2CHIA
C 159	16	28.6	782	6	E09024	CDNA encodi	232	16	28.6	2267	8	HSNCHIM	HSNCHIM
C 160	16	28.6	801	10	BV033140	Sequence	233	16	28.6	2267	11	SYNPKF18C	HSNCHIM
C 161	16	28.6	803	6	BD181875	Alveolar	234	16	28.6	2267	11	SYNPKF398	SYNPKF18C
C 162	16	28.6	803	6	I09321	Sequence	235	16	28.6	2267	11	SYNPKF399	SYNPKF398
C 163	16	28.6	814	10	BV532754	Sequence	236	16	28.6	2227	11	SYNHS399	SYNPKF399
C 164	16	28.6	848	6	I07562	Sequence	237	16	28.6	2237	11	SYNPKF16C	SYNHS399



238	16	28.6	2237	11	SYNPKF17C	D29829 Cloning vec	311	16	28.6	3494	11	AF074376	AF074376 Cloning v
239	16	28.6	2237	11	SYNPKF396	D29824 Cloning vec	312	16	28.6	3499	11	AY028642	AY028642 Cloning v
240	16	28.6	2237	11	SYNPKF397	D29825 Cloning vec	313	16	28.6	3558	11	BD269483	BD269483 Stable re
241	16	28.6	2246	11	SYNPSBL	DI0670 Unidentifile	C 314	16	28.6	3558	6	AX035432	AX035432 Sequence
242	16	28.6	2315	8	BC011393	BC011393 Homo sapi	315	16	28.6	3564	11	SYNBJSC73	K01092 Plasmid clone
243	16	28.6	2319	11	PSU8	X53939 Plasmid vec	316	16	28.6	3564	11	SYNBJSC73V	L08920 pJSC73 pJON
244	16	28.6	2338	11	SYNSU2718	M64731 Cloning vec	317	16	28.6	3565	11	AY262832	AY262832 Expressio
245	16	28.6	2338	11	SYNSU2719A	M64732 Cloning vec	318	16	28.6	3575	11	AY386205	AY386205 Cloning v
246	16	28.6	2397	11	PSU237	X53937 Plasmid vec	319	16	28.6	3604	11	AF062078	AF062078 Cloning v
247	16	28.6	2408	11	ASTNMAX9	Z50123 Artificial	320	16	28.6	3604	11	AF083407	AF083407 Cloning v
248	16	28.6	2449	11	ASTNMAX10	Z50124 Artificial	C 321	16	28.6	3666	11	U66309	U66309 Expression
249	16	28.6	2504	6	A11245	A11245 vector pDSI	322	16	28.6	3715	2	AY128426	AY128426 Drosohphil
250	16	28.6	2535	11	AY822454	AY822454 Yeast exp	323	16	28.6	3776	11	AF544403	AF544403 Expressio
251	16	28.6	2535	11	AY822455	AY822455 Yeast exp	C 324	16	28.6	3788	11	SYNPMAC78V	L08931 pMAC7-8 clo
252	16	28.6	2535	11	AY822456	AY822456 Yeast exp	C 325	16	28.6	3801	6	AR493833	AR493833 Sequence
253	16	28.6	2535	11	AY822457	AY822457 Yeast exp	C 326	16	28.6	3803	6	A06419	A06419 Synthetic n
254	16	28.6	2566	11	SYNCCDBB	L38948 Cloning vec	C 327	16	28.6	3803	6	A10238	A10238 Synthetic D
255	16	28.6	2566	11	SYNCCDBB	L38949 Cloning vec	C 328	16	28.6	3803	6	A21892	A21892 Nucleotide
256	16	28.6	2594	6	AX364327	AX364327 Sequence	C 329	16	28.6	3803	11	SYNPMAC58V	L08930 pMAC5-8 clo
257	16	28.6	2655	11	AY222813	AY222813 Cloning v	330	16	28.6	3833	6	A10359	A10359 Artificial
258	16	28.6	2684	11	AY523576	AY523576 Expressio	331	16	28.6	3840	2	DMDNAME12	X89241 D.melanog
259	16	28.6	2701	11	AF060240	AF060240 Mobile an	332	16	28.6	3843	11	EVE507406	AJ507406 Expressio
260	16	28.6	2738	5	BC077483	BC077483 Xenopus 1	333	16	28.6	3851	11	AY597271	AY597271 Chloramph
261	16	28.6	2758	6	C0578286	C0578286 Sequence	334	16	28.6	3876	6	AX035988	AX035988 Sequence
262	16	28.6	2801	11	AY952934	AY952934 Cloning v	335	16	28.6	3876	6	AX035989	AX035989 Sequence
263	16	28.6	2804	11	AY048742	AY048742 Template	336	16	28.6	3879	6	AX035966	AX035966 Sequence
264	16	28.6	2839	11	AY222812	AY222812 Cloning v	337	16	28.6	3879	6	AX035967	AX035967 Sequence
265	16	28.6	2863	11	AY576605	AY576605 Brucella	338	16	28.6	3879	6	AX035968	AX035968 Sequence
266	16	28.6	2885	11	ASTNMAX6	Z50121 Artificial	339	16	28.6	3879	6	AX035982	AX035982 Sequence
267	16	28.6	2933	15	AY781400	AY781400 Synthetic	340	16	28.6	3879	6	AX035985	AX035985 Sequence
268	16	28.6	3032	15	AK066132	AK066132 Oryza sat	341	16	28.6	3879	6	AX035987	AX035987 Sequence
269	16	28.6	3064	11	AB019609	AB019609 Cloning v	342	16	28.6	3881	6	BD270597	BD270597 Method fo
270	16	28.6	3064	11	AB019610	AB019610 Cloning v	343	16	28.6	3881	6	AR649152	AR649152 Sequence
271	16	28.6	3064	11	AB019611	AB019611 Cloning v	344	16	28.6	3885	6	AX035964	AX035964 Sequence
272	16	28.6	3064	11	AB019612	AB019612 Cloning v	345	16	28.6	3888	6	BD269485	BD269485 Stable re
273	16	28.6	3064	11	AB019613	AB019613 Cloning v	346	16	28.6	3888	6	AX035434	AX035434 Sequence
274	16	28.6	3064	11	AB019614	AB019614 Cloning v	347	16	28.6	3888	6	AX352676	AX352676 Sequence
275	16	28.6	3176	1	TN21TNPA	X04891 Transposon	348	16	28.6	3888	6	AX362234	AX362234 Sequence
276	16	28.6	3178	6	CQ963625	CQ963625 Sequence	349	16	28.6	3897	6	AX035981	AX035981 Sequence
277	16	28.6	3181	6	CQ963626	CQ963626 Sequence	350	16	28.6	3900	6	AX035970	AX035970 Sequence
278	16	28.6	3200	11	AB001897	AB001897 Cloning v	351	16	28.6	3910	2	DMLETHAL2	Z48443 D.melanog
279	16	28.6	3210	11	AF361440	AF361440 Cloning v	352	16	28.6	3912	6	AX035969	AX035969 Sequence
280	16	28.6	3225	6	AR300363	AR300363 Sequence	353	16	28.6	3912	6	AX035978	AX035978 Sequence
281	16	28.6	3225	6	AX079026	AX079026 Sequence	C 354	16	28.6	3914	11	AY584600	AY584600 Expressio
282	16	28.6	3245	6	I84556	I84556 Sequence 4	355	16	28.6	3919	2	DROWSL2G	L42553 Drosohphila
283	16	28.6	3283	11	AY219690	AY219690 Shuttle v	356	16	28.6	3919	6	AX035979	AX035979 Sequence
284	16	28.6	3345	11	XXU35235	U35235 Plasmid pBS	357	16	28.6	3927	6	AX035977	AX035977 Sequence
285	16	28.6	3357	11	XXU35132	U35132 Plasmid pBS	358	16	28.6	3927	6	AX035983	AX035983 Sequence
286	16	28.6	3369	1	AY515701	AY515701 Achromoba	359	16	28.6	3927	6	AX035984	AX035984 Sequence
287	16	28.6	3399	11	CVU46018	U46018 Cloning vec	C 360	16	28.6	3930	11	AB001326	AB001326 Cloning v
288	16	28.6	3400	6	AR477289	AR477289 Sequence	361	16	28.6	3932	6	AX035975	AX035975 Sequence
289	16	28.6	3403	6	A02228	A02228 Plasmid pDS	362	16	28.6	3936	6	AX035974	AX035974 Sequence
290	16	28.6	3416	6	A02230	A02230 Plasmid pDS	363	16	28.6	3946	6	CS071214	CS071214 Sequence
291	16	28.6	3416	6	A19609	A19609 Artificial	C 364	16	28.6	3946	6	CS071214	CS071214 Sequence
292	16	28.6	3416	6	A30440	A30440 Plasmid pDS	365	16	28.6	3957	6	AX035985	AX035985 Sequence
293	16	28.6	3416	6	A30442	A30442 Plasmid pDS	366	16	28.6	3975	6	BD270596	BD270596 Method fo
294	16	28.6	3417	11	AF153422	AF153422 Cloning v	367	16	28.6	3975	6	AR649151	AR649151 Sequence
295	16	28.6	3420	6	AX035962	AX035962 Sequence	368	16	28.6	3977	6	A18756	A18756 Tumour necr
296	16	28.6	3420	6	AX035963	AX035963 Sequence	369	16	28.6	3977	6	A39903	A39903 Sequence 1
297	16	28.6	3420	6	AX082905	AX082905 Sequence	370	16	28.6	3977	6	A78780	A78780 Sequence 1
298	16	28.6	3420	6	AX146692	AX146692 Sequence	371	16	28.6	3977	6	I12243	I12243 Sequence 2
299	16	28.6	3427	6	A30446	A30446 Plasmid pDS	372	16	28.6	3977	6	I12244	I12244 Sequence 13
300	16	28.6	3431	6	AX818055	AX818055 Sequence	373	16	28.6	3977	6	I17237	I17237 Sequence 1
301	16	28.6	3433	6	CQ973730	CQ973730 Sequence	374	16	28.6	3977	6	I34461	I34461 Sequence 1
302	16	28.6	3440	6	A30444	A30444 Plasmid pDS	375	16	28.6	3977	6	I58765	I58765 Sequence 2
303	16	28.6	3462	6	AR317284	AR317284 Sequence	376	16	28.6	3977	6	I58766	I58766 Sequence 13
304	16	28.6	3462	6	AX133356	AX133356 Sequence	377	16	28.6	3989	6	AX035976	AX035976 Sequence
305	16	28.6	3462	6	AX377527	AX377527 Sequence	378	16	28.6	3999	6	E36264	E36264 Human Gemap
306	16	28.6	3462	6	BD016294	BD016294 Human pro	379	16	28.6	3999	6	AX001328	AX001328 Sequence
307	16	28.6	3474	11	AY327140	AY327140 Expressio	380	16	28.6	4003	6	A30448	A30448 Plasmid pDS
308	16	28.6	3475	11	D88215	D88215 Cloning vec	381	16	28.6	4004	6	A30450	A30450 Plasmid pDH
309	16	28.6	3485	11	AF178449	AF178449 Integrati	C 382	16	28.6	4005	6	A23997	A23997 pMAC5-19 ex
310	16	28.6	3485	11	AF178450	AF178450 Integrati	C 383	16	28.6	4019	6	E36263	E36263 Human Gemap



384	16	28.6	4019	6	AX001327	AX001327 Sequence	C 457	16	28.6	4721	6	AX352678	AX352678 Sequence
385	16	28.6	4027	11	RVU57024	U57024 Reporter ve	C 458	16	28.6	4721	6	AX362236	AX362236 Sequence
386	16	28.6	4041	6	A10360	A10360 Artificial	C 459	16	28.6	4752	11	CVPCATCON	X65319 Cloning vec
387	16	28.6	4045	6	ARS59888	ARS59888 Sequence	C 460	16	28.6	4753	11	AF129432	AF129432 Cloning v
388	16	28.6	4051	6	AX078902	AX078902 Sequence	C 461	16	28.6	4755	6	AR240212	AR240212 Sequence
C 389	16	28.6	4051	11	XXU35126	U35126 Plasmid PBS	C 462	16	28.6	4755	6	AX347591	AX347591 Sequence
C 390	16	28.6	4055	6	AR339215	AR339215 Sequence	C 463	16	28.6	4765	6	CQ826738	CQ826738 Sequence
C 391	16	28.6	4055	6	AR339215	AR339215 Sequence	C 464	16	28.6	4765	6	CQ826740	CQ826740 Sequence
C 392	16	28.6	4060	11	XXU1846	U3846 pcm7 clonin	C 465	16	28.6	4803	6	AY243506	AY243506 Cloning v
C 393	16	28.6	4062	14	AC091011	AC091011 Homo sapi	C 466	16	28.6	4810	6	CQ578285	CQ578285 Sequence
C 394	16	28.6	4068	6	A00781	A00781 Plasmid pBS	C 467	16	28.6	4827	14	AC135911	AC135911 Homo sapi
C 395	16	28.6	4068	6	A02229	A02229 Plasmid pBS	C 468	16	28.6	4842	11	XXU35125	AY242863 Cloning v
C 396	16	28.6	4068	6	A19607	A19607 Artificial	C 469	16	28.6	4892	11	AY423863	AY423863 Cloning v
C 397	16	28.6	4100	6	CS119871	CS119871 Sequence	C 470	16	28.6	4907	11	SYNBR328V	AY584602 Rpl23-fus
C 398	16	28.6	4144	11	XXU35131	U35131 Plasmid PBS	C 471	16	28.6	4934	11	AY584602	AY584602 Rpl23-fus
C 399	16	28.6	4150	11	SYNBR329	U01753 Plasmid pBR	C 472	16	28.6	4938	6	AX594148	AX594148 Sequence
C 400	16	28.6	4151	11	SYNBR329V	L08855 pBR329 clon	C 473	16	28.6	4939	6	BD263387	BD263387 Sequence
C 401	16	28.6	4152	11	AY219693	AY219693 Shuttle v	C 474	16	28.6	4968	11	AY219687	AY219687 Expression
C 402	16	28.6	4154	11	CVB403982	AY403982 Cloning v	C 475	16	28.6	5003	11	SYNPSV2CAT	M77788 pSV2-Cat c1
C 403	16	28.6	4165	6	BD263380	BD263380 Compositi	C 476	16	28.6	5024	6	CQ846977	CQ846977 Sequence
C 404	16	28.6	4174	11	AF074852	AF074852 Synthetic	C 477	16	28.6	5026	11	DO075935	DO075935 Expression
C 405	16	28.6	4204	6	BD263378	BD263378 Compositi	C 478	16	28.6	5064	6	AX035972	AX035972 Sequence
C 406	16	28.6	4208	6	BD263379	BD263379 Compositi	C 479	16	28.6	5071	11	PKSM710	U04883 Cloning vec
C 407	16	28.6	4219	11	RVU57027	U57027 Reporter ve	C 480	16	28.6	5090	11	AY902486	AY902486 Expression
C 408	16	28.6	4228	11	BPL313516	APJ13516 Expression	C 481	16	28.6	5094	11	XXU13859	U13859 PKC32-8 c1
C 409	16	28.6	4245	6	AR069365	AR069365 Sequence	C 482	16	28.6	5109	6	CS072923	CS072923 Sequence
C 410	16	28.6	4245	11	PACYC184	X06403 Cloning vec	C 483	16	28.6	5135	11	SVE133193	AF133193 Shuttle v
C 411	16	28.6	4252	11	AY423865	AY423865 Cloning v	C 484	16	28.6	5148	6	AX306527	AX306527 Sequence
C 412	16	28.6	4252	11	XXU35133	U51313 Plasmid pBS	C 485	16	28.6	5156	6	BD263382	BD263382 Compositi
C 413	16	28.6	4256	11	SYNCA1BLA	M80484 Cloning vec	C 486	16	28.6	5157	11	AY902485	AY902485 Expression
C 414	16	28.6	4273	11	RVU57026	U57026 Reporter ve	C 487	16	28.6	5157	11	AY952933	AY952933 Cloning v
C 415	16	28.6	4291	11	ABCVP	X99398 Artificial	C 488	16	28.6	5178	6	CQ759171	CQ759171 Sequence
C 416	16	28.6	4297	11	AY219685	AY219685 Expressio	C 489	16	28.6	5201	6	AR493834	AR493835 Sequence
C 417	16	28.6	4311	6	AX244155	AX244155 Sequence	C 490	16	28.6	5201	6	AR493835	AR493835 Shuttle v
C 418	16	28.6	4313	11	CVPCATBAS	X65322 Cloning vec	C 491	16	28.6	5223	11	AY827555	AB052891 Cloning v
C 419	16	28.6	4334	11	AF074853	AF074853 Synthetic	C 492	16	28.6	5240	11	AB052891	AB052891 Cloning v
C 420	16	28.6	4343	6	BD269484	BD269484 Stable re	C 493	16	28.6	5241	6	A49695	A49695 Sequence 1
C 421	16	28.6	4343	6	AX035433	AX035433 Sequence	C 494	16	28.6	5241	6	A49696	A49696 Sequence 2
C 422	16	28.6	4344	11	BLCAT3DNA	X64409 Plasmid pBL	C 495	16	28.6	5241	6	A77043	A77043 Sequence 1
C 423	16	28.6	4354	11	STNPMAMA	M36637 Artificial	C 496	16	28.6	5241	6	A77044	A77044 Sequence 2
C 424	16	28.6	4376	6	AX035971	AX035971 Sequence	C 497	16	28.6	5241	6	AR282755	AR282755 Sequence
C 425	16	28.6	4376	11	SFU81140	U81140 Shigella fl	C 498	16	28.6	5241	6	AR282756	AR282756 Sequence
C 426	16	28.6	4377	11	CVCATLIC	U25271 Ligatcion-in	C 499	16	28.6	5262	6	AR126256	AR126256 Sequence
C 427	16	28.6	4380	6	AX035973	AX035973 Sequence	C 500	16	28.6	5262	11	CVU65077	U65077 Promoter-pr
C 428	16	28.6	4398	11	AR061929	AR061929 Plasmoson	C 501	16	28.6	5273	11	EVU51556	U51556 Expression
C 429	16	28.6	4401	11	STNCA1BLB	M80483 Cloning vec	C 502	16	28.6	5281	11	SCU2104	U2104 Cloning vec
C 430	16	28.6	4411	6	AR069366	AR069366 Sequence	C 503	16	28.6	5286	11	AY489048	AY489048 Cloning v
C 431	16	28.6	4423	11	AVE401047	AJ401047 Artificial	C 504	16	28.6	5300	11	ECPBHR1	Y14439 Becherichia
C 432	16	28.6	4441	11	AP258339	AP258339 Expressio	C 505	16	28.6	5321	6	CS060991	CS060991 Sequence
C 433	16	28.6	4442	11	AY584601	AY584601 Rpl23-fus	C 506	16	28.6	5324	11	AY584597	AY584597 Rpl23-fus
C 434	16	28.6	4454	11	AY170009	AY170009 Cloning v	C 507	16	28.6	5376	6	A00783	A00783 Plasmid pB/
C 435	16	28.6	4462	11	VFO551314	AJ551314 Transfect	C 508	16	28.6	5376	6	A00784	A00784 Plasmid pB/
C 436	16	28.6	4465	11	RVU57025	U57025 Reporter ve	C 509	16	28.6	5406	11	ECOT7660	AJ007660 Cloning v
C 437	16	28.6	4470	6	BD263377	BD263377 Compositi	C 510	16	28.6	5424	11	AY818379	AY818379 Gateway d
C 438	16	28.6	4484	11	UCU89964	U89964 Cloning vec	C 511	16	28.6	5443	11	AY796342	AY796342 Cloning v
C 439	16	28.6	4484	6	AX082906	AX082906 Sequence	C 512	16	28.6	5498	6	BD270602	BD270602 Method fo
C 440	16	28.6	4491	6	AR240211	AR240211 Sequence	C 513	16	28.6	5498	6	ARE49157	ARE49157 Sequence
C 441	16	28.6	4491	6	AX347580	AX347580 Sequence	C 514	16	28.6	5498	11	AY222821	AY222821 Shuttle v
C 442	16	28.6	4496	11	BLCAT8DNA	X64410 Plasmid pBL	C 515	16	28.6	5517	6	AX352679	AX352679 Sequence
C 443	16	28.6	4499	11	EVB243877	AJ243877 Expressio	C 516	16	28.6	5517	6	AX362237	AX362237 Sequence
C 444	16	28.6	4500	6	AX352677	AX352677 Sequence	C 517	16	28.6	5525	6	BD270599	BD270599 Method fo
C 445	16	28.6	4500	6	AX362235	AX362235 Sequence	C 518	16	28.6	5525	6	ARE49154	ARE49154 Sequence
C 446	16	28.6	4506	6	CVPCATPRO	X65320 Cloning vec	C 519	16	28.6	5528	6	BD270603	BD270603 Method fo
C 447	16	28.6	4554	6	BD263394	BD263394 Compositi	C 520	16	28.6	5528	6	ARE49158	ARE49158 Sequence
C 448	16	28.6	4559	11	CVPCATENH	X65319 Cloning vec	C 521	16	28.6	5534	11	AF361302	AF361302 Cloning v
C 449	16	28.6	4570	11	AY327141	M23363 Plasmid pFL	C 522	16	28.6	5555	6	BD270598	BD270598 Method fo
C 450	16	28.6	4589	11	SYN261CAT	M23363 Plasmid pFL	C 523	16	28.6	5555	6	ARE49153	ARE49153 Sequence
C 451	16	28.6	4590	11	AY584598	AY584598 Rpl23-fus	C 524	16	28.6	5557	6	BD270600	BD270600 Method fo
C 452	16	28.6	4658	11	AY584599	AY584599 Rpl23-fus	C 525	16	28.6	5557	6	ARE49155	ARE49155 Sequence
C 453	16	28.6	4676	11	AF061918	AF061918 Plasmoson	C 526	16	28.6	5558	6	CQ794769	CQ794769 Sequence
C 454	16	28.6	4676	11	AF061919	AF061919 Plasmoson	C 527	16	28.6	5563	6	CS135707	CS135707 Sequence
C 455	16	28.6	4707	11	XXU02374	U02374 Cloning vec	C 528	16	28.6	5584	6	BD263402	BD263402 Compositi
C 456	16	28.6	4716	6	AX742856	AX742856 Sequence	C 529	16	28.6	5587	6	CS135706	CS135706 Sequence



530	16	28.6	5593	11	AF519766	AF519766 Cloning v	c	603	16	28.6	6640	11	AF110459	AF110459 Cloning v
531	16	28.6	5611	6	BD270601	BD270601 Method fo	c	604	16	28.6	6652	6	BD263373	BD263373 Compositi
532	16	28.6	5611	6	AR649156	AR649156 Sequence	c	605	16	28.6	6658	6	BD263367	BD263367 Compositi
533	16	28.6	5635	11	ASVPSKAN8	X84307 Artificial	c	606	16	28.6	6675	6	BD263364	BD263364 Compositi
534	16	28.6	5641	6	AR629176	AR629176 Sequence	c	607	16	28.6	6686	11	EV081999	U81999 Expression
535	16	28.6	5641	6	AX113748	AX113748 Sequence	c	608	16	28.6	6708	6	BD263358	BD263358 Compositi
536	16	28.6	5670	6	AR629177	AR629177 Sequence	c	609	16	28.6	6716	11	AY995139	AY995139 Cloning v
537	16	28.6	5670	6	AX113749	AX113749 Sequence	c	610	16	28.6	6716	11	AY995140	AY995140 Cloning v
538	16	28.6	5677	6	A21895	A21895 Nucleotide	c	611	16	28.6	6758	11	AF121784	AF121784 Expressio
539	16	28.6	5699	6	AX352680	AX352680 Sequence	c	612	16	28.6	6781	11	AY995136	AY995136 Cloning v
540	16	28.6	5699	6	AX362238	AX362238 Sequence	c	613	16	28.6	6781	11	AY995138	AY995138 Cloning v
541	16	28.6	5777	6	CQ974070	CQ974070 Sequence	c	614	16	28.6	6823	6	BD263351	BD263351 Compositi
542	16	28.6	5793	6	CS072929	CS072929 Sequence	c	615	16	28.6	6900	11	AY643800	AY643800 Large-ins
543	16	28.6	5825	6	AR629174	AR629174 Sequence	c	616	16	28.6	6941	11	CVU51114	US1114 Cloning vec
544	16	28.6	5825	6	AX113745	AX113745 Sequence	c	617	16	28.6	6949	11	AB095955	AB095955 Cloning v
545	16	28.6	5838	6	AR072535	AR072535 Sequence	c	618	16	28.6	6949	11	AB095956	AB095956 Cloning v
546	16	28.6	5838	6	AR079410	AR079410 Sequence	c	619	16	28.6	6956	11	AY219682	AY219682 Shuttle e
547	16	28.6	5848	6	BD064199	BD064199 System fo	c	620	16	28.6	6961	6	BD263372	BD263372 Compositi
548	16	28.6	5848	6	BD263361	BD263361 Sequence	c	621	16	28.6	6964	6	BD263352	BD263352 Compositi
549	16	28.6	5874	11	AY737006	AY737006 Cloning v	c	622	16	28.6	6971	6	BD131875	BD131875 Novel met
550	16	28.6	5957	6	BD263353	BD263353 Compositi	c	623	16	28.6	6971	6	AR439946	AR439946 Sequence
551	16	28.6	5957	6	BD263354	BD263354 Compositi	c	624	16	28.6	6971	6	AX006030	AX006030 Sequence
552	16	28.6	5986	6	AX377528	AX377528 Sequence	c	625	16	28.6	6978	11	AY451994	AY451994 BAC cloni
553	16	28.6	5996	11	SYNBR325V	L08855 PBR325 clon	c	626	16	28.6	6981	11	AY423864	AY423864 Cloning v
554	16	28.6	6015	11	SYNCAITLAC	L25311 Cloning vec	c	627	16	28.6	7013	6	BD263363	BD263363 Compositi
555	16	28.6	6023	11	AF102577	AF102577 Cloning v	c	628	16	28.6	7026	6	BD263359	BD263359 Compositi
556	16	28.6	6025	6	BD263355	BD263355 Compositi	c	629	16	28.6	7027	11	CVU10457	U10457 Binary clon
557	16	28.6	6043	6	AR399301	AR399301 Sequence	c	630	16	28.6	7027	11	CVU10486	U10486 Binary clon
558	16	28.6	6043	6	AX370644	AX370644 Sequence	c	631	16	28.6	7055	6	BD131874	BD131874 Novel met
559	16	28.6	6060	11	AF061927	AF061927 Plaspodon	c	632	16	28.6	7055	6	AR439945	AR439945 Sequence
560	16	28.6	6060	11	AF061928	AF061928 Plaspodon	c	633	16	28.6	7055	6	AX006017	AX006017 Sequence
561	16	28.6	6071	6	AR629175	AR629175 Sequence	c	634	16	28.6	7066	6	BD263368	BD263368 Compositi
562	16	28.6	6071	6	AX113747	AX113747 Sequence	c	635	16	28.6	7114	6	BD263401	BD263401 Compositi
563	16	28.6	6078	11	AY737004	AY737004 Cloning v	c	636	16	28.6	7141	6	BD263395	BD263395 Compositi
564	16	28.6	6096	6	B01216	B01216 Genomic DNA	c	637	16	28.6	7144	11	AF108217	AF108217 Cloning v
565	16	28.6	6101	11	SIN41788	AX554413 Sequence	c	638	16	28.6	7151	11	AY042185	AY042185 Cloning v
566	16	28.6	6122	6	AX554413	AX554413 Sequence	c	639	16	28.6	7156	6	BD263396	BD263396 Compositi
567	16	28.6	6122	6	AX554422	AX554422 Sequence	c	640	16	28.6	7224	11	SYNMACG14	L08932 pMAC5-bp14
568	16	28.6	6122	6	AX642149	AX642149 Sequence	c	641	16	28.6	7232	11	AF179893	AF179893 Cloning v
569	16	28.6	6123	11	SIN417449	AX554420 Sequence	c	642	16	28.6	7236	11	EV082000	U82000 Expression
570	16	28.6	6125	6	AX554420	AX554420 Sequence	c	643	16	28.6	7278	6	BD263360	BD263360 Compositi
571	16	28.6	6166	11	PPA05339	U75332 Cloning vec	c	644	16	28.6	7286	6	XXU13206	U13306 Cloning vec
572	16	28.6	6227	11	CVU75332	U23732 Cloning vec	c	645	16	28.6	7313	14	AC069583	AR364483 Sequence
573	16	28.6	6241	11	AP092036	U42372 Cloning vec	c	646	16	28.6	7326	6	AR364483	AR364483 Sequence
574	16	28.6	6243	11	XXU42372	AY81837 Gateway d	c	647	16	28.6	7336	6	A05160	A05160 Nucleotide
575	16	28.6	6252	11	AY818372	BD263371 Compositi	c	648	16	28.6	7336	6	A08030	A08030 Synthetic n
576	16	28.6	6264	6	BD263371	AY818370 Gateway d	c	649	16	28.6	7336	6	A13198	A13198 complete pl
577	16	28.6	6288	11	AY818370	U42373 Cloning vec	c	650	16	28.6	7336	6	A20502	A20502 Hind III fr
578	16	28.6	6289	11	XXU42373	AX005323 PCPI(-) K	c	651	16	28.6	7336	6	AR033984	AR033984 Sequence
579	16	28.6	6340	11	ASAF5323	AX005323 PCPI(-) S	c	652	16	28.6	7336	6	AR123993	AR123993 Sequence
580	16	28.6	6340	11	ASAF5324	L05081 Cloning vec	c	653	16	28.6	7336	6	AR154323	AR154323 Sequence
581	16	28.6	6347	11	SYNPRLA	BD263365 Compositi	c	654	16	28.6	7336	6	AR408644	AR408644 Sequence
582	16	28.6	6354	6	BD263365	BD263365 Compositi	c	655	16	28.6	7340	11	AF286455	AF286455 Promoter
583	16	28.6	6363	6	AR069367	AY661563 Arabidena	c	656	16	28.6	7343	11	AF286456	AF286456 Promoter
584	16	28.6	6389	11	AY661563	BD263362 Compositi	c	657	16	28.6	7366	11	DQ086480	DQ086480 Integrati
585	16	28.6	6422	6	BD263362	Y15337 Sheep astro	c	658	16	28.6	7382	11	AF286457	AF286457 Promoter
586	16	28.6	6440	13	SACAPSID	AF2884421 Synthetic	c	659	16	28.6	7382	11	AF286459	AF286459 Promoter
587	16	28.6	6447	11	AF288421	AF2884421 Synthetic	c	660	16	28.6	7382	11	AF286461	AF286461 Promoter
588	16	28.6	6464	11	AY608912	AF2884421 Synthetic	c	661	16	28.6	7385	11	AF286458	AF286458 Promoter
589	16	28.6	6464	6	BD263349	U46126 Saccharomyc	c	662	16	28.6	7385	11	AF286460	AF286460 Promoter
590	16	28.6	6494	11	XXU46126	AY955141 Cloning v	c	663	16	28.6	7385	11	AF286462	AF286462 Promoter
591	16	28.6	6500	11	AY955141	AR349929 Sequence	c	664	16	28.6	7405	8	AC105380	AC105380 Homo sapi
592	16	28.6	6501	6	AR349929	AR349930 Sequence	c	665	16	28.6	7413	11	AY842153	AY842153 Synthetic
593	16	28.6	6501	6	AR349930	AX594150 Sequence	c	666	16	28.6	7413	11	AY842153	AY842153 Synthetic
594	16	28.6	6525	6	AX594150	BD263356 Compositi	c	667	16	28.6	7481	6	AX594151	AX594151 Sequence
595	16	28.6	6526	6	BD263356	BD263356 Compositi	c	668	16	28.6	7487	6	AX594151	AX594151 Sequence
596	16	28.6	6553	6	BD263350	AB183146 Integrati	c	669	16	28.6	7507	11	CVU51113	US1113 Cloning vec
597	16	28.6	6555	11	AB183146	AY955137 Cloning v	c	670	16	28.6	7509	11	AJ885178	AJ885178 Shuttle p
598	16	28.6	6565	11	AY955137	AJ1313195 Shuttle v	c	671	16	28.6	7544	6	BD263397	BD263397 Cloning v
599	16	28.6	6601	11	SVR133195	BD263366 Compositi	c	672	16	28.6	7553	11	AY928469	AY928469 Compositi
600	16	28.6	6601	6	BD263366	Z50120 Artificial	c	673	16	28.6	7559	6	BD263398	BD263398 Compositi
601	16	28.6	6614	11	ASTNMAYS	U10456 Binary clon	c	674	16	28.6	7564	11	AB015619	AB015619 Cloning v
602	16	28.6	6636	11	CVU10456		c	675	16	28.6	7566	6	A24783	A24783 plasmid pps



676	16	28.6	7566	6	AR074388	AR074388 Sequence	c 749	16	28.6	9737	6	AR568594	AR568594 Sequence
c 678	16	28.6	7620	1	RC0277653	AR277653 Escherich	c 750	16	28.6	9737	6	AR568599	AR568599 Sequence
679	16	28.6	7639	6	A24782	A27782 Plasmid pUD	c 751	16	28.6	9737	6	AR568614	AR568614 Sequence
c 680	16	28.6	7697	14	AC131589	AR074387 Sequence	c 752	16	28.6	9737	6	AR568620	AR568620 Sequence
681	16	28.6	7775	11	AF464139	AC131589 Homo sapi	c 753	16	28.6	9737	6	AR568625	AR568625 Sequence
682	16	28.6	7783	6	BD131871	AF464139 Filamento	c 754	16	28.6	9871	6	AR215120	AR215120 Sequence
683	16	28.6	7783	6	AR433942	BD131871 Novel met	c 755	16	28.6	9871	6	AR302362	AR302362 Sequence
684	16	28.6	7783	6	AX006002	AR433942 Sequence	c 756	16	28.6	9871	6	AR373234	AR373234 Sequence
c 685	16	28.6	7801	6	E03388	AX006002 Sequence	c 757	16	28.6	9871	6	AR401620	AR401620 Sequence
686	16	28.6	7811	6	AR078675	E03388 Xylose isom	c 758	16	28.6	9871	6	AR442953	AR442953 Sequence
687	16	28.6	7814	6	AX554978	AR078675 Sequence	c 759	16	28.6	9871	6	AR568595	AR568595 Sequence
688	16	28.6	7830	11	AY428809	AX554978 Sequence	c 760	16	28.6	9871	6	AR568616	AR568616 Sequence
c 689	16	28.6	7964	11	AB070708	AY428809 Cloning v	c 761	16	28.6	9905	6	CS079704	CS079704 Sequence
690	16	28.6	8097	11	SCU46780	AB070708 Cloning v	c 762	16	28.6	9905	6	CS079705	CS079705 Sequence
691	16	28.6	8123	6	BD263375	U66780 Synthetic c	c 763	16	28.6	10060	6	AR215121	AR215121 Sequence
c 692	16	28.6	8201	11	CVE278228	BD263375 Compositi	c 764	16	28.6	10060	6	AR302363	AR302363 Sequence
693	16	28.6	8247	11	AY737284	A278278 Cloning v	c 765	16	28.6	10060	6	AR373235	AR373235 Sequence
c 694	16	28.6	8296	11	EVU82001	AY737284 Cloning v	c 766	16	28.6	10060	6	AR401621	AR401621 Sequence
695	16	28.6	8405	11	XXU13861	U82001 Expressio	c 767	16	28.6	10060	6	AR442954	AR442954 Sequence
696	16	28.6	8408	6	CO859238	U13861 PMSG-CAT c1	c 768	16	28.6	10060	6	AR568596	AR568596 Sequence
697	16	28.6	8408	6	CO873569	CO859238 Sequence	c 769	16	28.6	10060	6	AR568617	AR568617 Sequence
698	16	28.6	8416	11	AF403427	CO873569 Sequence	c 770	16	28.6	10295	11	AJ868288	AJ868288 Transcon
c 699	16	28.6	8500	6	BD105249	AF403427 Cloning v	c 771	16	28.6	10429	6	CS079700	CS079700 Sequence
700	16	28.6	8520	14	AC115095	BD105249 A process	c 772	16	28.6	10429	6	CS079706	CS079706 Sequence
c 701	16	28.6	8530	11	AY289598	AC115095 Homo sapi	c 773	16	28.6	10580	6	A27169	A27169 Artificial
702	16	28.6	8547	6	CS072825	AY289598 Cloning v	c 774	16	28.6	10580	6	I45935	I45935 Sequence
c 703	16	28.6	8621	6	AX085883	CS072825 Sequence	c 775	16	28.6	10580	6	AY553053	AY553053 Reporter
c 704	16	28.6	8626	11	CVU10459	AX085883 Sequence	c 776	16	28.6	10907	11	AY310333	AY310333 Cloning v
c 705	16	28.6	8626	11	CVU10488	U10459 Binary clon	c 777	16	28.6	11000	15	AF286114	AF286114 Broomhac
706	16	28.6	8774	11	AY386222	U10488 Binary clon	c 778	16	28.6	11005	11	AY196824	AY196824 Piggybac
c 707	16	28.6	8774	11	IYU69267	AY386222 Cloning v	c 779	16	28.6	11241	6	AX548647	AX548647 Sequence
708	16	28.6	8815	6	BD263400	U69267 Integratio	c 780	16	28.6	11241	11	AY180162	AY180162 Shuttle v
c 709	16	28.6	8850	11	AF403425	BD263400 Compositi	c 781	16	28.6	11378	11	AF234294	AF234294 Binary ve
c 710	16	28.6	8894	11	AF234313	AF403425 Cloning v	c 782	16	28.6	11378	11	AF234295	AF234295 Binary ve
c 711	16	28.6	8909	11	CVU10458	AF234313 Binary ve	c 783	16	28.6	11457	14	AC119286	AC119286 Homo sapi
c 712	16	28.6	8909	11	CVU10487	U10458 Binary clon	c 784	16	28.6	11612	11	CVU80929	CVU80929 Compositi
713	16	28.6	8923	6	BD263370	U10487 Binary clon	c 785	16	28.6	11713	6	BD263369	BD263369 Cloning v
c 714	16	28.6	9019	11	AR408413	BD263370 Compositi	c 786	16	28.6	11785	11	AF234314	AF234314 Binary ve
c 715	16	28.6	9019	11	AR408413	AR408413 Binary ve	c 787	16	28.6	11827	11	SVS509853	SVS509853 Cloning v
c 716	16	28.6	9065	11	AF405698	AR408413 Binary ve	c 788	16	28.6	11918	11	CVU72488	CVU72488 Shuttle v
717	16	28.6	9071	11	AB057644	AF405698 Reporte	c 789	16	28.6	11925	11	AY303237	AY303237 Binary ve
c 718	16	28.6	9077	11	AY292466	AB057644 Shuttle v	c 790	16	28.6	12001	11	AF234293	AF234293 Binary ve
c 719	16	28.6	9110	11	AF234292	AY292466 BAC clon	c 791	16	28.6	12168	11	AF405696	AF405696 Reporter
720	16	28.6	9113	11	CYPCG1408	AF234292 Binary ve	c 792	16	28.6	12248	11	AF405697	AF405697 Reporter
c 721	16	28.6	9114	11	AF100174	U12228 Promoter-pr	c 793	16	28.6	12288	6	BD263399	BD263399 Compositi
722	16	28.6	9184	11	XXU02431	AF100174 Cloning v	c 794	16	28.6	12416	6	BD263357	BD263357 Compositi
c 723	16	28.6	9231	11	AF100176	U02431 Cloning vec	c 795	16	28.6	12464	6	BD263357	BD263357 Binary ve
c 724	16	28.6	9233	11	AY237646	AF100176 Cloning v	c 796	16	28.6	12483	11	AY995142	AY995142 Binary ve
725	16	28.6	9265	6	AX554979	AY237646 Sequence	c 797	16	28.6	12537	11	AY788908	AY788908 N-termina
c 726	16	28.6	9311	11	SYNPMB206	AX554979 Sequence	c 798	16	28.6	12607	11	AY737283	AY737283 C-termina
727	16	28.6	9388	11	AF187996	MJ7847 Bacterial c	c 799	16	28.6	12634	14	AC100977	AC100977 Mus muscu
728	16	28.6	9460	6	AX097932	AF187996 Promoter	c 800	16	28.6	12677	11	AY196825	AY196825 PiggyBac
c 729	16	28.6	9583	11	PLMCG	AX097932 Sequence	c 801	16	28.6	12677	11	AY196825	AY196825 PiggyBac
730	16	28.6	9583	11	SYNPA37XV	M11320 Plasmid pAA	c 802	16	28.6	12796	14	AC100945	AC100945 Mus muscu
c 731	16	28.6	9652	6	AX548648	L08817 pAA3.7X c1o	c 803	16	28.6	12796	14	AC100945	AC100945 Mus muscu
732	16	28.6	9652	11	CVU38900	AX548648 Sequence	c 804	16	28.6	12905	14	AC111168	AC111168 Sequence
c 733	16	28.6	9692	6	AR215118	U89900 Yeast-Dacte	c 805	16	28.6	13974	6	AX356862	AX356862 Sequence
c 734	16	28.6	9737	6	AR215119	AR215118 Sequence	c 806	16	28.6	13974	11	AY487253	AY487253 Cloning v
c 735	16	28.6	9737	6	AR215124	AR215119 Sequence	c 807	16	28.6	13974	11	AY487253	AY487253 Cloning v
c 736	16	28.6	9737	6	AR302360	AR215124 Sequence	c 808	16	28.6	13466	11	AY665170	AY665170 Expressio
c 737	16	28.6	9737	6	AR302361	AR302360 Sequence	c 809	16	28.6	13466	6	AX641919	AX641919 Sequence
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c 740	16	28.6	9737	6	AR373233	AR373232 Sequence	c 812	16	28.6	14105	11	AY572837	AY572837 Cloning v
c 741	16	28.6	9737	6	AR373238	AR373233 Sequence	c 813	16	28.6	14105	11	AY572837	AY572837 Cloning v
c 742	16	28.6	9737	6	AR401618	AR401618 Sequence	c 814	16	28.6	14928	11	AY230218	AY230218 Expressio
c 743	16	28.6	9737	6	AR401619	AR401619 Sequence	c 815	16	28.6	15111	14	AC015661	AC015661 Homo sapi
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c 745	16	28.6	9737	6	AR442951	AR401624 Sequence	c 817	16	28.6	15781	14	AC100973	AC100973 Mus muscu
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c 747	16	28.6	9737	6	AR442957	AR442952 Sequence	c 819	16	28.6	16437	11	AF123770	AF123770 Shuttle v
c 748	16	28.6	9737	6	AR568593	AR442957 Sequence	c 820	16	28.6	16520	11	AY178048	AY178048 Expressio
						AR568593 Sequence	c 821	16	28.6	16537	11	AY995145	AY995145 Binary ve



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C 825	16	28.6	18658	14	XXU73849	U73849 Synthetic t	C 898	16	28.6	44350	14	AC105039	AC105039 Homo sapi
C 826	16	28.6	18691	11	CV831184	CV831184 Cloning v	C 899	16	28.6	44456	6	AX059475	AX059475 Sequence
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C 828	16	28.6	22960	11	AY192024	AY192024 BAC clon1	C 901	16	28.6	44764	14	AC100016	AC100016 Mus muscu
C 829	16	28.6	24357	14	AC100557	AC100557 Mus muscu	C 902	16	28.6	44826	14	AC100612	AC100612 Mus muscu
C 830	16	28.6	25053	14	AC107242	AC107242 Homo sapi	C 903	16	28.6	44871	14	AC100057	AC100057 Mus muscu
C 831	16	28.6	25136	14	AC099801	AC099801 Trypanoso	C 904	16	28.6	44873	14	AC107889	AC107889 Homo sapi
C 832	16	28.6	25244	14	AC131903	AC131903 Homo sapi	C 905	16	28.6	44899	14	AC114992	AC114992 Homo sapi
C 833	16	28.6	25421	14	AC116005	AC116005 Homo sapi	C 906	16	28.6	45092	14	AC130487	AC130487 Homo sapi
C 834	16	28.6	26773	14	AC016238	AC016238 Homo sapi	C 907	16	28.6	45195	8	AC090421	AC090421 Homo sapi
C 835	16	28.6	27352	14	AC126372	AC126372 Homo sapi	C 908	16	28.6	45325	1	AY123253	AY123253 Klebsiell
C 836	16	28.6	27825	14	AC015763	AC015763 Homo sapi	C 909	16	28.6	45594	14	AC090823	AC090823 Homo sapi
C 837	16	28.6	29623	14	AC133146	AC133146 Homo sapi	C 910	16	28.6	45701	14	CERT4	CERT4 Caenorhabdi
C 838	16	28.6	30130	14	AC091281	AC091281 Mus muscu	C 911	16	28.6	45702	14	AC061982	AC061982 Homo sapi
C 839	16	28.6	30210	14	AC100104	AC100104 Mus muscu	C 912	16	28.6	45908	14	AC105240	AC105240 Homo sapi
C 840	16	28.6	30210	14	AC100104	AC100104 Mus muscu	C 913	16	28.6	46010	14	AC100091	AC100091 Mus muscu
C 841	16	28.6	30237	14	AC115096	AC115096 Homo sapi	C 914	16	28.6	46044	14	AC100534	AC100534 Mus muscu
C 842	16	28.6	30381	14	AC104251	AC104251 Homo sapi	C 915	16	28.6	46069	14	AC133288	AC133288 Homo sapi
C 843	16	28.6	31166	14	AC024379	AC024379 Homo sapi	C 916	16	28.6	46069	14	AC133288	AC133288 Homo sapi
C 844	16	28.6	32037	14	AC101089	AC101089 Mus muscu	C 917	16	28.6	46070	14	AC121561	AC121561 Homo sapi
C 845	16	28.6	32479	14	AC090240	AC090240 Homo sapi	C 918	16	28.6	46146	14	AC108918	AC108918 Mus muscu
C 846	16	28.6	33298	14	AC113520	AC113520 Mus muscu	C 919	16	28.6	46185	14	AC129485	AC129485 Homo sapi
C 847	16	28.6	33952	14	AC137879	AC137879 Homo sapi	C 920	16	28.6	46201	14	AC099961	AC099961 Mus muscu
C 848	16	28.6	34164	14	AC090913	AC090913 Homo sapi	C 921	16	28.6	46278	14	AC132815	AC132815 Homo sapi
C 849	16	28.6	34429	14	AC117791	AC117791 Mus muscu	C 922	16	28.6	46320	14	AC100390	AC100390 Mus muscu
C 850	16	28.6	34525	14	AC100355	AC100355 Mus muscu	C 923	16	28.6	46613	14	AC131052	AC131052 Homo sapi
C 851	16	28.6	34525	14	AC100355	AC100355 Mus muscu	C 924	16	28.6	46784	14	AC104230	AC104230 Homo sapi
C 852	16	28.6	34699	14	AC101104	AC101104 Mus muscu	C 925	16	28.6	47221	14	AC115854	AC115854 Mus muscu
C 853	16	28.6	35173	14	AC157371	AC157371 Medicago	C 926	16	28.6	47296	14	AC136985	AC136985 Mus muscu
C 854	16	28.6	35252	14	AC101051	AC101051 Mus muscu	C 927	16	28.6	47296	14	AC136985	AC136985 Mus muscu
C 855	16	28.6	35260	14	AC083761	AC083761 Homo sapi	C 928	16	28.6	47302	14	AC100458	AC100458 Mus muscu
C 856	16	28.6	35383	14	AC099956	AC099956 Mus muscu	C 929	16	28.6	47436	14	AC106032	AC106032 Homo sapi
C 857	16	28.6	35711	14	AC100058	AC100058 Mus muscu	C 930	16	28.6	47599	14	AC144984	AC144984 Mus muscu
C 858	16	28.6	36154	14	AC100446	AC100446 Mus muscu	C 931	16	28.6	47655	14	AC100064	AC100064 Mus muscu
C 859	16	28.6	36545	14	AC110055	AC110055 Mus muscu	C 932	16	28.6	47698	14	AC090207	AC090207 Homo sapi
C 860	16	28.6	36625	14	AC111166	AC111166 Homo sapi	C 933	16	28.6	47736	14	AC136356	AC136356 Homo sapi
C 861	16	28.6	36652	14	AC110598	AC110598 Homo sapi	C 934	16	28.6	47840	6	AX059458	AX059458 Sequence
C 862	16	28.6	36884	14	AC101081	AC101081 Mus muscu	C 935	16	28.6	47950	6	AX059460	AX059460 Sequence
C 863	16	28.6	37159	14	AC100259	AC100259 Mus muscu	C 936	16	28.6	47950	14	AC099985	AC099985 Mus muscu
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C 865	16	28.6	38022	14	AC068244	AC068244 Homo sapi	C 938	16	28.6	48000	14	AC149655	AC149655 Homo sapi
C 866	16	28.6	38275	14	AC069372	AC069372 Homo sapi	C 939	16	28.6	48179	14	AC149992	AC149992 Strongylo
C 867	16	28.6	38486	14	AC135624	AC135624 Homo sapi	C 940	16	28.6	48330	14	AC069086	AC069086 Homo sapi
C 868	16	28.6	39245	14	AC136734	AC136734 Mus muscu	C 941	16	28.6	48348	14	AC107907	AC107907 Homo sapi
C 869	16	28.6	39547	14	AC016460	AC016460 Homo sapi	C 942	16	28.6	48433	14	AC120152	AC120152 Mus muscu
C 870	16	28.6	39549	14	AC105140	AC105140 Homo sapi	C 943	16	28.6	48522	14	AC105112	AC105112 Homo sapi
C 871	16	28.6	40035	14	AC101084	AC101084 Mus muscu	C 944	16	28.6	48601	14	AC100101	AC100101 Mus muscu
C 872	16	28.6	40205	14	AC104254	AC104254 Homo sapi	C 945	16	28.6	48603	14	AC100169	AC100169 Mus muscu
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C 874	16	28.6	40442	14	CERT8	AL022307 Caenorhab	C 947	16	28.6	49074	14	AC068356	AC068356 Homo sapi
C 875	16	28.6	40696	14	AC099859	AC099859 Mus muscu	C 948	16	28.6	49101	14	AC110278	AC110278 Homo sapi
C 876	16	28.6	40774	14	AC100658	AC100658 Mus muscu	C 949	16	28.6	49137	14	AC100074	AC100074 Mus muscu
C 877	16	28.6	40908	14	AC100713	AC100713 Mus muscu	C 950	16	28.6	49323	14	AC107455	AC107455 Mus muscu
C 878	16	28.6	41065	14	AC024533	AC024533 Homo sapi	C 951	16	28.6	49348	14	AC100527	AC100527 Mus muscu
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C 880	16	28.6	41722	14	AC100593	AC100593 Mus muscu	C 953	16	28.6	49507	14	AC129982	AC129982 Mus muscu
C 881	16	28.6	41857	14	AC068098	AC068098 Homo sapi	C 954	16	28.6	49515	14	AC138584	AC138584 Mus muscu
C 882	16	28.6	41939	14	AC126371	AC126371 Homo sapi	C 955	16	28.6	49532	14	AC100565	AC100565 Mus muscu
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C 884	16	28.6	41939	14	AC101045	AC101045 Mus muscu	C 957	16	28.6	49676	14	AC103761	AC103761 Homo sapi
C 885	16	28.6	41974	14	AC144976	AC144976 Xenopus t	C 958	16	28.6	49685	14	AC133148	AC133148 Homo sapi
C 886	16	28.6	42271	14	AC100593	AC100593 Mus muscu	C 959	16	28.6	49739	14	AC100909	AC100909 Mus muscu
C 887	16	28.6	42441	14	AC109339	AC109339 Homo sapi	C 960	16	28.6	50054	14	AC134410	AC134410 Homo sapi
C 888	16	28.6	42502	14	AC024330	AC024330 Homo sapi	C 961	16	28.6	50234	14	AC144977	AC144977 Xenopus t
C 889	16	28.6	42786	14	AC106000	AC106000 Homo sapi	C 962	16	28.6	50283	14	AC136982	AC136982 Mus muscu
C 890	16	28.6	42856	14	AC100075	AC100075 Mus muscu	C 963	16	28.6	50320	14	AC126373	AC126373 Homo sapi
C 891	16	28.6	42998	14	AC103869	AC103869 Homo sapi	C 964	16	28.6	50362	14	AC091572	AC091572 Homo sapi
C 892	16	28.6	43274	14	AC101233	AC101233 Mus muscu	C 965	16	28.6	50406	14	AC027739	AC027739 Homo sapi
C 893	16	28.6	44031	8	AC116360	AC116360 Homo sapi	C 966	16	28.6	50440	14	AC026825	AC026825 Homo sapi
C 894	16	28.6	44080	6	AX059463	AX059463 Sequence	C 967	16	28.6	50499	14	AC125272	AC125272 Mus muscu



C 968	16	28.6	51191	14	AC011870	AC011870 Homo sapi
C 969	16	28.6	51256	14	AC129530	AC129530 Homo sapi
C 970	16	28.6	51313	14	AC111025	AC111025 Mus muscu
C 971	16	28.6	51422	14	AC101444	AC101444 Ciona sav
C 972	16	28.6	51564	14	AC102921	AC102921 Mus muscu
C 973	16	28.6	51637	14	AC144959	AC144959 Xenopus t
C 974	16	28.6	51751	14	AC011918	AC011918 Homo sapi
C 975	16	28.6	51770	14	AC011178	AC011178 Homo sapi
C 976	16	28.6	51803	14	AC126378	AC126378 Homo sapi
C 977	16	28.6	51815	14	AC068454	AC068454 Homo sapi
C 978	16	28.6	51837	14	AC100132	AC100132 Mus muscu
C 979	16	28.6	51860	9	AL808109	AL808109 Mouse DNA
C 980	16	28.6	51874	14	AC129511	AC129511 Homo sapi
C 981	16	28.6	51883	14	AC135993	AC135993 Homo sapi
C 982	16	28.6	51991	14	AC101447	AC101447 Ciona sav
C 983	16	28.6	51997	14	AC137886	AC137886 Mus muscu
C 984	16	28.6	52032	14	AC101080	AC101080 Mus muscu
C 985	16	28.6	52035	14	AC100409	AC100409 Mus muscu
C 986	16	28.6	52170	14	AC100053	AC100053 Mus muscu
C 987	16	28.6	52189	14	AC100695	AC100695 Mus muscu
C 988	16	28.6	52347	14	AC068214	AC068214 Homo sapi
C 989	16	28.6	52390	14	AC100498	AC100498 Mus muscu
C 990	16	28.6	52420	14	AC102002	AC102002 Mus muscu
C 991	16	28.6	52453	14	AC116153	AC116153 Homo sapi
C 992	16	28.6	52500	14	AC101026	AC101026 Mus muscu
C 993	16	28.6	52611	14	AC100025	AC100025 Mus muscu
C 994	16	28.6	52687	14	AC068390	AC068390 Homo sapi
C 995	16	28.6	52765	14	AC125425	AC125425 Homo sapi
C 996	16	28.6	52940	14	AC104969	AC104969 Homo sapi
C 997	16	28.6	52943	14	AC139208	AC139208 Mus muscu
C 998	16	28.6	52954	14	AC103677	AC103677 Homo sapi
C 999	16	28.6	53035	14	AC104987	AC104987 Homo sapi
C1000	16	28.6	53035	14	AC104987	AC104987 Homo sapi

## ALIGNMENTS

RESULT 1  
BACCAPAC  
LOCUS B.anthraxis encapsulation protein genes (capA, capB, and capC),  
DEFINITION complete cds.  
M24150  
ACCESSION M24150.1 GI:142630  
VERSION M24150.1  
KEYWORDS encapsulation protein; membrane-associated protein.  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 3244)  
AUTHORS Makino,S., Uchida,I., Terakado,N., Sasakawa,C. and Yoshikawa,M.  
TITLE Molecular characterization and protein analysis of the cap region,  
JOURNAL which is essential for encapsulation in Bacillus anthracis  
PUBMED J. Bacteriol. 171 (2), 722-730 (1989)  
COMMENT 253679  
Original source text: B.anthraxis (strain TE702; isolate pCAP1)

Draft entry and computer-readable sequence for [1] kindly provided  
by I.Uchida, 01-MAY-1989.  
Location/Qualifiers

FEATURES  
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282..1475  
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## CDS

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LAVABALGIDEBTAFRGMANAPDPGAMRTIRFADQSKPAFVFGFAMPSPSTLRIM  
ERYDDRGVSNLAPVIMNCRPDRIRTEOPARADLPYIKAEIVAIIGETTAPISAFE  
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SMNPDLVLRQISKADPRKGNADLVVNTVHGEYDKNPSPROALAKANVADADII  
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## CDS

ORIGIN 748 bp upstream of HindIII site.

Query Match 100.0%; Score 56; DB 1; Length 3244;  
Best Local Similarity 100.0%; Pred. No. 4.1e-23;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTCCGTGATGTTGATGCTCATCCGATCCAGAGCAATGAGATTAACAG 56  
Db 975 GCATTCCGTGATGTTGATGCTCATCCGATCCAGAGCAATGAGATTAACAG 1030

RESULT 2  
AB011191/c  
LOCUS AB011191 94829 bp DNA circular BCT 14-JUN-2002  
DEFINITION Bacillus anthracis str. A2012 plasmid pXO2, complete sequence.  
ACCESSION AB011191  
VERSION AB011191.1 GI:20520280  
KEYWORDS  
SOURCE Bacillus anthracis str. A2012  
ORGANISM Bacillus anthracis str. A2012  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 94829)  
AUTHORS Reed,T.D., Salzbary,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapfel,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Comparative genome sequencing for discovery of novel polymorphisms  
JOURNAL in Bacillus anthracis  
PUBMED Science 296 (5575), 2028-2033 (2002)  
COMMENT 12004073

REFERENCE 2 (bases 1 to 94829)  
AUTHORS Reed,T.D., Salzbary,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L.,  
Holtzapfel,E., Busch,J.D., Smith,K.L., Schnupp,J.M., Solomon,D.,  
Keim,P. and Frazer,C.M.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2002) The Institute for Genomic Research, 9712  
Medical Center Dr, Rockville, MD 20850, USA  
Location/Qualifiers

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ACCESSION AB017335
VERSION    AB017335.3 GI:50118566
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SOURCE      Bacillus anthracis str. 'Ames Ancestor'
ORGANISM    Bacillus anthracis; Bacillales; Bacillaceae; Bacillus; Bacillus
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AUTHORS     Ravel,U., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
             Federova,N.B., Wilson,M., Stanley,S., Decker,S., Read,T.D.,
             Salzberg,S. and Fraser,C.M.
             Bacillus anthracis comparative genomics
             Unpublished
             2 (bases 1 to 94830)
             Ravel,U., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
             Federova,N.B., Salzberg,S. and Fraser,C.M.
             Direct Submision
             Submitted (17-MAY-2004) Microbial Genomics, The Institute for
             Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850,
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AUTHORS     Ravel,U., Rasko,D.A., Shumway,M.F., Jiang,L., Cer,R.Z.,
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             Salzberg,S. and Fraser,C.M.
             Direct Submission
             Submitted (09-JUN-2004) Microbial Genomics, The Institute for
             Genomic Research, 9712 Medical Center Drive, Rockville, MD 20850,
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REMARK     Sequence update by submitter
COMMENT     On Jul 9, 2004 this sequence version replaced gi:47552342.
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<p>RESULT 4</p> <p>AP188935/c</p> <p>LOCUS AP188935 96231 bp DNA circular BCT 01-OCT-2003</p> <p>DEFINITION Bacillus anthracis plasmid pX02, complete sequence.</p> <p>ACCESSION AP188935</p> <p>VERSION AP188935.1 GI:6470151</p> <p>KEYWORDS</p> <p>SOURCE</p> <p>ORGANISM</p> <p>Bacillus anthracis</p> <p>Bacillus anthracis</p> <p>Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.</p> <p>1 (bases 1 to 96231)</p> <p>Okinaka,R.T., Cloud,K., Hampton,O., Hill,K.K., Keim,P., Lanke,G., Kumano,S., Manter,D., Martinez,Y., Svensson,R., Tatum,L.R., Brown,A.E. and Jackson,P.J.</p> <p>Direct Submission</p> <p>Submitted (01-NOV-1999) Bioscience Division, Los Alamos National Laboratory, M888, Los Alamos, NM 87545, USA</p> <p>Location/Qualifiers</p> <p>1..96231</p> <p>/organism="Bacillus anthracis"</p> <p>/mol_type="genomic DNA"</p> <p>/db_xref="taxon:1392"</p> <p>/plasmid="pX02"</p> <p>complement (19..477)</p> <p>/note="hypothetical protein"</p> <p>/codon_start=1</p> <p>/evidence=not experimental</p> <p>/transl_table=11</p> <p>/product="pX02-01"</p> <p>/protein_id="AAI13606.1"</p> <p>/db_xref="GI:6470152"</p> <p>/translation="MRBGKQDDVLSIKKEVKDKLQKSVNTMKQDMLIKLNMELIAQ SGSNLSLEKLEQVKSRIASVTSKSGKGPRTVKEPILENNQEHQRIQREKVTISF VKPELPMTDVOIWMKKGKPHQVVPVTRLTGYQETIEWEIOIPHRKKELE"</p> <p>complement (482..1018)</p> <p>/note="hypothetical protein"</p> <p>/codon_start=1</p> <p>/evidence=not experimental</p> <p>/transl_table=11</p> <p>/product="pX02-02"</p> <p>/protein_id="AAI13607.1"</p> <p>/db_xref="GI:6470153"</p> <p>/translation="MKSPEIILITSGYTI PNKSPFTTVDYCMRKALKDGHLLTNT ELTBLSLQNAIDSPMEROSPHSNQKQSVSEKKAAPAYLTLSPNSFNTTDPKRY SYNGRKALESKRKMTKEEEVSLNKKHIEDLSPENKGGKKGIKAEIITISGVPSK DKWVITSDINIEIKDIR"</p>	



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IRGPKARDVYTVVQOOGKILIDSGVQDESEVETGMINPLEPATYKIKTNGAVDEKQ  
SFIOHISKVTMMIFLNTPEDDTVIOFRKILVAFYIEMGLVPGSGDRPYKVTGYP  
NHVPLDEPVYKLSNLKLEAGATPQRHLEAIIQVEDMTVYGDMFNHGTLLNFE  
NEQIVPFDIGISIKYDSVFNQCLFTALLIWSHALNGRMKYLIREKNLSIDVYK  
PMVFLDECHVINSQNFAPRYVLEFEREMKRFAGIIFATOSQEMLPFGSTVYVS  
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/translation="MKVATAAKVYNNRKOIESSEKNGKQSFISTIFASPNQTDASIV  
DIAPYKLEOKTGILVDHNNILQVYLKVTDLSPMODDKRPMNQLTSCRYVHEP  
FKILSYSTSTTEQQYVYKEMALRPGMSQBSSEKKEHLWYORSLAIBNRYLV  
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complement (7910. .8224)  
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/transl\_table=1  
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GFGRIHFVLTGTGLFCIFPHNSPTNRNIFVILDMIKMNKNTHPLEWNTISSEK  
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complement (8227. .8430)  
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/evidence=not\_experimental  
/transl\_table=1  
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/protein\_id="AAFI3617.1"  
/db\_xref="GI:6470163"  
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TNAIYLDNPFKKGKQDKKEDH"  
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/protein\_id="AAFI3618.1"  
/db\_xref="GI:6470164"  
/translation="MKVIDIANRRRIYEMKQOELRASIMTVAGFIAPALIVPOIS  
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/product="PX02-14"
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/db_xref="GI:6470165"
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FLGKADVTREKVAFLQWEMIQYADFLASIMQSTGGIITKLTVLAEGLIPDTER
FPLDKDGLNDPASFSLIKGLFVALFVALFVILGIRITIIQKPPKSVGNLIPDTER
LLGGLNELMADQMOKSTDPFSEBTITNSAKDGLMDLVKQWTADLIYLSKGFEPLOS
KKENEPALSTDSKPKNGMSKDIPLKALGIVVTGPKVEMTSGODIPEKEVEYVYKI
TNDGDKETVEKINDSVENPFKDKFPGGVVRIPMANGTIFMGLLMLGVAVLFTVEVFW

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Query Match 100.0%; Score 56; DB 1; Length 96231;  
 Best Local Similarity 100.0%; Pred. No. 4,9e-23;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTCGGTGTATGTGATGCTCATCCGATCCAGACGAGCAATGAAATTACACG 56  
 |||  
 Db 56589 GCATTCGGTGTATGTGATGCTCATCCGATCCAGACGAGCAATGAAATTACACG 56534

RESULT 5  
 BV618443/c 825 bp DNA linear STS 15-APR-2005  
 DEFINITION S217P61053FB4.T0 Noemie Pan troglodytes troglodytes STS genomic,  
 sequence tagged site.  
 BV618443  
 BV618443.1 GI:62608621  
 STS.  
 Pan troglodytes troglodytes  
 Pan troglodytes troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Pan.  
 1 (bases 1 to 825)  
 Mikkel, J. S., Hillier, W. L., Eichler, E. E., Zody, M. C. and  
 Jaffe, D. B.  
 Initial Sequence of the Chimpanzee Genome and Comparison with the  
 Human Genome  
 Unpublished (2005)

JOURNAL  
 TITLE  
 AUTHORS  
 COMMENT

Contact: Michael C. Zody  
 Broad Institute of MIT and Harvard  
 320 Charles Street, Cambridge, MA 02141, USA  
 Tel: 6172580933  
 Fax: 6172580903  
 Email: mczody@broad.mit.edu  
 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 825

Protocol:  
 23,021,928 chimpanzee whole genome shotgun reads were aligned to  
 the Human genome (NCBI  
 Build 34 (hg16, July 2003). Chimp WGS reads were from 9 donors,  
 including Clint (Pan  
 troglodytes verus), 3 other Pan troglodytes verus chimps  
 (Donald, Karlien, Yvonne), 3 Pan  
 troglodytes troglodytes chimps (Noemie, Masuku, Clara) and 2 chimps  
 of unknown origin  
 (Gon, Unknown Chimp). Common names: Pan troglodytes verus is the  
 western chimp and Pan  
 troglodytes troglodytes is the central chimp. To be included in  
 chimpanzee SNP discovery, a  
 read must be at least 500bp in length, at least 50% of its base  
 calls must have Phred  
 score >= 20, at least 30% of its base calls must satisfy  
 SNOS (30,25) (single strand NOS), the  
 base in question has Phred score >= 30, the surrounding 10 bases in  
 the read have Phred  
 score >= 25), and the read must have at least 200 bp SNOS (30,25)  
 bases. Reads not uniquely  
 placed in the genome and read pairs whose two ends were not  
 consistently placed were  
 discarded. After above filtering, NOS (30,25) standard was applied  
 to all pairs of

overlapping reads to call NOS bases and SNPs. Alignments (between  
 two reads) with less  
 than 100 NOS bases or with SNP rate > 0.01 were discarded. To  
 exclude alignment between two  
 copies of a single read, comparisons between two reads that share  
 95% of their genome  
 alignments (>=95% bases of read A and >=95% bases of read B were  
 placed at the same locus  
 of human genome) were discarded.

FEATURES  
 source  
 Location/Qualifiers  
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 /organism="Pan troglodytes troglodytes"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:37011"  
 /clone\_id="Noemie"  
 <1..>825

ORIGIN  
 STS

Query Match 32.1%; Score 18; DB 10; Length 825;  
 Best Local Similarity 100.0%; Pred. No. 9.1;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GAGCAATGAGATTACAC 55  
 |||  
 Db 314 GAGCAATGAGATTACAC 297

RESULT 6  
 AC068685 60211 bp DNA linear HTG 13-JUL-2000  
 LOCUS Homo sapiens chromosome 10 clone RP11-149B5 map 10, LOW-PASS  
 DEFINITION SEQUENCE SAMPLING.  
 AC068685  
 AC068685.1 GI:7712172  
 HTG; HTGS PHASEO.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homiidae; Homo.  
 1 (bases 1 to 60211)  
 Birren, B., Linton, L., Nusbaum, C. and Lander, E.  
 Homo sapiens chromosome 10, clone RP11-149B5  
 Unpublished  
 2 (bases 1 to 60211)  
 Anderson, S., Baldwin, D., Barna, N., Bastien, V., Bada, F.,  
 Boguslavsky, L., Bouhgalter, B., Brown, A., Burkett, G.,  
 Campoliano, A., Casale, A., Choepel, Y., Colangelo, M., Collins, S.,  
 Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S.,  
 Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D.,  
 Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L.,  
 Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L.,  
 Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A.,  
 Klein, J., Laboche, K., Lamazares, R., Landers, T., Lehotzky, D.,  
 Levine, R., Lieu, C., Liu, G., Locke, K., MacDonald, P., Marquis, N.,  
 McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R.,  
 Meldrum, J., Menus, L., Mihova, T., Miranda, C., Mlenga, V., Morrow, J.,  
 Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P.,  
 O'Neill, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N.,  
 Pisani, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D.,  
 Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B.,  
 Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J.,  
 Tesfaye, S., Theodore, D., Tirrell, A., Travers, M., Trigilio, D.,  
 Vassiliou, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J.,  
 Young, G., Zaitoun, J., Zimmer, A. and Zody, M.

Direct Submission  
 Submitted (06-MAY-2000) Whitehead Institute/MIT Center for Genome  
 Research, 320 Charles Street, Cambridge, MA 02141, USA  
 All repeats were identified using RepeatMasker:  
 Smit, A. F. A. & Green, P. (1996-1997)  
 http://ftp.genome.washington.edu/RM/RepeatMasker.html

JOURNAL  
 TITLE  
 AUTHORS  
 COMMENT



```
-----Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIRB
Web site: http://www-seq.wi.mit.edu
Contact: sequence submissions@genome.wi.mit.edu
-----Project Information
Center project name: L7183
Center clone name: 149_B_5
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* NOTE: This record contains 74 individual
* sequencing reads that have not been assembled into
* contigs. Runs of N are used to separate the reads
* and the order in which they appear is completely
* arbitrary. Low-pass sequence sampling is useful for
* identifying clones that may be gene-rich and allows
* overlap relationships among clones to be deduced.
* However, it should not be assumed that this clone
* will be sequenced to completion. In the event that
* the record is updated, the accession number will
* be preserved.
1
* 723: contig of 722 bp in length
* 723 822: gap of 100 bp
* 823 1551: contig of 729 bp in length
* 1552 1651: gap of 100 bp
* 1652 2378: contig of 727 bp in length
* 2379 2478: gap of 100 bp
* 2479 3170: contig of 692 bp in length
* 3171 3270: gap of 100 bp
* 3271 3983: contig of 713 bp in length
* 3984 4083: gap of 100 bp
* 4084 4797: contig of 714 bp in length
* 4798 4897: gap of 100 bp
* 4898 5614: contig of 717 bp in length
* 5615 5714: gap of 100 bp
* 5715 6428: contig of 714 bp in length
* 6429 6529: gap of 100 bp
* 6529 7250: contig of 722 bp in length
* 7251 7350: gap of 100 bp
* 7351 8062: contig of 712 bp in length
* 8063 8162: gap of 100 bp
* 8163 8875: contig of 713 bp in length
* 8876 8975: gap of 100 bp
* 8976 9682: contig of 707 bp in length
* 9683 9782: gap of 100 bp
* 9783 10509: contig of 727 bp in length
* 10510 10609: gap of 100 bp
* 10610 11324: contig of 715 bp in length
* 11325 11424: gap of 100 bp
* 11425 12136: contig of 712 bp in length
* 12137 12226: gap of 100 bp
* 12237 12958: contig of 722 bp in length
* 12959 13058: gap of 100 bp
* 13059 13785: contig of 727 bp in length
* 13786 13885: gap of 100 bp
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* 14689 15423: contig of 735 bp in length
* 15424 15523: gap of 100 bp
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* 16225 16324: gap of 100 bp
* 16325 17030: contig of 706 bp in length
* 17031 17130: gap of 100 bp
* 17131 17871: contig of 741 bp in length
* 17872 17971: gap of 100 bp
* 17972 18685: contig of 714 bp in length
* 18686 18785: gap of 100 bp
* 18786 19509: contig of 724 bp in length
* 19510 19609: gap of 100 bp
* 19610 20321: contig of 712 bp in length
* 20322 20421: gap of 100 bp
* 20422 21123: contig of 702 bp in length
* 21124 21223: gap of 100 bp
* 21224 21938: contig of 715 bp in length
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* 21939 22038: gap of 100 bp
* 22039 22759: contig of 721 bp in length
* 22760 22859: gap of 100 bp
* 22860 23575: contig of 716 bp in length
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* 23676 24391: contig of 716 bp in length
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* 24492 25204: contig of 713 bp in length
* 25205 25304: gap of 100 bp
* 25305 26017: contig of 713 bp in length
* 26018 26117: gap of 100 bp
* 26118 26843: contig of 726 bp in length
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* 26944 27652: contig of 709 bp in length
* 27653 27752: gap of 100 bp
* 27753 28477: contig of 725 bp in length
* 28478 28577: gap of 100 bp
* 28578 29292: contig of 715 bp in length
* 29293 29392: gap of 100 bp
* 29393 30107: contig of 715 bp in length
* 30108 30207: gap of 100 bp
* 30208 30927: contig of 720 bp in length
* 30928 31027: gap of 100 bp
* 31028 31756: contig of 729 bp in length
* 31757 31856: gap of 100 bp
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* 34205 34304: gap of 100 bp
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* 35128 35829: contig of 702 bp in length
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* 38363 39088: contig of 726 bp in length
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* 39189 39915: contig of 727 bp in length
* 39916 40015: gap of 100 bp
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* 40748 40847: gap of 100 bp
* 40848 41561: contig of 714 bp in length
* 41562 41661: gap of 100 bp
* 41662 42381: contig of 720 bp in length
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* 42482 43193: contig of 712 bp in length
* 43194 43293: gap of 100 bp
* 43294 44002: contig of 709 bp in length
* 44003 44102: gap of 100 bp
* 44103 44810: contig of 708 bp in length
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* 44911 45636: contig of 726 bp in length
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* 45737 46472: contig of 736 bp in length
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* 46573 47301: contig of 729 bp in length
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* 47402 48088: contig of 687 bp in length
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* 48993 49708: contig of 716 bp in length
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repeat_region 13877..14787
/rpt_family="RUTR13D1"
repeat_region 15460..15705
/rpt_family="L1_Mm"
repeat_region 15706..15927
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repeat_region 15928..15940
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repeat_region 17227..17274
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repeat_region 18181..18208
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repeat_region 18211..18363
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repeat_region 20355..20658
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repeat_region 25480..25480
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repeat_region 25807..25909
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repeat_region 30036..30036
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Query Match 32.1% Score 18; DB 9; Length 145190;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 32 ATCCAGAGCAATGAGAA 49
Db 132489 ATCCAGAGCAATGAGAA 132506

RESULT 8
CNS07BD1 163784 bp DNA linear PRI 10-SEP-2002
LOCUS Human chromosome 14 DNA sequence BAC R-12619 of library RPCT-11
DEFINITION from chromosome 14 of Homo sapiens (Human), complete sequence.
ACCESSION AL445385
VERSION AL445385.4 GI:22859119
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
1 (bases 1 to 163784)
Heilig, R., Petit, J., Vico, V., Dailly, C., Robert, C., Wincker, P.,
Brotier, P., Cactolico, L., Barbe, V., Pelletier, E., Artiguenave, F.,
Levy, M., Beckenbach, R., Bruls, T., deBardine, V., Crund, C.,
Gyapay, G., Saurin, W. and Weissenbach, J.
Sequencing of the human chromosome 14
Unpublished
2 (bases 1 to 163784)
Genoscope.
Direct Submission
Submitted (09-SEP-2002) Genoscope - Centre National de Sequencage :
BP 191 91006 Evry cedex - FRANCE (E-mail : segref@genoscope.cns.fr)
- Web : www.genoscope.cns.fr)
On Sep 14, 2002 this sequence version replaced gi.12655361.
----- Genome Center
Center: Genoscope / Centre National de Sequencage
Center code: GS
Web site: http://www.genoscope.cns.fr/
Contact: segref@genoscope.cns.fr)

The following BAC sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : R-338B12
Downstream BAC (overlapping the SP6 end) : R-611H21 (AC=AL513143)
----- Finishing boundaries
FINISHED SEGMENT STARTS AT BASE 13680
FINISHED SEGMENT ENDS AT BASE 163783
----- Summary Statistics
Assembly program: Phrap; version 2.0
Quality coverage: 13.66x in Q20 bases; sum-of-contigs

Range : bases
0 - 9 : 6
10 - 19 : 11
20 - 29 : 99
30 - 39 : 2479
40 - 49 : 10651
50 - 59 : 7641
60 - 69 : 12564
70 - 79 : 34298
80 - 89 : 96035
90 - 99 : 96035

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Percentage of bases with a quality value >= 40 : 99 %.

FEATURES  
source  
1. 163784  
/organism="Homo sapiens"  
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/db\_xref="taxon:9606"  
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/clone\_lib="RPC1-11"

ORIGIN

Query Match 32.1%; Score 18; DB 8; Length 163784;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 38 GAGCAATGAGATTACAC 55  
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Db 66632 GAGCAATGAGATTACAC 66649

RESULT 9  
AC017102 184648 bp DNA linear HTG 07-JUL-2000  
LOCUS Homo sapiens chromosome 14 clone RP11-557H24, WORKING DRAFT  
DEFINITION  
SEQUENCE, 22 unordered pieces.  
AC017102  
AC017102.5 GI:7232209  
VERSION  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT.  
SOURCE  
Homo sapiens (human)  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homniidae; Homo.  
1 (bases 1 to 184648)  
Waterston, R.H.  
The sequence of Homo sapiens clone  
Unpublished  
2 (bases 1 to 184648)  
Waterston, R.H.  
Direct Submission  
Submitted (09-DEC-1999) Genome Sequencing Center, Washington  
University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
MO 63108, USA  
On Mar 13, 2000 this sequence version replaced gi:7024128.

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: http://genome.wustl.edu/gsc/index.shtml  
----- Project Information -----  
Center project name: H\_NH057H24  
----- Summary Statistics -----  
Sequencing vector: M13, 87%  
Sequencing vector: plasmid, 13%  
Chemistry: Dye-primer ET; 87% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 173296 bases at least Q40  
Consensus quality: 177295 bases at least Q20  
Consensus quality: 178880 bases at least Q20  
Insert size: 194000; agarose-fp  
Insert size: 182548; sum-of-contigs  
Quality coverage: 3.52 in Q20 bases; agarose-fp  
Quality coverage: 3.74 in Q20 bases; sum-of-contigs  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 22 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.

1 1605: contig of 1605 bp in length  
1606 1705: gap of unknown length  
1706 3856: contig of 2151 bp in length  
3857 3956: gap of unknown length  
3957 6882: contig of 2926 bp in length  
6883 6982: gap of unknown length  
6983 10326: contig of 3344 bp in length  
10327 10427: gap of unknown length  
10427 13261: contig of 2835 bp in length  
13262 13361: gap of unknown length  
13362 16982: contig of 3621 bp in length  
16983 17082: gap of unknown length  
17083 20746: contig of 3664 bp in length  
20747 20846: gap of unknown length  
20847 23664: contig of 2818 bp in length  
23665 23764: gap of unknown length  
23765 28197: contig of 4433 bp in length  
28198 28297: gap of unknown length  
28298 32465: contig of 4168 bp in length  
32466 32565: gap of unknown length  
32566 35460: contig of 2895 bp in length  
35461 35560: gap of unknown length  
35561 40394: contig of 4834 bp in length  
40395 40494: gap of unknown length  
40495 45499: contig of 5005 bp in length  
45500 45599: gap of unknown length  
45600 52236: contig of 6637 bp in length  
52237 52336: gap of unknown length  
52337 58619: contig of 6283 bp in length  
58620 58719: gap of unknown length  
58720 64507: contig of 5788 bp in length  
64508 64607: gap of unknown length  
64609 73094: contig of 8487 bp in length  
73095 73194: gap of unknown length  
73195 83563: contig of 10369 bp in length  
83564 83663: gap of unknown length  
83664 94814: contig of 11151 bp in length  
94815 94914: gap of unknown length  
94915 107896: contig of 12982 bp in length  
107897 107996: gap of unknown length  
107997 140282: contig of 32286 bp in length  
140283 140383: gap of unknown length  
140383 140383: contig of 44266 bp in length.

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1606. 1705  
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10427. 13361  
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13362. 16982  
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Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
38 GAGCAATGAGATTACAC 55
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Db 130020 GAGCAATGAGATTACAC 130037

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RESULT 10
AL592113      191501 bp DNA linear HTG 23-NOV-2001
LOCUS Homo sapiens chromosome 1 clone RP11-158A1, 11 unordered pieces.
DEFINITION AL592113
ACCESSION AL592113
VERSION 6 GI:15591595
KEYWORDS HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
            Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
            Homidae; Homo.
REFERENCE 1
AUTHORS McJury,K.
TITLE Direct Submission
JOURNAL Submitted (23-NOV-2001) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequest@sanger.ac.uk
On Sep 12, 2001 this sequence version replaced gi:15021041.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BAI58A1
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Consensus quality: 189346 bases at least Q40
Consensus quality: 189958 bases at least Q20
Insert size: 190501; sum-of-contigs
Insert size: 51968; 4.5% error; agarose-fp
Quality coverage: 6.00x in Q20 bases; sum-of-contigs Quality
coverage: 22.36x in Q20 bases; agarose-fp

```

\* NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.

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* 1 4036: contig of 4036 bp in length
* 4037 4136: gap of 100 bp
* 4137 22116: contig of 17980 bp in length
* 22117 22216: gap of 100 bp
* 22217 49401: contig of 27185 bp in length
* 49402 49501: gap of 100 bp
* 49502 54698: contig of 5197 bp in length
* 54699 54798: gap of 100 bp
* 54799 57475: contig of 2677 bp in length
* 57476 57575: gap of 100 bp
* 57576 83314: contig of 25739 bp in length
* 83315 83414: gap of 100 bp
* 83415 91544: contig of 8130 bp in length
* 91545 91644: gap of 100 bp
* 91645 128399: contig of 36755 bp in length
* 128400 128499: gap of 100 bp
* 128500 174592: contig of 46093 bp in length
* 174593 174692: gap of 100 bp
* 174693 180968: contig of 6276 bp in length
* 180969 181068: gap of 100 bp
* 181069 191501: contig of 10433 bp in length.

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/chromosome="6"
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repeat_region
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complement(2096..2158)
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2160..2611
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3702..3898
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3899..4212
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complement(7200..7445)
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/rpt_family="B1_Mu82"
complement(12095..12398)
/rpt_family="MLT1D"
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12810..12836
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complement(13611..13957)
/rpt_family="ORR1C1"
repeat_region
14515..14539
/rpt_family="(CAGA)n"
complement(16568..16623)
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16625..17149
/rpt_family="L1_Mm"
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17302..17544
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repeat_region
17546..17648
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23275..23460
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27494..27552
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complement(28701..29377)
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complement(30391..36680)
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Query Match      32.1%; Score 18; DB 9; Length 193221;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      32 ATCCAGAGCAATGAGAA 49
DB      124196 ATCCAGAGCAATGAGAA 124213

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RESULT 12
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LOCUS
DEFINITION
Rattus norvegicus clone CH230-1084, WORKING DRAFT SEQUENCE, 2
unrounded pieces.
AC136487
AC136487.2 GI:25188608
HTG, HTGS_PHASE1, HTGS_DRAFT, HTGS_FULLTOP.
Rattus norvegicus (Norway rat)
SOURCE
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Murinae; Rattus.
1 (bases 1 to 226128)
Muzny,D,Marie, Metzker,M, Lee, A, Abramson, S, Adams, C, Alder, J,
Allen, C, Allen, H, Alsbrooks, S, Amth, A, Anguiano, D,
Anyalebech, V, Ayodeji, A, Ayodeji, M, Baca, E, Baden, H,
Baldwin, D, Bandaranaike, D, Barber, M, Barnstead, M, Benahmed, F,
Biswal, K, Blair, J, Blankenburg, K, Blyth, P, Brown, M,
Bryant, N, Buhay, C, Burch, P, Butrell, K, Calderon, B,
Cardenas, V, Carter, K, Cavazos, I, Caesar, H, Center, A,
Chacko, J, Chavez, D, Chen, G, Chen, R, Chen, Y, Chen, Z, Chu, J,
Cleveland, C, Cockrell, R, Cox, C, Coyle, M, Cree, A, D'Souza, L,
Davila, M, L, Davis, C, Davy-Carroll, L, De Anda, C, Dederich, D,
Delgado, O, Denson, S, Deramo, C, Ding, Y, Dinh, H, Divya, K,
Draper, H, Dugan-Rocha, S, Dunn, A, Durbin, K, Duval, B, Evans, K,
Egan, A, Escotto, M, Eugene, C, Evans, C, A, Falls, T, Fan, G,
Fernandez, S, Finley, M, Flagg, N, Forbes, L, Foster, M, Foster, P,
Fraser, C, M, Gabisi, A, Ganta, R, Garcia, A, Garner, T, Garza, M,

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Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Day-Carroll, L., De Anda, C., Dederich, D., Delgado, O., Denison, S., Detamco, C., Ding, Y., Dinh, H., Diya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Dublin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Falls, T., Fan, G., Fernandez, S., Finley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M., Gebregeorgis, E., Geer, K., Gill, R., Grady, M., Guerra, W., Guevara, W., Gunaratne, P., Haland, M., Hamill, C., Hamilton, C., Hamilton, K., Harvey, Y., Havlak, P., Hawes, A., Henderson, N., Hernandez, J., Hernandez, R., Hines, S., Hladun, S.L., Hodgson, A., Hogues, M., Hollins, B., Howells, S., Huliy, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Jolivet, A., Kapachny, S., Kelly, S., Kelly, S., Khan, Z., King, L., Koyar, C., Kowals, C., Kraft, C.L., Lebow, H., Levan, U., Lewis, L., Li, Z., Liu, J., Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J., Lorenshaw, L., Louisaged, H., Lozada, R. J., Lu, X., Ma, J., Maheswari, M., Mahindaratne, M., Mahmood, M., Malloy, K., Mangum, A., Mangum, B., Mapa, P., Martin, K., Martin, R., Martineau, E., Manthey, S., McLeod, M.P., McNeill, T.Z., Meenen, B., Milesavljevic, A., Miner, G., Ming, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Muidasa, M., Murphy, M., Nair, L., Narkavicius, C., Neal, D., Newton, N., Nguyen, N., Norris, S., Nwokoleh, O., Okunolu, G., Olariu, S., Pal, S., Parke, K., Pasternak, S., Paul, H., Perez, A., Perez, L., Pfannkuch, C., Plopper, F., Poidexter, A., Popovic, D., Primm, E., Pu, L., L., Puzo, M., Quiroz, J., Rachlin, E., Reeves, K., Regier, M.A., Reigh, R., Kelly, B., Reilly, M., Ren, Y., Reuter, M., Richards, S., Riggs, F., Rives, C., Rodkey, T., Rojas, A., Rose, M., Rose, R., Ruiz, S.J., Sanders, W., Savery, G., Scherer, S., Scott, G., Shatsman, S., Shen, H., Shetty, J., Shvartsbeyn, A., Slason, I., Sitter, C.D., Smajs, D., Sneed, A., Sodergren, E., Song, X.-Z., Sorelle, R., Sosa, J., Steidle, M., Strong, R., Sutton, A., Svatek, A., Tabac, P., Taylor, C., Taylor, T., Thomas, N., Thomas, S., Tingley, A., Trejo, Z., Usmani, K., Valas, R., Vera, V., Villaseña, D., Waldron, L., Walker, B., Wang, J., Wang, Q., Wang, S., Warren, J., Warren, R., Wei, X., White, F., Williams, G., Willson, R., Wleczky, R., Wooden, H., Worley, K., Wright, D., Wright, R., Wu, J., Yakub, S., Yen, J., Yoon, L., Yoon, V., Yu, P., Zhang, J., Zhou, J., Zhou, X., Zhao, S., Zhou, D., von Niederhausern, A., Weiss, R., Smith, D.R., Holt, R.A., Smith, H.O., Weinstock, G. and Gibbs, R.A.

Direct Submission  
Unpublished  
2 (bases 1 to 266188)  
Worley, K.C.  
Direct Submission  
Submitted (24-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
3 (bases 1 to 266188)  
Rat Genome Sequencing Consortium.  
Direct Submission  
Submitted (13-MAY-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA  
On May 13, 2003 this sequence version replaced gi:23664651.  
The sequence in this assembly is a combination of BAC based reads and whole genome shotgun sequencing reads assembled using Atlas (<http://www.hgsc.bcm.tmc.edu/projects/rat/>). Each contig described in the feature table below represents a scaffold in the Atlas assembly (a 'contig-scaffold'). Within each contig-scaffold, individual sequence contigs are ordered and oriented, and separated by sized gaps filled with Ns to the estimated size. The sequence may extend beyond the ends of the clone and there may be sequence contigs within a contig-scaffold that consist entirely of whole genome shotgun sequence reads. Both end sequences and whole genome shotgun sequence only contigs will be indicated in the feature table.

----- Genome Center  
Center: Baylor College of Medicine  
Center code: BCM  
Web site: <http://www.hgsc.bcm.tmc.edu/>



RESULT 14  
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 LOCUS AX505342  
 DEFINITION Sequence 37 from Patent WO0216655.  
 ACCSSION AX505342  
 VERSION AX505342.1 GI:23386579  
 KEYWORDS  
 ORGANISM Arabidopsis thaliana (thale cress)  
 Arabidopsis thaliana  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosid II; Brassicales; Brassicaceae; Arabidopsis.

REFERENCE 1  
 Harper, J.F., Kreps, J., Wang, X. and Zhu, T.  
 Stress-regulated genes of plants, transgenic plants containing same, and methods of use  
 Patent: WO 0216655-A 37 28-FEB-2002;  
 The Scripps Research Institute (US) ; Syngenta Participations AG (CH)

FEATURES  
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 /db\_xref="taxon:3702"

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 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 TTCCGTGATGATGAA 20  
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 161 TTCCGTGATGATGAA 177

RESULT 15  
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 LOCUS BV240969/c  
 DEFINITION S234P6228RC7.T0 Englishshepherd Canis familiaris STS genomic,  
 sequence tagged site.  
 ACCSSION BV240969  
 VERSION BV240969.1 GI:57303511  
 KEYWORDS STS.  
 SOURCE Canis familiaris (dog)  
 ORGANISM Canis familiaris  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae; Canis.  
 1 (bases 1 to 527)  
 Lindblad-Toh, K.  
 The genome sequence of Canis familiaris  
 Unpublished (2004)

REFERENCE 1  
 AUTHORS Lindblad-Toh, K.  
 TITLE The genome sequence of Canis familiaris  
 JOURNAL Unpublished (2004)

COMMENT  
 Contact: Kerstin Lindblad-Toh  
 Whitehead Institute for Biomedical Research, Center for Genome  
 Research  
 320 Charles Street, Cambridge, MA 02141, USA  
 Tel.: 6172521477  
 Fax: 6172580903  
 Email: kersti@genome.wi.mit.edu  
 Primer A: No sequence submitted  
 Primer B: No sequence submitted  
 STS size: 527  
 Protocol:  
 WGS-discovery (WGS):  
 Paired-end low-coverage whole genome shotgun reads were generated from 9 breeds  
 (German Shepherd, Rotweiler, Bedlington Terrier, Beagle, Labrador Retriever, English Shepherd, Italian Greyhound, Alaskan Malamute and the Portuguese Water Dog -100,000 each)  
 and five other canids (Chinese, Alaskan, Indian and Spanish Gray Wolf as well as the

Californian Coyote).  
 The WGS reads were placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSANA-SNP. 863872 reads were annotated as STSs and 485941 SNPs were annotated with alleles from the boxer and the breed or canid from which the particular read came. The validation rate for these SNPs was estimated at approximately 98%.  
 WGS-discovery (WGA) of Boxer/Poodle SNPs:  
 A second set of SNPs was generated using a similar methodology except that the contigs from the 1.5x poodle assembly (Kirkness 2003) were used instead of WGS reads. Since this sequence lacked base quality scores, arbitrary quality scores of pined 40 were assigned before the poodle sequence was placed uniquely on the CanFam1.0 boxer assembly and SNP detection was carried out by SSANA-SNP. 1637780 SNPs were annotated with alleles from the boxer and the poodle. The validation rate for these SNPs was estimated at approximately TBD%.  
 Internal-WGA-discovery (I-WGA):  
 A third set of SNPs were discovered by comparing reads in the WGA assembly. SNPs were defined as mismatch positions that had a base quality of >= 30 on both reads in a region that aligned without gaps, and with at most one additional mismatch in the ten flanking bases. For each allele, at least one additional read had to confirm it. 731476 SNPs were annotated with alleles between the two boxer alleles. The validation rate for these SNPs was estimated at approximately TBD%.  
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 Best Local Similarity 100.0%; Pred. No. 37;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGGAGCAATGAGAAATT 51  
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 Db 359 CAGGAGCAATGAGAAATT 343

RESULT 16  
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 LOCUS AY696754  
 DEFINITION Shigella boydii strain 3097-02 cytolethal distending toxin A (cdtA) and truncated cytolethal distending toxin B (cdtB) genes, complete cds; and cytolethal distending toxin C (cdtC) gene, partial cds.  
 ACCSSION AY696754  
 VERSION AY696754.1 GI:52854785  
 KEYWORDS  
 SOURCE Shigella boydii  
 ORGANISM Shigella boydii  
 Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.  
 1 (bases 1 to 1997)  
 Hyma, K.E., Lachner, D.W., Nelson, A.M., Bumbaugh, A.C., Janda, J.M., Stroockbine, N.A., Young, V.B. and Whittem, T.S.  
 Evolutionary Genetics of a New Pathogenic Escherichia Species: Escherichia albertii and Related Shigella boydii Strains  
 J. Bacteriol. 187 (2), 619-628 (2005)



PUBMED 15629933  
REFERENCE 2 (bases 1 to 1997)  
AUTHORS Hyma,K.E., Lacher,D.W., Abu-Ali,G.S., Nelson,A.M., Janda,J.M., Stroockbine,N.A., Young,V.B. and Whittam,T.S.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-2004) Microbial Evolution Laboratory, National Food Safety and Toxicology Center, Michigan State University, 190B Food Safety and Toxicology, East Lansing, MI 48824, USA  
FEATURES Location/Qualifiers  
source 1..1997  
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ORIGIN  
Query Match 30.4%; Score 17; DB 1; Length 1997;  
Best Local Similarity 100.0%; Pred.No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 GTTGATGCTCATCCGG 31  
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DB 831 GTTGATGCTCATCCGG 815  
RESULT 17  
AY696752/c  
LOCUS AY696752 1999 bp DNA linear BCT 05-JAN-2005  
DEFINITION Shigella boydii strain K-694 cytolethal distending toxin A (cdtA)  
and truncated cytolethal distending toxin B (cdtB) genes, complete  
cds; and cytolethal distending toxin C (cdtC) gene, partial cds.  
ACCESSION AY696752  
VERSION AY696752.1 GI:52854777  
KEYWORDS Shigella boydii  
SOURCE

ORGANISM Shigella boydii  
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
Enterobacteriaceae; Shigella.  
REFERENCE 1 (bases 1 to 1999)  
AUTHORS Hyma,K.E., Lacher,D.W., Nelson,A.M., Bumbaugh,A.C., Janda,J.M., Stroockbine,N.A., Young,V.B. and Whittam,T.S.  
TITLE Evolutionary Genetics of a New Pathogenic Escherichia Species: Escherichia albertii and Related Shigella boydii Strains  
JOURNAL J. Bacteriol. 187 (2), 619-628 (2005)  
PUBMED 15629933  
REFERENCE 2 (bases 1 to 1999)  
AUTHORS Hyma,K.E., Lacher,D.W., Abu-Ali,G.S., Nelson,A.M., Janda,J.M., Stroockbine,N.A., Young,V.B. and Whittam,T.S.  
TITLE Direct Submission  
JOURNAL Submitted (26-JUL-2004) Microbial Evolution Laboratory, National Food Safety and Toxicology Center, Michigan State University, 190B Food Safety and Toxicology, East Lansing, MI 48824, USA  
FEATURES Location/Qualifiers  
source 1..1999  
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/strain="K-694"  
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/db\_xref="taxon:621"  
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/db\_xref="GI:52854779"  
/translation="MKKYITSLIVFLSFAQADLTDFRVATNMQASATTESK"  
1670..>1999  
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/transl\_table=11  
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/protein\_id="AAU88261.1"  
/db\_xref="GI:52854780"  
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LMTCNPT"  
ORIGIN  
Query Match 30.4%; Score 17; DB 1; Length 1999;  
Best Local Similarity 100.0%; Pred.No. 39;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 15 GTTGATGCTCATCCGG 31  
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DB 833 GTTGATGCTCATCCGG 817  
RESULT 18



Query Match	30.4%	Score 17	DB 1	Length 2202
Best Local Similarity	100.0%	Pred. No. 40		
Matches	17	Conservative 0	Mismatches 0	Indels 0; Gaps 0
QY	15	GTGATGCTCATCCGG	31	
DB	815	GTGATGCTCATCCGG	799	
RESULT 19				
LOCUS	AY696753/c			
DEFINITION	Shigella boydii strain K-1 cytolethal distending toxin A (cdta), cytolethal distending toxin B (cdtb), and cytolethal distending toxin C (cdtc) genes, complete cds.			
ACCESSION	AY696753			
VERSION	AY696753.1			
KEYWORDS	GI:52854781			
SOURCE	Shigella boydii			
ORGANISM	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales; Enterobacteriaceae; Shigella.			
REFERENCE	1 (bases 1 to 2231)			
AUTHORS	Hyma, K.E., Lachner, D.W., Nelson, A.M., Bumbaugh, A.C., Janda, J.M., Strochbine, N.A., Young, V.B. and Whitlam, T.S.			
TITLE	Evolutionary Genetics of a New Pathogenic Escherichia Species: Escherichia albertii and Related Shigella boydii Strains			
JOURNAL	J. Bacteriol. 187 (2), 619-628 (2005)			
PUBMED	15629933			
REFERENCE	2 (bases 1 to 2231)			
AUTHORS	Hyma, K.E., Lachner, D.W., Abu-Ali, G.S., Nelson, A.M., Janda, J.M., Strochbine, N.A., Young, V.B. and Whitlam, T.S.			
TITLE	Direct Submission			
JOURNAL	Submitted (26-JUL-2004) Microbial Evolution Laboratory, National Food Safety and Toxicology Center, Michigan State University, 190B Food Safety and Toxicology, East Lansing, MI 48824, USA			
FEATURES	Location/Qualifiers			
SOURCE	1..2231			
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CDs	/transl_table=11			
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CDs	/protein_id="NAU88262.1"			
gene	/db_xref="GI:52854782"			
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gene	846..1655			
CDs	/gene="cdtB"			
gene	/codon_start=1			
CDs	/transl_table=11			
gene	/product="cytolethal distending toxin B"			
CDs	/protein_id="NAU88264.1"			
gene	/db_xref="GI:52854784"			
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SNPTWSEDAITALEAVRLGHMSINOAIIHNL PYSSLYGRFKRGKYEEPTVGEISQ

GGATCCAGGAG 40  
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GGATCCAGGAG 1249

LOCUS	3362 bp	mrna	linear	INV 16-FEB-2001
AF315555				

mRNA, partial cds.  
ACCESSION AF315555  
VERSION AF315555.1 GI:12231944

ORGANISM  
Caenorhabditis briggsae  
Eukaryote; Metazoa; Nematoda; Rhabditida;  
Rhabditidae; Rhabditidae; Pelodierinae; Caenorhabditis.  
1 (Passes 1 to 3362)  
Rudel, D. and Kimble, J.  
Conservation of gld-1 regulation and function in nematodes  
Genetics 157 (2), 639-654 (2001)  
11156985

AUTHORS  
 TITLE  
 JOURNAL  
 FEATURES  
 source  
 Ruedel,D.J. and Kimble,J.B.  
 Direct Submission  
 Submitted (23-OCT-2000) Biochemistry, University of  
 Wisconsin-Madison, 433 Babcock Drive, Madison, WI 53706, USA  
 Location/Qualifiers  
 1..3362  
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30.4%; Score 17; DB 2; Length 3362;  
 Query Match 100.0%; Pred. No. 40;  
 Best Local Similarity



Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GATCCAGAGCAATGAG 47  
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Db 54 GATCCAGAGCAATGAG 38

RESULT 22  
AF315554/c  
LOCUS AF315554  
DEFINITION Caenorhabditis briggsae notch-like transmembrane receptor (gfp-1)  
ACCESSION AF315554  
VERSION AF315554.1 GI:12231942  
KEYWORDS  
SOURCE  
ORGANISM

Caenorhabditis briggsae  
Caenorhabditis briggsae  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditioidea; Rhabditidae; Peloderinae; Caenorhabditis.

REFERENCE  
AUTHORS Rudel, D. and Kimble, J.  
TITLE Conservation of gfp-1 regulation and function in nematodes  
JOURNAL Genetics 157 (2), 639-654 (2001)  
PUBMED 11156985  
2 (bases 1 to 7881)

REFERENCE  
AUTHORS Rudel, D.J., Friedman, L.C. and Kimble, J.E.  
TITLE Direct Submission  
JOURNAL Submitted (23-OCT-2000) Biochemistry, University of  
Wisconsin-Madison, 433 Babcock Drive, Madison, WI 53706, USA  
LOCATION/Qualifiers  
1. 7881  
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CDEYGEFCTKDKNECLQMGCAHGCYVLACGSPVACGKGFNCGHNVNMGES  
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CYNGVCGNGGCKCPSTPTDRCLELNRTAVLPMYSCHNPNQNDGKCVDDGYACT  
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DEDCNVACQPDGDCSGQOPSPRCMTPACASFAEIGCNPCNNBCKLYDMDQ  
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LSHIIIRRYNGITGVVITYLEVERICQPKSTCRSTASVNLIAAGLISNGRQSLG  
FSITEAMVAAPRRHGGVWSNRQILIALVAFLALGTVAAGVVRAGEPRSRKRI  
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TPMLAAKGNLAKYKTLACGASVTVYDGEKTAQOAFHDVAFHVDVLSNKNL  
PEVPODPRSRVCKNRBSANTKGRQTKVKRNGSKTPIIQTNLTPHSGSSPS  
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ORIGIN

Query Match 30.4%; Score 17; DB 2; Length 7881;  
Best Local Similarity 100.0%; Pred. No. 42;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 31 GATCCAGAGCAATGAG 47  
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Db 4125 GATCCAGAGCAATGAG 4109

RESULT 23  
A93560/c  
LOCUS A93560  
DEFINITION Sequence 5 from Patent WO9738105.  
ACCESSION A93560  
VERSION A93560.1 GI:6741765  
KEYWORDS  
SOURCE  
ORGANISM

REFERENCE  
AUTHORS Baier, M. and Metzner, K.  
TITLE GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH CODE FOR POLYPEPTIDES  
WITH IL-16 ACTIVITY, PROCESSES FOR THE PRODUCTION THEREOF AND THEIR  
USE  
JOURNAL Patent: WO 9738105-A 5 16-OCT-1997;  
BUNDESREP DEUTSCHLAND (DE); BAIER MICHAEL (DE)  
LOCATION/Qualifiers  
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/db\_xref="taxon:32644"  
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664..832  
833..2870  
2871..2972  
2973..5224  
5225..5483  
5484..5737  
5738..5863  
5864..7926  
7927..9096

ORIGIN  
Query Match 30.4%; Score 17; DB 6; Length 9096;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTAGTTGATGCT 24  
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Db 3452 GTGGTAGTTGATGCT 3436

RESULT 24  
AR182400/c  
LOCUS AR182400  
DEFINITION Sequence 5 from patent US 6338844.  
ACCESSION AR182400  
VERSION AR182400.1 GI:20225607  
KEYWORDS  
SOURCE  
ORGANISM

Unknown.  
Unclassified.  
1 (bases 1 to 9096)  
REFERENCE  
AUTHORS Kurth, R., Baier, M., Bannert, N., Metzner, K. and Werner, A.  
TITLE Genomic nucleic acids, cDNA and mRNA which code for polypeptides  
with IL-16 activity, processes for the production thereof and their  
use  
JOURNAL Patent: US 6338844-A 5 15-JAN-2002;  
LOCATION/Qualifiers  
1. 9096  
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ORIGIN /mol\_type="unassigned DNA"

Query Match 30.4%; Score 17; DB 6; Length 9096;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTATGTTGAATGCT 24  
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Db 3452 GTGGTATGTTGAATGCT 3436

RESULT 25  
LOCUS A93556 15936 bp DNA linear PAT 22-JAN-2000  
DEFINITION Sequence 1 from Patent WO9738105.  
ACCESSION A93556  
VERSION A93556.1 GI:6741761  
KEYWORDS  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE  
AUTHORS 1 (bases 1 to 15936)  
TITLE Baier,M. and Metzner,K.  
GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESSES FOR THE PRODUCTION THEREOF AND THEIR USE  
PATENT: WO 9738105-A 1 16-OCT-1997;  
JOURNAL BUNDESREP DEUTSCHLAND (DE); BAIER MICHAEL (DE)  
FEATURES  
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exon 5540..6635  
exon 7504..7672  
exon 9711..9812  
exon 12065..12323  
exon 12578..12703  
exon 14767..15936  
ORIGIN

Query Match 30.4%; Score 17; DB 6; Length 15936;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTATGTTGAATGCT 24  
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Db 10292 GTGGTATGTTGAATGCT 10276

RESULT 26  
LOCUS ARI82396 15936 bp DNA linear PAT 20-APR-2002  
DEFINITION Sequence 1 from patent US 6338844.  
ACCESSION ARI82396  
VERSION ARI82396.1 GI:20225603  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE  
AUTHORS 1 (bases 1 to 15936)  
TITLE Kurth,R., Baier,M., Bannert,N., Metzner,K. and Werner,A.  
Genomic nucleic acids, cDNA and mRNA which code for polypeptides with IL-16 activity, processes for the production thereof and their use  
PATENT: US 6338844-A 1 15-JAN-2002;  
JOURNAL Patent: US 6338844-A 1 15-JAN-2002;  
FEATURES  
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ORIGIN

Query Match 30.4%; Score 17; DB 6; Length 15936;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTATGTTGAATGCT 24  
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Db 10292 GTGGTATGTTGAATGCT 10276

RESULT 27  
LOCUS AF077011 15936 bp DNA linear PRI 07-JUN-1999  
DEFINITION Homo sapiens interleukin 16 (IL16) gene, complete cds.  
ACCESSION AF077011  
VERSION AF077011.1 GI:4322270  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 15936)  
TITLE Bannert,N., Avots,A., Baier,M., Seifling,E. and Kurth,R.  
GA-binding protein factors, in concert with the coactivator CREB binding protein/p300, control the induction of the interleukin 16 promoter in T lymphocytes  
Proc. Natl. Acad. Sci. U.S.A. 96 (4), 1541-1546 (1999)  
JOURNAL  
PUBMED 9990060  
REFERENCE  
AUTHORS 2 (bases 1 to 15936)  
TITLE Bannert,N., Baier,M. and Kurth,R.  
Direct Submision  
Submitted (10-JUL-1998) Paul-Ehrlich-Institut,  
Paul-Ehrlich-Str. 51-59, Langen 63225, Germany  
JOURNAL  
FEATURES  
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OEGTIOKNEVLSINGSLKGTTHDAIILROARPGQAVIVTKLTPKAPMNDNS  
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ORIGIN



Query Match 30.4%; Score 17; DB 8; Length 15936;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 GTGGTATGTGAATGCT 24  
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Db 10292 GTGGTATGTGAATGCT 10276

RESULT 28  
CEY10666G/c 20244 bp DNA linear INV 09-AUG-2005

LOCUS Caenorhabditis elegans YAC Y10666G, complete sequence.  
DEFINITION  
ACCESSION AL033508  
VERSION AL033508.1 GI:3873422  
KEYWORDS HTG.  
SOURCE  
ORGANISM  
Caenorhabditis elegans  
Caenorhabditis elegans  
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
Rhabditidae; Rhabditidae; Peloderinae; Caenorhabditis.  
REFERENCE  
AUTHORS  
CONSTRM  
TITLE  
1 (bases 1 to 20244)  
C. elegans Sequencing Consortium  
Genome sequence of the nematode C. elegans: a platform for  
investigating biology  
Science 282 (5396), 2012-2018 (1998)

JOURNAL 9851916  
PUBMED 2 (bases 1 to 20244)  
REFERENCE MCMurray, A.A.  
AUTHORS Direct Submission  
TITLE Submitted (12-NOV-1998) Nematode Sequencing Project, Sanger  
Institute, Hinxton, Cambridge CB10 1SA, England and Department of  
Genetics, Washington University, St. Louis, MO 63110, USA. E-mail:  
worm@sanger.ac.uk  
JOURNAL  
COMMENT  
Coding sequences below are predicted from computer analysis, using  
predictions from GeneFinder (P. Green, U. Washington), and other  
available information.  
Current sequence finishing criteria for the C. elegans genome  
sequencing consortium are that all bases are either sequenced  
unambiguously on both strands, or on a single strand with both a  
dye primer and dye terminator reaction, from distinct subclones.  
Exceptions are indicated by an explicit note.  
IMPORTANT: This sequence is NOT necessarily the entire insert of  
the specified clone. It may be shorter because we only sequence  
overlapping sections once, or longer because we arrange for a small  
overlap between neighbouring submissions.  
For a graphical representation of this sequence and its analysis  
see: - [http://www.wormbase.org/perl/ace/elegans/seq/sequence?](http://www.wormbase.org/perl/ace/elegans/seq/sequence?name=Y10666G;class=Sequence)  
name=Y10666G;class=Sequence  
IMPORTANT: This sequence is not the entire insert of clone Y10666G.  
It may be shorter because we only sequence overlapping sections  
once, or longer because we arrange for a small overlap between  
neighbouring submissions.  
The true left end of clone ZC434 is at 10139 in this sequence. The  
true right end of clone T20F10 is at 104 in this sequence. The  
start of this sequence (1..104) overlaps with the end of sequence  
Z81594.  
The end of this sequence (20139..20244) overlaps with the start of  
sequence Z75714.

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CDS

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gene  
CDS



KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Bakaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.
REFERENCE	1 (bases 1 to 21072)
AUTHORS	Rieder,M.J., Daniels,R.L., da Ponte,S.H., Hastings,N.C., Ahearn,M.O., Rajkumar,N., Yi,Q. and Nickerson,D.A.
TITLE	Direct Submission
JOURNAL	Submitted (09-BBC-2003) Genome Sciences, University of Washington, 1705 NE Pacific, Seattle, WA 98195, USA
COMMENT	To cite this work please use: SeattleSNP. NHLBI HL66682 Program for Genomic Applications, UW-FHCRC, Seattle, WA (URL: <a href="http://pga.gs.washington.edu">http://pga.gs.washington.edu</a> ).
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variation	1985



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RESULT 30	
LOCUS CO870229/c	
DEFINITION Sequence 650 from Patent WO2004074320.	
ACCESSION CO870229	
VERSION CO870229.1 GI:51999852	
KEYWORDS	.
SOURCE Homo sapiens (human)	
ORGANISM Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eumetazoa; Euarchontoglires; Primates; Catarrhini; Hominoidea; Hominidae; Homo.	
REFERENCE 1 Morris,D.W., Morris,D.W. and Malandro,M.S.	



TITLE Novel therapeutic targets in cancer  
JOURNAL Patent: WO 2004/074320-A 650 02-SEP-2004;  
Sagres Discovery, Inc. (US)  
FEATURES  
Source Location/Qualifiers  
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Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 8 GTGGTATGTTGAATGCT 24  
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Db 21309 GTGGTATGTTGAATGCT 21293  
RESULT 31  
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LOCUS Arabidopsis thaliana genomic DNA, chromosome 3, P1 clone: MCP4.  
DEFINITION  
AB028610 BA000014  
ACCESSION  
AB028610.1 GI:5041963  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Arabidopsis thaliana (thale cress)  
Arabidopsis thaliana  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Arabidopsids.  
REFERENCE  
1 Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asaniz, E. and Tabata, S.  
AUTHORS  
TITLE  
Structural analysis of Arabidopsis thaliana chromosome 3. I.  
Sequence features of the regions of 4,504,864 bp covered by sixty  
P1 and TAC clones  
DNA Res. 7 (2), 131-135 (2000)  
10819329  
2 (bases 1 to 38810)  
Sato, S., Nakamura, Y., Kaneko, T., Katoh, T., Asaniz, E. and Tabata, S.  
JOURNAL  
PUBMED  
REFERENCE  
AUTHORS  
TITLE  
Direct Submission  
Submitted (09-JUN-1999) Yasukazu Nakamura, Kazusa DNA Research  
Institute, Department of Plant Gene Research; 1532-3, Yana,  
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,  
Tel: 81-438-52-3935, Fax: 81-438-52-3934)  
COMMENT  
Address for correspondence: kaos@kazusa.or.jp  
For the latest information on annotation of this clone, please see  
http://www.kazusa.or.jp/kaos/cgi-bin/agd\_graph.cgi?c=MCP4  
Genes with similarity to proteins in the databases are described in  
'product' or 'note' qualifiers. Genes that have no significant  
protein similarity are described as 'unknown protein'.  
The software programs used to predict genes include: Grail  
(Informatics Group, Oak Ridge National Laboratory,  
http://combio.ornl.gov/Grail-1.3/),  
GENSCAN (Chris Burge, MIT, http://CCR-081.mit.edu/GENSCAN.html),  
NetGene2 (S.M. Hebsgaard, et al., CBS, Technical University of  
Denmark, http://www.cbs.dtu.dk/services/NetGene2/) and  
SplicePredictor (Volker Brendel, Stanford University,  
http://gremli.ni.zool.laebate.edu/cgi-bin/sp.cgi).  
Genes encoding tRNAs are predicted by tRNAscan-SE  
(Sean Eddy, Washington University School of Medicine, St. Louis,  
http://genome.wustl.edu/eddy/tRNAscan-SE/).  
This sequence may not be the entire insert of this clone. It may be  
shorter because we remove overlaps between neighboring submissions.  
The 5' clone is NM17 and the 3' clone is MD16.  
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EEDDEYEDDDVTPKCNFLCPTTTRRPPRLILPNNPVEETVALSCIGERTLVN  
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CDS

HKIFRKLVSGGYEYISFKSDSKWLDLVNLDGESTELCELSVLSKNAFYFVITKEE  
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CDS

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/translation="MPGKSSVPLPHKPTPLKPSSTSSSSNNSTNOACAACKYOR  
RKCAPDCLAPYFPHDRHROPILNAHLFGVSNITKIKSLTPEKDAAMTIMQSOA  
RANDPVDGCGIILKLOYLETNELBEIYVQLAMPDRDGHQHHOEPHIOMEOED  
LSFSSSCDLNNNSIPYNYPLNIHQEPNOQYSSGNNBSGLDEDMWCQDSSITI  
VNKAAGTIDCEEDVKEVBEVSSERHEPHEAFVQRKLDLPSAQYITIS"

snRNA

25224..25328  
/product="U6 snRNA"

CDS

/note="gene\_id:MCP4.9"

/evidence=not\_experimental  
complement (join(25824..25923,26017..26095,26187..26292,  
26382..26485,26570..26669,26750..26845,26946..27023,  
27100..27168,27247..27417,27535..27621,27699..27803,  
27885..27980,28072..28247,28360..28519,28623..28754,  
29074..29095,29216..29253))  
/note="gene\_id:MCP4.10"

/codon\_start=1  
/evidence=not\_experimental

/product="chaperonin; similar to GroEL protein"

/protein\_id="BAB02911.1"

/db\_xref="GI:9294610"

/translation="MYRVLSKSSISGSSSRKLVSGRITSSRYAKDIFSGIGARA  
AMLOGSEVAVAKVTMGPKRNYIISSGPKITTDGTVASISFOAKAKITGAE  
LVKOVASATNKVADGTTCAVTLQALIBGCKSVAGVVMVDLRVGINMAIAVSD  
LKSRAVMISTEPETIOTATISANGEBIGELIARAMEKVGEGVITVADNTLDNEE  
VVEGMKLARGYISPYFTDEKQCELENPIILHEKSIDINSILVLEAAVKSRR  
LLIYAEVDESALAMLINKHGGLKVCALKAPFGDNRKASLDLAVLGAEYISRP  
RGLSEKIRPELIGTAKKVTYTRDITLILGGGKLIERCELSRANKSTSPD  
EKYDERLSKSGVAVFKVGSASSEYGEKDRKTDKTLNTRAIVEGIIPGGVALL  
YATIALNLTQENEDQRRGOVIVGNALKAPEFTIANAAGVDGSLVKKLEQDDCNG  
FDAQKGYDMVAKGIIDPVKIRLTALTDAAVSGLLTTEASVLYKADENTPHVED  
MASMG"

CDS

complement (join(29885..30097,30208..30304,30407..30501,  
30719..30823,30933..31094,31194..31290,31381..31643,  
30719..30823,30933..31094,31194..31290,31381..31643,

31757..31881,31989..32154,32296..32374,32509..32600,  
32690..32758,32846..33004,33137..33193,33278..33340,

Query Match

30.4%; Score 17; DB 15; Length 38810;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

12 TATGTTGAAGCTCATC 28

Db

11517 TATGTTGAAGCTCATC 11533

RESULT 32

CBRG44L02

LOCUS

CBRG44L02 43429 bp DNA linear INV 04-NOV-2000

DEFINITION

Caenorhabditis briggsae cosmid G44L02, complete sequence.

ACCESSION

AC084620

VERSION

AC084620.1 GI:11095069

KEYWORDS

HTG.

SOURCE

Caenorhabditis briggsae

ORGANISM

Caenorhabditis briggsae

REFERENCE

1 (bases 1 to 43429)  
Washington University Genome Sequencing Center.

AUTHORS

The C. briggsae Genome Sequencing Project

JOURNAL

Unpublished

TITL

The sequence of C. briggsae cosmid G44L02

AUTHORS

3 (bases 1 to 43429)

REFERENCE

Unpublished

TITL

Submitted

JOURNAL

Submitted (04-NOV-2000) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA

COMMENT

Submitted by:

Genome Sequencing Center

Department of Genetics, Washington University,

St. Louis, MO 63110, USA

e-mail: jlepith@wuston.wustl.edu

NOTICE: This sequence may not be the entire insert of this clone.

It may be shorter because we only sequence overlapping sections

once, or longer because we provide a small overlap between

neighboring submissions.

Location/Qualifiers

FEATURES

1..43429  
/organism="Caenorhabditis briggsae"

source

/mol\_type="genomic DNA"

ORIGIN

/strain="Gujarat G16"

Query Match

30.4%; Score 17; DB 2; Length 43429;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy

31 GATCCAGGACCAATGAG 47

Db

3292 GATCCAGGACCAATGAG 3308

RESULT 33

AL355875/c

LOCUS

AL355875 49362 bp DNA linear PRI 18-MAY-2005

DEFINITION

Human DNA sequence from clone Rp4-685N8 on chromosome 1p34.3-36.11,

ACCESSION

AL355875

VERSION

AL355875.10 GI:16972865

KEYWORDS

HTG.



```

SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominiidae; Homo.
REFERENCE   1 (bases 1 to 49362)
AUTHORS     Tracey,A.
JOURNAL     Direct Submission
            Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgehire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
COMMENT     On Nov 16, 2001 this sequence version replaced gi:15590941.
            The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Bm., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WormPeP; Information
on the WormPeP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
RP4-685N8 is from the library RPCI-4 constructed by the group of
Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pCYPAC2

----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
-----

This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (l.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.

Location/Qualifiers
        1..49362
           /organism="Homo sapiens"
           /mol_type="genomic DNA"
           /db_xref="RZPD:RPCI7D:4N08685"
           /db_xref="taxon:9606"
           /chromosome="1"
           /map="p34.3-36.11"
           /clone="RP4-685N8"
           /clone_1fb="RPCI-4"
misc_feature       2000
                    /note="Clone_right_end: RP4-732F8"
misc_feature       49362
                    /note="Clone_right_end: RP4-685N8"
ORIGIN
Query Match          30.4%; Score 17; DB 8; Length 49362;
Best Local Similarity 100.0%; Fred.No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0

QY      34 CCAGGCGCATGTGAAT 50
|||||
Db      28399 CCGAGCGCATGTGAAT 28377

RESULT 34
AC108345.3
WPCOMMENT
Sequence split into 4 fragments LOCUS AC108345 Accession AC108345
Fragment Name Begin End
AC108345_0 1 110000
AC108345_1 10001 210000
AC108345_2 20001 310000
AC108345_3 30001 351828
Continuation (4 of 4) of AC108345 from base 300001 (AC108345 Rattus norvegicus

```

Query Match 30.4%; Score 17; DB 14; Length 51828;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**RESULT 35**  
 AC118389\_5/c  
 WPCOMMENT  
 Sequence split into 6 fragments  
 Fragment Name Begin End  
 AC118389\_0 1 110000  
 AC118389\_1 100001 210000  
 AC118389\_2 200001 310000  
 AC118389\_3 300001 410000  
 AC118389\_4 400001 510000  
 AC118389\_5 500001 568550  
 Continuation 76 of 6) of AC118389 from base 500001 (AC118389 Rattus norvegicus clone C

Query Match 30.4%; Score 17; DB 14; Length 68550;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

**Db** 20510 GTATGTGAATGCTCAT 20526  
**Qy** 11 GTATGTGAATGCTCAT 27  
 |||||  
 |||||

**RESULT 36**  
 AC087682  
 LOCUS  
 DEFINITION  
 AC087682 Homo sapiens chromosome 18 clone RP11-886K22 map 18, LOW-PASS  
 SEQUENCE SAMPLING.  
 AC087682 AC087682.1 GI:12223457  
 HTG: HTGS PHASE0.  
 Homo sapiens (human)  
 Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 68589)  
 Birren,B., Linton,L., Nusbaum,C. and Lander,B.  
 Homo sapiens chromosome 18, clone RP11-886K22  
 Unpublished  
 2 (bases 1 to 68589)  
 Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,  
 Barris,N., Bastien,V., Boguski,M., Bouckgeat,B., Brown,A.,  
 Camarata,P., Campopiano,A., Choquet,Y., Colangelo,M., Collins,S.,  
 Collumore,A., Cooke,P., DeRellano,K., Dewar,K., Diaz,J.S.,  
 Dodge,S., Fero,S., Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J.,  
 Gargus,S., Ginde,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
 Hagos,B., Heatford,A., Horton,L., Hulme,W., Iliev,I., Johnson,R.,  
 Jones,C., Karatas,A., Larocque,K., Lamazares,R., Landers,T.,  
 Lehoczy,J., Levine,R., Liu,G., Maclean,C., Macdonald,P.,  
 Marquis,N., Matthews,C., McCarthy,M., McSwan,P., McKernan,K.,  
 McPheeters,R., Meldrum,J., Menus,L., Mihova,T., Mlenga,V.,  
 Murphy,T., Naylor,J., Nguyen,C., Norbu,C., Norman,C.H.,  
 O'Connor,T., O'Donnell,P., O'Neill,D., Oliver,J., Peterson,K.,  
 Phunkhang,P., Pletre,N., Pollara,V., Raymond,C., Retta,R.,  
 Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M.,  
 Roy,A., Santos,R., Schauer,S., Schuppach,R., Seaman,S., Severy,P.,  
 Sounez,C., Spencer,B., Strange-Thomann,N., Stojanovic,N.,  
 Strauss,N., Sudramanian,A., Talamas,J., Teste,S., Theodore,J.,  
 Travers,M., Travis,N., Triggillo,J., Vassiliev,H., Viel,R., Vo,A.,  
 Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zaitoun,J.,  
 Zembek,L., Zimmer,A. and Zody,M.  
 Direct Submission  
 Submitted (15-JAN-2001) Whitehead Institute/MIT Center for Genome



## COMMENT

Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBR

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## Project Information

Center project name: L12306

Center clone name: 866\_K\_22

NOTE: This record contains 85 individual  
sequencing reads that have not been assembled into  
contigs. Runs of N are used to separate the reads  
and the order in which they appear is completely  
arbitrary. Low-pass sequence sampling is useful for  
identifying clones that may be gene-rich and allows  
overlap relationships among clones to be deduced.  
However, it should not be assumed that this clone  
will be sequenced to completion. In the event that  
the record is updated, the accession number will  
be preserved.

1 714: contig of 714 bp in length  
715 814: gap of 100 bp  
815 1522: contig of 708 bp in length  
1523 1622: gap of 100 bp in length  
1623 2330: contig of 708 bp in length  
2331 2430: gap of 100 bp in length  
2431 3132: contig of 702 bp in length  
3133 3232: gap of 100 bp in length  
3233 3944: contig of 712 bp in length  
3945 4044: gap of 100 bp in length  
4045 4741: contig of 697 bp in length  
4742 4841: gap of 100 bp in length  
4842 5570: contig of 729 bp in length  
5571 5670: gap of 100 bp in length  
5671 6387: contig of 717 bp in length  
6388 6487: gap of 100 bp in length  
6488 7189: contig of 702 bp in length  
7190 7289: gap of 100 bp in length  
7290 7992: contig of 703 bp in length  
7993 8092: gap of 100 bp in length  
8093 8796: contig of 704 bp in length  
8797 8896: gap of 100 bp in length  
8897 9603: contig of 707 bp in length  
9604 9703: gap of 100 bp in length  
9704 10405: contig of 702 bp in length  
10406 10505: gap of 100 bp in length  
10506 11206: contig of 701 bp in length  
11207 11306: gap of 100 bp in length  
11307 12042: contig of 736 bp in length  
12043 12142: gap of 100 bp in length  
12143 12855: contig of 713 bp in length  
12856 12955: gap of 100 bp in length  
12957 13654: contig of 693 bp in length  
13655 13754: gap of 100 bp in length  
13755 14489: contig of 735 bp in length  
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14590 15269: contig of 680 bp in length  
15270 15369: gap of 100 bp in length  
15370 16083: contig of 714 bp in length  
16084 16183: gap of 100 bp in length  
16184 16887: contig of 704 bp in length  
16888 16987: gap of 100 bp in length  
16989 17677: contig of 690 bp in length  
17678 17777: gap of 100 bp in length  
17779 18483: contig of 706 bp in length  
18484 18583: gap of 100 bp in length  
18584 19299: contig of 716 bp in length  
19300 19399: gap of 100 bp in length  
19400 20119: contig of 720 bp in length

20120 20219: gap of 100 bp in length  
20220 20945: contig of 726 bp in length  
20946 21045: gap of 100 bp in length  
21046 21763: contig of 718 bp in length  
21764 21863: gap of 100 bp in length  
21864 22556: contig of 693 bp in length  
22557 22657: gap of 100 bp in length  
22657 23376: contig of 719 bp in length  
23376 23475: gap of 100 bp in length  
23475 24179: contig of 704 bp in length  
24179 24279: gap of 100 bp in length  
24279 24973: contig of 694 bp in length  
24973 25073: gap of 100 bp in length  
25073 25788: contig of 715 bp in length  
25788 25889: gap of 100 bp in length  
25889 26602: contig of 714 bp in length  
26602 26702: gap of 100 bp in length  
26702 27398: contig of 696 bp in length  
27398 27498: gap of 100 bp in length  
27498 28190: contig of 692 bp in length  
28190 28290: gap of 100 bp in length  
28290 29008: contig of 718 bp in length  
29008 29108: gap of 100 bp in length  
29108 29825: contig of 717 bp in length  
29825 29926: gap of 100 bp in length  
29926 30628: contig of 703 bp in length  
30628 30728: gap of 100 bp in length  
30728 31426: contig of 698 bp in length  
31426 31526: gap of 100 bp in length  
31526 32222: contig of 696 bp in length  
32222 32323: gap of 100 bp in length  
32323 33015: contig of 693 bp in length  
33015 33115: gap of 100 bp in length  
33115 33833: contig of 717 bp in length  
33833 33933: gap of 100 bp in length  
33933 34659: contig of 727 bp in length  
34659 34759: gap of 100 bp in length  
34759 35450: contig of 691 bp in length  
35450 35550: gap of 100 bp in length  
35550 36270: contig of 720 bp in length  
36270 36371: gap of 100 bp in length  
36371 37078: contig of 708 bp in length  
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37178 37892: contig of 714 bp in length  
37892 37992: gap of 100 bp in length  
37992 38715: contig of 723 bp in length  
38715 38815: gap of 100 bp in length  
38815 39528: contig of 713 bp in length  
39528 39628: gap of 100 bp in length  
39628 40340: contig of 712 bp in length  
40340 40440: gap of 100 bp in length  
40440 41084: contig of 644 bp in length  
41084 41184: gap of 100 bp in length  
41184 41877: contig of 693 bp in length  
41877 41977: gap of 100 bp in length  
41977 42655: contig of 678 bp in length  
42655 42755: gap of 100 bp in length  
42755 43464: contig of 709 bp in length  
43464 43564: gap of 100 bp in length  
43564 44301: contig of 737 bp in length  
44301 44401: gap of 100 bp in length  
44401 45116: contig of 715 bp in length  
45116 45216: gap of 100 bp in length  
45216 45927: contig of 711 bp in length  
45927 46027: gap of 100 bp in length  
46027 46702: contig of 675 bp in length  
46702 46802: gap of 100 bp in length  
46802 47515: contig of 713 bp in length  
47515 47615: gap of 100 bp in length  
47615 48326: contig of 711 bp in length  
48326 48427: gap of 100 bp in length  
48427 49125: contig of 699 bp in length  
49125 49225: gap of 100 bp in length



```

* 49226 49930: contig of 705 bp in length
* 49931 50030: gap of 100 bp
* 50031 50744: contig of 714 bp in length
* 50745 50844: gap of 100 bp
* 50845 51534: contig of 690 bp in length
* 51535 51634: gap of 100 bp
* 51635 52348: contig of 714 bp in length
* 52349 52448: gap of 100 bp
* 52449 53192: contig of 744 bp in length
* 53193 53292: gap of 100 bp
* 53293 53930: contig of 638 bp in length
* 53931 54030: gap of 100 bp
* 54031 54736: contig of 706 bp in length
* 54737 54836: gap of 100 bp
* 54837 55331: contig of 695 bp in length

Query Match 30.4%; Score 17; DB 14; Length 68589;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 17 TGAATGCTCATCCGAT 33
Db 13988 TGAATGCTCATCCGAT 14004

RESULT 37
AC161705 68689 bp DNA linear HTG 18-MAY-2005
DEFINITION Bos taurus clone CH240-24P11, *** SEQUENCING IN PROGRESS ***, 16
unordered pieces.
AC161705.1 GI:66267863
AC161705.1 HTG: HTGS_PHASE1.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
MAMMALIA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eukaryota; Eumetazoa; Laurasiatheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
1 (bases 1 to 68689)
Munzy,D., Adams,C., Agbai II,O., Allen,C., Alsbrooks,S., Archer,P.,
Aireddondo,H., Bandarnaike,D., Bangura,L., Beltran,B., Beltman,R.,
Berducci,A., Biewalo,K., Blyth,P., Bonham,H., Buhay,C., Burch,P.,
Cadoree,I., Canada,A., Cardenas,V., Carter,K., Cavazos,I.,
Chacko,J., Chahrouh,M., Chavez,D., Chen,A., Chen,G., Chen,R.,
Cheng,M.-T., Chu,J., Clerc,K., Cockrell,R., Coyle,M., Cree,A.,
Curry,S., Dai,W., Davila,M.L., Davis,C., Davy-Carroll,L., De
Ande,C., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H.,
Donlin,J., McCauley,S., Dugan-Rocha,S., Dunn,A., Durbin,K.,
Dzinda,D., Egan,A., Escotto,M., Espinosa,V., Eugene,C., Fa,M.,
Fernandez,S., Fernando,P., Flagg,N., Forbes,L., Foster,P.,
Fowler,G., Fu,Q., Fuh,E., Garcia,A., Garcia,R., Garner,T.,
Gaslin,C., Gench,S., Ghose,S., Gill,R., Gonzalez,D.,
Gonzalez-Garay,M., Guevara,W., Holder,M., Haaland,W., Haeblerlen,K.,
Hall,B., Hamid,H., Hamilton,K., Harber,B., Harris,R., Haylak,P.,
Hawes,A., Hawkins,E., Hayes,S., Hemphill,L., Hernandez,J.,
Hines,S., Hitchens,M., Hodgson,A., Hoques,M., Hollins,B.,
Howell,L.T., Hulys,S., Hume,J., Imo,K., Jackson,A., Jackson,L.,
Jacob,L., Jiang,H., Johnson,B., Johnson,R., Kalafut,K., Kelly,S.,
Keye,T., Khan,Z., King,L., Kovar,C., Kowis,A., Kowis,C., Lara,F.,
Leal,S., Lee,K., Lee,S., Legall,F.I., Lemmon,S., Lewis,L., Li,B.,
Li,Y., Li,Z., Linnell,M., Liu,W., Liu,Y.-S., Liu,Y., Llyanage,D.,
London,P., Lopez,J., Lorenshewa,L., Lozado,R., Luk,T., Madu,D.,
Maheshwari,M., Mahoney,C., Malloy,K., Mansouri,D., Martinez,E.,
McClelland,H., McPherson,J., Mercadao,C., Metzker,M.,
Milosavljevic,A., Minja,E., Morgan,M., Morris,S., Mundaasa,M.,
Murray,D., Nazarihi,I., Ngo,D., Nguyen,N., Norwig-Bastnaugh,E.,
Nott,A., Nwaokemelehen,O., Obregon,M., Ochi-Okorie,C., Oden,E.,
Okwunonu,G., Okwunonu,K., Parker,D., Pasternak,S., Patel,B.,
Patel,V., Paul,H., Perez,A., Perez,L., Petrosino,J., Pham,T.,
Primas,B., Pu,L.-L., Puazo,M., Qin,X., Quinn,A., Quiroz,J.,
Rabata,D., Rachlin,E., Reigh,R., Ren,Y., Reuter,M., Richards,S.,
Rives,C., Rodriguez,F., Rojas,A., Ruiz,S.J., Sana,M., Sanders,W.,
Sanluis,J., Santos,R., Savery,G., Scherer,S., Shen,H., Shen,Y.,

```

```

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Sisson,I., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R.,
Svatek,A., Taylor,B., Taylor,T., Thomas,N., Thorn,R., Thornton,R.,
Trezek,Z., Usmani,K., Varigo,C., Verduzco,D., Villasana,D., Vitek,D.,
Volkov,A., Waldron,L., Walker,B., Wang,Q., Wang,S., Warren,J.,
Wei,X., Wheeler,D., Williams,G., Williams,R., Wolley,K., Wright,R.,
Wu,J., Yakub,S., Yan,K., Yuan,Y., Yu,F., Zhang,J., Zhang,L.,
Zhang,Z., Zhou,J., Weinstein,G. and Gibbs,R.
Direct Submission
Unpublished
2 (bases 1 to 68689)
Morley,K.C.
Direct Submission
Submitted (18-MAY-2005) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
-----Genome Center
Center: Baylor College of Medicine
Center code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
Contact: hgsc-help.tmc.edu
-----Project Information
Center project name: FBKY
Center clone name: CH240-24P11
-----Summary Statistics
Sequencing vector: Plasmid;
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.990329
Consensus quality: 71426 bases at least Q40
Consensus quality: 74385 bases at least Q30
Consensus quality: 76736 bases at least Q20
Estimated insert size: 91774; sum-of-contigs estimation
Quality coverage: 1x in Q20 bases; sum-of-contigs estimation
-----
* NOTE: Estimated insert size may differ from sequence length
* (see http://www.hgsc.bcm.tmc.edu/docs/genbank_drift_data.html).
* NOTE: This is a "working draft" sequence. It currently
* consists of 16 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4341: contig of 4341 bp in length
* 4342 4441: gap of unknown length
* 4442 6717: contig of 2276 bp in length
* 6718 6817: gap of unknown length
* 6818 9332: contig of 2515 bp in length
* 9333 9432: gap of unknown length
* 9433 13498: contig of 4066 bp in length
* 13499 13598: gap of unknown length
* 13599 16153: contig of 2555 bp in length
* 16154 16253: gap of unknown length
* 16254 19809: contig of 3556 bp in length
* 19810 19909: gap of unknown length
* 19910 23838: contig of 3929 bp in length
* 23839 23938: gap of unknown length
* 23939 31168: contig of 7230 bp in length
* 31169 31268: gap of unknown length
* 31269 34204: contig of 2926 bp in length
* 34205 34304: gap of unknown length
* 34305 37959: contig of 3655 bp in length
* 37960 38059: gap of unknown length
* 38060 46017: contig of 7958 bp in length
* 46018 46117: gap of unknown length
* 46118 48808: contig of 2691 bp in length
* 48809 48908: gap of unknown length
* 48909 55388: contig of 6480 bp in length
* 55389 55488: gap of unknown length
* 55489 59659: contig of 4371 bp in length
* 59660 64939: gap of unknown length
* 64940 65039: contig of 4980 bp in length

```



FEATURES \* 65040 66689: contig of 3650 bp in length.  
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SOURCE 1..66689  
/organism="Bos taurus"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9913"  
/clone="CH240-24F11"  
4342..4441  
gap /estimated\_length=unknown  
6718..6817  
gap /estimated\_length=unknown  
9333..9432  
gap /estimated\_length=unknown  
13489..13598  
gap /estimated\_length=unknown  
16154..16253  
gap /estimated\_length=unknown  
19810..19909  
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23839..23938  
gap /estimated\_length=unknown  
31169..31268  
gap /estimated\_length=unknown  
34205..34304  
gap /estimated\_length=unknown  
37960..38059  
gap /estimated\_length=unknown  
46018..46117  
gap /estimated\_length=unknown  
48809..48908  
gap /estimated\_length=unknown  
55389..55488  
gap /estimated\_length=unknown  
59860..59959  
gap /estimated\_length=unknown  
64940..65039  
gap /estimated\_length=unknown  
ORIGIN  
Query Match 30.4%; Score 17; DB 14; Length 66689;  
Best Local Similarity 100.0%; Pred. No. 47;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 11 GTATGTAATGCTCAT 27  
Db 29866 GTATGTAATGCTCAT 29882  
RESULT 38  
AC101430/c 69049 bp DNA linear HTG 23-NOV-2001  
LOCUS Mus musculus clone RP23-302L24, LOW-PASS SEQUENCE SAMPLING.  
DEFINITION AC101430  
AC101430.1 GI:17060205  
VERSION HTG; HTGS PHASEO.  
KEYWORDS Mus musculus (house mouse)  
SOURCE Mus musculus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 69049)  
Birren,B., Linton,L., Nusbaum,C. and Lander,E.  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
REFERENCE  
AUTHORS  
2 (bases 1 to 69049)  
Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,  
Anderson,S., Batra,N., Bastien,V., Boguski,K., Bouckgeater,B.,  
Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B.,  
Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A.,  
Cooke,P., Dearrellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S.,  
Ferreira,P., Fitzhugh,W., Gage,D., Galagan,J., Gardyna,S.,  
Gilde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N.,  
Hagos,B., Heatford,A., Horton,L., Hulme,W., Illiev,I., Johnson,R.,

Jones,C., Kamat,A., Karatas,A., Kells,C., Labrecque,K.,  
Lamazeres,R., Landers,T., Lehotzky,J., Levine,R., Liu,G.,  
MacLean,C., Macdonald,P., Major,J., Marguis,N., Matthews,C.,  
McCartney,M., McEwan,P., McKernan,K., McPheters,R., Melitini,J.,  
Meneva,L., Mihova,T., Mienga,V., Murphy,T., Naylor,J., Nguyen,C.,  
Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neill,D.,  
Oliver,J., Peterson,K., Phunhang,P., Pierre,N., Pollara,V.,  
Raymond,C., Retta,R., Riedack,W., Riley,R., Rise,C., Rogov,P.,  
Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupack,R.,  
Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N.,  
Strauss,N., Subramanian,A., Talamas,J., Teefaye,S., Theodore,J.,  
Topham,K., Travers,M., Travis,N., Trigglio,J., Vassiliev,H.,  
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,  
Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.  
Direct Submission  
Submitted (23-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Snit, A.P.A. & Green, P. (1996-1997)  
http://ftp.genome.washington.edu/RM/RepeatMasker.html  
----- Genome Center  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: MIBR  
Web site: http://www-seq.wi.mit.edu  
Contact: sequence\_submissions@genome.wi.mit.edu  
----- Project Information  
Center project name: L16686  
Center clone name: 302\_L\_24  
-----  
\* NOTE: This record contains 84 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.  
1 713: contig of 713 bp in length  
\* 1 813: gap of 100 bp  
\* 814 1506: contig of 693 bp in length  
\* 1507 1606: gap of 100 bp  
\* 1607 2309: contig of 703 bp in length  
\* 2310 2409: gap of 100 bp  
\* 2410 3128: contig of 719 bp in length  
\* 3129 3228: gap of 100 bp  
\* 3229 3932: contig of 704 bp in length  
\* 3933 4032: gap of 100 bp  
\* 4033 4751: contig of 719 bp in length  
\* 4752 4851: gap of 100 bp  
\* 4852 5580: contig of 729 bp in length  
\* 5581 5680: gap of 100 bp  
\* 5681 6408: contig of 728 bp in length  
\* 6409 6508: gap of 100 bp  
\* 6509 7242: contig of 734 bp in length  
\* 7243 7343: gap of 100 bp  
\* 7344 8041: contig of 699 bp in length  
\* 8042 8141: gap of 100 bp  
\* 8142 8870: contig of 729 bp in length  
\* 8871 8970: gap of 100 bp  
\* 8971 9698: contig of 728 bp in length  
\* 9699 9799: gap of 100 bp  
\* 9799 10517: contig of 719 bp in length  
\* 10518 10617: gap of 100 bp  
\* 10618 11337: contig of 720 bp in length  
\* 11338 11437: gap of 100 bp  
\* 11438 12151: contig of 714 bp in length  
\* 12152 12251: gap of 100 bp  
\* 12252 12962: contig of 711 bp in length  
\* 12963 13062: gap of 100 bp  
\* 13063 13806: contig of 744 bp in length



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* 13807 13906: gap of 100 bp
* 13907 14671: contig of 765 bp in length
* 14672 14771: gap of 100 bp
* 14772 15507: contig of 736 bp in length
* 15508 15607: gap of 100 bp
* 15608 16325: contig of 718 bp in length
* 16326 16425: gap of 100 bp
* 16426 17137: contig of 712 bp in length
* 17138 17237: gap of 100 bp
* 17238 17966: contig of 729 bp in length
* 17967 18066: gap of 100 bp
* 18067 18759: contig of 693 bp in length
* 18760 18859: gap of 100 bp
* 18860 19594: contig of 735 bp in length
* 19595 19694: gap of 100 bp
* 19695 20399: contig of 705 bp in length
* 20400 20499: gap of 100 bp
* 20500 21221: contig of 722 bp in length
* 21222 21321: gap of 100 bp
* 21322 22032: contig of 711 bp in length
* 22033 22132: gap of 100 bp
* 22133 22856: contig of 724 bp in length
* 22857 22956: gap of 100 bp
* 22957 23691: contig of 735 bp in length
* 23692 23791: gap of 100 bp
* 23792 24538: contig of 747 bp in length
* 24539 24638: gap of 100 bp
* 24639 25350: contig of 712 bp in length
* 25351 25450: gap of 100 bp
* 25451 26182: contig of 732 bp in length
* 26183 26282: gap of 100 bp
* 26283 27021: contig of 739 bp in length
* 27022 27121: gap of 100 bp
* 27122 27843: contig of 722 bp in length
* 27844 27944: gap of 100 bp
* 27944 28666: contig of 723 bp in length
* 28667 28766: gap of 100 bp
* 28767 29462: contig of 696 bp in length
* 29463 29562: gap of 100 bp
* 29563 30273: contig of 711 bp in length
* 30274 30373: gap of 100 bp
* 30374 31100: contig of 727 bp in length
* 31101 31200: gap of 100 bp
* 31201 31935: contig of 735 bp in length
* 31936 32035: gap of 100 bp
* 32036 32765: contig of 730 bp in length
* 32766 32865: gap of 100 bp
* 32866 33580: contig of 715 bp in length
* 33581 33680: gap of 100 bp
* 33681 34410: contig of 730 bp in length
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* 34511 35231: contig of 721 bp in length
* 35232 35331: gap of 100 bp
* 35332 36063: contig of 732 bp in length
* 36064 36163: gap of 100 bp
* 36164 36891: contig of 726 bp in length
* 36892 36991: gap of 100 bp
* 36992 37705: contig of 714 bp in length
* 37706 37805: gap of 100 bp
* 37806 38527: contig of 722 bp in length
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* 38629 39354: contig of 727 bp in length
* 39355 39454: gap of 100 bp
* 39455 40192: contig of 738 bp in length
* 40193 40292: gap of 100 bp
* 40293 41001: contig of 709 bp in length
* 41002 41101: gap of 100 bp
* 41102 41853: contig of 752 bp in length
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* 43529 43628: gap of 100 bp

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* 43629 44360: contig of 732 bp in length
* 44361 44460: gap of 100 bp
* 44461 45165: contig of 705 bp in length
* 45166 45265: gap of 100 bp
* 45266 45985: contig of 720 bp in length
* 45986 46085: gap of 100 bp
* 46086 46816: contig of 731 bp in length
* 46817 46916: gap of 100 bp
* 46917 47629: contig of 713 bp in length
* 47630 47729: gap of 100 bp
* 47730 48430: contig of 701 bp in length
* 48431 48530: gap of 100 bp
* 48531 49246: contig of 716 bp in length
* 49247 49346: gap of 100 bp
* 49347 50084: contig of 738 bp in length
* 50085 50184: gap of 100 bp
* 50185 50932: contig of 748 bp in length
* 50933 51032: gap of 100 bp
* 51033 51762: contig of 730 bp in length
* 51763 51862: gap of 100 bp
* 51863 52587: contig of 725 bp in length
* 52588 52687: gap of 100 bp
* 52688 53400: contig of 713 bp in length
* 53401 53500: gap of 100 bp
* 53501 54247: contig of 747 bp in length
* 54248 54347: gap of 100 bp
* 54348 55064: contig of 717 bp in length
* 55065 55164: gap of 100 bp
* 55165 55867: contig of 703 bp in length
* 55868 55967: gap of 100 bp
* 55968 56705: contig of 738 bp in length

Query Match
Best Local Similarity 30.4%; Score 17; DB 14; Length 69049;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 33 TCACGACGACATGAGAA 49
Db 41844 TCACGACGACATGAGAA 41828

RESULT 39
AL391804/c
LOCUS
DEFINITION
Human DNA sequence from clone Rpl1-384H3 on chromosome 13, complete
sequence.
ACCESSION
AL391804
VERSION
AL391804.8 GI:11121080
KEYWORDS
HTG.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo.
REFERENCE
1 (bases 1 to 69966)
Oliver K.
Direct Submission
Submitted (17-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegase@sanger.ac.uk
Clone request: clonerequest@sanger.ac.uk
On Nov 8, 2000 this sequence version replaced GI:11096501.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
Rpl1-384H3 is from the library RPl1-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm

```



VECTOR: pBACe3.6  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)

-----  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

## FEATURES

location/Qualifiers

source  
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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="RZPD:RPC18753H03384"  
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 /chromosome="13"  
 /clone="RP11-384H3"  
 /clone\_1lb="RPC1-11.2"  
 /note="Clone\_right\_end: RP11-25J23"  
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 14399  
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 misc\_feature  
 69966  
 /note="Clone\_right\_end: RP11-384H3"

## ORIGIN

Query Match 30.4%; Score 17; DB 8; Length 69966;  
 Best Local Similarity 100.0%; Pred. No. 47;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 33 TCCAGAGCAATGAGAA 49  
 |||||  
 Db 7058 TCCAGAGCAATGAGAA 7042

## RESULT 40

AL445677 84732 bp DNA linear PRI 18-MAY-2005  
 LOCUS AL445677

DEFINITION Human DNA sequence from clone RP11-59D5 on chromosome 6 Contains two novel genes, a pseudogene similar to part of platelet-activating factor acetylhydrolase variant 1 alpha subunit (PAFAH1B1) and the gene for a novel EGF-like domain containing protein, complete sequence.

ACCESSION AL445677  
 VERSION AL445677.1 GI:11022573  
 KEYWORDS HTG; EGF; PAFAH1B1; platelet activating factor acetylhydrolase.

SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo  
 1 (bases 1 to 84732)  
 Babbage, A.  
 Direct Submission

REFERENCE Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)

COMMENT Cloned requests: [clonerequests@sanger.ac.uk](mailto:clonerequests@sanger.ac.uk)  
 The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:  
 Em, EMBL; Sw, SWISSPROT; Tr, TREMBL; Wp, WORMPEP; Information on the WORMPEP database can be found at  
[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) This sequence was generated from part of bacterial clone contigs of human chromosome 6, constructed by the Sanger Centre Chromosome 6 Mapping Group. Further information can be found at  
<http://www.sanger.ac.uk/HGP/Chr6>

----- Genome Center  
 Center: Wellcome Trust Sanger Institute

Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: [vega@sanger.ac.uk](mailto:vega@sanger.ac.uk)

-----  
 This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.  
 RP11-59D5 is from the library RPC1-11.1 constructed by the group of Pieter de Jong. For further details see  
<http://www.chori.org/bacpac/home.htm>

## FEATURES

location/Qualifiers

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 /organism="Homo sapiens"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="6"  
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 /clone\_1lb="RPC1-11.1"  
 /note="Clone\_right\_end: RP1-22117"  
 misc\_feature  
 30175  
 /note="Clone\_left\_end: RP11-69018"  
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 /locus\_tag="RP11-59D5\_B.1-001"  
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 /note="match: ESTs: AV711464 BG430182 BM837077"  
 55627..56469  
 /locus\_tag="RP11-59D5\_B.3-001"  
 /pseudo  
 55627..56469  
 /locus\_tag="RP11-59D5\_B.3-001"  
 /note="match: proteins: AA932483 AAL90338 O31261 O96698 P43033 P43034 P43035 Q8WZ88 Q8WZ89 Q90ZL4 Q9GL51 Q9NDC9 Q9PTR5 Q9VVI0"  
 /pseudo  
 /codon\_start=1  
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 /locus\_tag="RP11-59D5\_B.2-001"  
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 /locus\_tag="RP11-59D5\_B.2-001"  
 /note="match: ESTs: AL523195 AL523196 BG498125 U82785"  
 84732  
 /note="Clone\_right\_end: RP11-59D5"

## ORIGIN

Query Match 30.4%; Score 17; DB 8; Length 84732;  
 Best Local Similarity 100.0%; Pred. No. 48;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 34 CCAAGAGCAATGAGAA 50  
 |||||  
 Db 59686 CCAAGAGCAATGAGAA 59702

Search completed: April 11, 2006, 18:06:26  
 Job time : 377.008 secs



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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - nucleic search, using bw model

Run on: April 11, 2006, 14:24:17 ; Search time 78.0231 Seconds  
(without alignments)  
4783.489 Million cell updates/sec

Title: US-10-712-654-26

Perfect score: 56  
Sequence: 1 gcatccgctggtatgttga.....ggagcaatggaattacacg 56

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database:

N\_Geneseq\_21: \*  
1: geneseqn1980s: \*  
2: geneseqn1990s: \*  
3: geneseqn2000s: \*  
4: geneseqn2001as: \*  
5: geneseqn2001bs: \*  
6: geneseqn2002as: \*  
7: geneseqn2002bs: \*  
8: geneseqn2003as: \*  
9: geneseqn2003bs: \*  
10: geneseqn2003cs: \*  
11: geneseqn2003ds: \*  
12: geneseqn2004as: \*  
13: geneseqn2004bs: \*  
14: geneseqn2005s: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	56	100.0	56	13	ADR48528
2	56	100.0	56	13	ADR48536
3	29	51.8	29	13	ADR48515
4	27	48.2	27	13	ADR48516
5	23	41.1	23	10	ADR44859
6	17	30.4	100	10	ABX61314
7	17	30.4	201	6	ABZ12232
8	17	30.4	500	6	ABZ12232
9	17	30.4	1743	12	ADOB1844
10	17	30.4	9096	13	AAT88015
11	17	30.4	36976	13	ABD32930
12	17	30.4	110000	4	AAI99682
13	17	30.4	110000	4	AAI99683
14	16	28.6	26	12	ADQ31362
15	16	28.6	30	8	ABZ70624
16	16	28.6	40	8	ABT17495
17	16	28.6	158	3	AAC05090
18	16	28.6	202	2	AAT69648
19	16	28.6	219	2	AAQ37002

20	16	28.6	226	2	AAQ03560	AAQ03560 Restricti
21	16	28.6	315	2	AAQ04767	AAQ04767 Sequence
22	16	28.6	324	5	AA67496	AA67496 DNA encod
23	16	28.6	350	4	AA184591	AA184591 Human pol
24	16	28.6	396	4	AAQ03563	AAQ03563 Sequence
25	16	28.6	405	5	AA571671	AA571671 DNA encod
26	16	28.6	414	2	AAT61810	AAT61810 T7 RNA se
27	16	28.6	496	5	AA577936	AA577936 DNA encod
28	16	28.6	497	2	AAQ72699	AAQ72699 pGM/E.14
29	16	28.6	561	6	ABK30710	ABK30710 Plant dwa
30	16	28.6	657	2	AAQ15266	AAQ15266 SP-C from
31	16	28.6	657	2	AAQ49262	AAQ49262 Vector de
32	16	28.6	658	6	ABL61148	ABL61148 CAT repor
33	16	28.6	658	10	ADP79371	ADP79371 Chloramph
34	16	28.6	658	13	ADP79371	ADP79371 Chloramph
35	16	28.6	660	2	AAV28374	AAV28374 Escherich
36	16	28.6	660	4	AAH02154	AAH02154 Escherich
37	16	28.6	660	12	ADQ36313	ADQ36313 Intracell
38	16	28.6	660	14	ADZ39850	ADZ39850 Chloramph
39	16	28.6	662	1	AAAN90107	AAAN90107 Sequence
40	16	28.6	666	5	AA575826	AA575826 DNA encod
41	16	28.6	666	5	AA565578	AA565578 DNA encod
42	16	28.6	672	2	AAQ72700	AAQ72700 pGM/B.9 t
43	16	28.6	679	2	AAQ62055	AAQ62055 Chloramph
44	16	28.6	679	2	AAQ62056	AAQ62056 Chloramph
45	16	28.6	690	5	AA571500	AA571500 DNA encod
46	16	28.6	723	1	AAAN90100	AAAN90100 ss sequen
47	16	28.6	723	2	AAQ03557	AAQ03557 Sequence
48	16	28.6	746	3	AA577360	AA577360 Polynucle
49	16	28.6	746	3	AA590392	AA590392 Chloramph
50	16	28.6	760	10	ADP55570	ADP55570 Cell-free
51	16	28.6	760	10	ADP66013	ADP66013 Cell-free
52	16	28.6	768	11	ACH98281	ACH98281 Klebsiell
53	16	28.6	781	2	AAV13116	AAV13116 Transposo
54	16	28.6	781	3	AAZ39902	AAZ39902 Chloramph
55	16	28.6	781	4	AAH26981	AAH26981 Chloramph
56	16	28.6	782	2	AAQ92253	AAQ92253 Donor vec
57	16	28.6	800	1	AAAN90101	AAAN90101 ss DNA in
58	16	28.6	801	5	AA579598	AA579598 DNA encod
59	16	28.6	803	2	AAQ15265	AAQ15265 SP-C from
60	16	28.6	848	2	AAQ03565	AAQ03565 SP-C expr
61	16	28.6	855	5	AA588738	AA588738 DNA encod
62	16	28.6	945	14	ADY30142	ADY30142 DNA sequ
63	16	28.6	945	14	AA577442	AA577442 DNA encod
64	16	28.6	974	2	AAQ03564	AAQ03564 SP-B expr
65	16	28.6	1002	5	AA582294	AA582294 DNA encod
66	16	28.6	1044	5	AA591786	AA591786 DNA encod
67	16	28.6	1059	5	AA590840	AA590840 DNA encod
68	16	28.6	1066	5	AA588715	AA588715 DNA encod
69	16	28.6	1086	5	AA585860	AA585860 DNA encod
70	16	28.6	1086	5	AA577622	AA577622 DNA encod
71	16	28.6	1113	1	AAAN80481	AAAN80481 XhoI/XbaI
72	16	28.6	1125	5	AA568472	AA568472 DNA encod
73	16	28.6	1137	12	ADN59026	ADN59026 Novel E c
74	16	28.6	1162	14	ADN88785	ADN88785 pA2 promo
75	16	28.6	1162	14	ADN937839	ADN937839 Plasmid p
76	16	28.6	1172	5	AA577423	AA577423 DNA encod
77	16	28.6	1188	13	ADT77871	ADT77871 Regulator
78	16	28.6	1191	12	ADN02068	ADN02068 m1c mutan
79	16	28.6	1221	1	AAAN81153	AAAN81153 XhoI/XbaI
80	16	28.6	1221	5	AA576539	AA576539 DNA encod
81	16	28.6	1233	5	AA588288	AA588288 DNA encod
82	16	28.6	1245	5	AA592782	AA592782 DNA encod
83	16	28.6	1254	5	AA578561	AA578561 DNA fragm
84	16	28.6	1270	10	ACF58169	ACF58169 Modified
85	16	28.6	1270	12	ADN59036	ADN59036 Novel E c
86	16	28.6	1284	5	AA589838	AA589838 DNA encod
87	16	28.6	1314	5	AA571508	AA571508 DNA encod
88	16	28.6	1317	5	AA574865	AA574865 DNA encod
89	16	28.6	1320	12	ADN59031	ADN59031 Novel E c
90	16	28.6	1349	6	AA517063	AA517063 Transposo
91	16	28.6	1350	5	AA591602	AA591602 DNA encod
92	16	28.6	1350	12	ADN76970	ADN76970 GalP-ptrc



C 93	16	28.6	1352	12	ADM76972	Adm76972 GLK-trc D	166	16	28.6	2504	1	AA60261	AA60261 Plasmid P
C 94	16	28.6	1362	10	ADC51775	Adc51775 Cm-resist	167	16	28.6	2527	8	ACC46205	ACC46205 Human dlt
95	16	28.6	1413	5	AA577551	AA577551 DNA encod	168	16	28.6	2538	5	AA586039	AA586039 DNA encod
96	16	28.6	1428	5	AA588734	AA588734 DNA encod	169	16	28.6	2544	5	AA568223	AA568223 DNA encod
97	16	28.6	1428	5	AA586007	AA586007 DNA encod	170	16	28.6	2589	14	AEBS3852	AEBS3852 Plasmid P
C 98	16	28.6	1440	5	AA592815	AA592815 DNA encod	C 171	16	28.6	2594	6	ABK30920	ABK30920 Plant dwa
99	16	28.6	1440	5	AA588813	AA588813 DNA encod	C 172	16	28.6	2601	5	AA571636	AA571636 DNA encod
100	16	28.6	1449	5	AA569797	AA569797 DNA encod	173	16	28.6	2628	5	AA585488	AA585488 DNA encod
101	16	28.6	1449	5	AA576656	AA576656 DNA encod	174	16	28.6	2694	5	AA588785	AA588785 DNA encod
102	16	28.6	1470	5	AA586009	AA586009 DNA encod	175	16	28.6	2714	10	ADP44786	ADP44786 De novo s
103	16	28.6	1470	5	AA577632	AA577632 DNA encod	176	16	28.6	2757	5	AA569873	AA569873 DNA encod
104	16	28.6	1470	5	AA588739	AA588739 DNA encod	177	16	28.6	2758	4	ABL05869	ABL05869 Drosophila
105	16	28.6	1494	5	AA593971	AA593971 DNA encod	C 178	16	28.6	2823	5	AA590026	AA590026 DNA encod
106	16	28.6	1494	5	AA577624	AA577624 DNA encod	C 179	16	28.6	3064	14	ADV09403	ADV09403 Plasmid P
107	16	28.6	1494	5	AA586001	AA586001 DNA encod	C 180	16	28.6	3178	14	ADU92114	ADU92114 Escherich
108	16	28.6	1494	5	AA588716	AA588716 DNA encod	C 181	16	28.6	3181	14	ADU92115	ADU92115 Escherich
C 109	16	28.6	1529	8	AB270622	AB270622 Plasmid P	182	16	28.6	3216	5	AA591100	AA591100 DNA encod
C 110	16	28.6	1529	8	AB270621	AB270621 Plasmid P	C 183	16	28.6	3216	5	AA577626	AA577626 DNA encod
111	16	28.6	1535	1	AA60260	AA60260 Plasmid P	184	16	28.6	3216	5	AA571304	AA571304 DNA encod
112	16	28.6	1542	1	AA60258	AA60258 Plasmid P	185	16	28.6	3216	5	AA588722	AA588722 DNA encod
113	16	28.6	1590	5	AA580619	AA580619 DNA encod	C 186	16	28.6	3216	5	AA577389	AA577389 DNA encod
114	16	28.6	1599	5	AA574854	AA574854 DNA encod	187	16	28.6	3225	4	AA572847	AA572847 EcORI-Hi
115	16	28.6	1599	5	AA568220	AA568220 DNA encod	188	16	28.6	3225	10	ADB88975	ADB88975 E. coli P
C 116	16	28.6	1599	10	ADF50272	ADF50272 Dog flavin	C 189	16	28.6	3225	12	ADU33432	ADU33432 EcORI-Hi
C 117	16	28.6	1599	10	ADF50274	ADF50274 Dog wild-	C 190	16	28.6	3249	2	AAQ73367	AAQ73367 E. coli/S.
C 118	16	28.6	1626	5	AA577404	AA577404 DNA encod	C 191	16	28.6	3249	13	ADU49869	ADU49869 Plasmid P
C 119	16	28.6	1626	6	ABK30789	ABK30789 Plant dha	C 192	16	28.6	3257	13	AAQ73367	AAQ73367 E. coli/S.
120	16	28.6	1626	6	ABK30756	ABK30756 Plant dha	C 193	16	28.6	3273	5	AA590355	AA590355 DNA encod
C 121	16	28.6	1653	5	AA577420	AA577420 DNA encod	C 194	16	28.6	3288	5	AA585789	AA585789 DNA encod
122	16	28.6	1680	5	AA591711	AA591711 DNA encod	C 195	16	28.6	3288	5	AA587346	AA587346 DNA encod
123	16	28.6	1712	5	AA571512	AA571512 DNA encod	C 196	16	28.6	3288	5	AA577395	AA577395 DNA encod
124	16	28.6	1719	5	AA590558	AA590558 DNA encod	C 197	16	28.6	3288	5	AA588746	AA588746 DNA encod
125	16	28.6	1750	6	ABQ75092	ABQ75092 Plasmid P	198	16	28.6	3288	5	AA586010	AA586010 DNA encod
126	16	28.6	1762	13	ADT18357	ADT18357 Plant CDN	199	16	28.6	3295	14	AEBS5419	AEBS5419 Nucleotid
C 127	16	28.6	1767	5	AA587797	AA587797 DNA encod	200	16	28.6	3384	4	AA559854	AA559854 Human nov
128	16	28.6	1767	5	AA588753	AA588753 DNA encod	201	16	28.6	3384	5	AA577630	AA577630 DNA encod
129	16	28.6	1797	5	AA577665	AA577665 DNA encod	202	16	28.6	3384	5	AA588731	AA588731 DNA encod
130	16	28.6	1825	2	AAO67563	AAO67563 TMV repli	203	16	28.6	3400	7	ADL18593	ADL18593 Plasmid P
131	16	28.6	1825	2	AAV54825	AAV54825 Replicon	204	16	28.6	3403	1	AA608956	AA608956 Plasmid P
132	16	28.6	1846	6	AAV44626	AAV44626 Gateway t	205	16	28.6	3414	2	AAQ12785	AAQ12785 PD56/RBS
133	16	28.6	1853	2	AAQ13156	AAQ13156 Self-cllea	206	16	28.6	3414	2	AAQ34609	AAQ34609 Expressio
134	16	28.6	1864	6	AAQ35079	AAQ35079 GeneHunte	207	16	28.6	3415	2	AAQ12784	AAQ12784 PD56/RBS
135	16	28.6	1866	1	AA60482	AA60482 XhoI/XbaI	208	16	28.6	3415	2	AAQ34608	AAQ34608 Expressio
136	16	28.6	1866	1	AA60482	AA60482 XhoI/XbaI	209	16	28.6	3415	1	AA608958	AA608958 Plasmid P
137	16	28.6	1866	1	AA60482	AA60482 XhoI/XbaI	210	16	28.6	3416	2	AAQ06302	AAQ06302 Sequence
138	16	28.6	1866	1	AA60482	AA60482 XhoI/XbaI	211	16	28.6	3416	2	AAQ12783	AAQ12783 PD56/RBS
139	16	28.6	1866	1	AA60482	AA60482 XhoI/XbaI	212	16	28.6	3416	2	AAQ12783	AAQ12783 PD56/RBS
140	16	28.6	1906	10	ADP44789	ADP44789 De novo s	C 213	16	28.6	3420	4	AAH20728	AAH20728 Expressio
141	16	28.6	1953	5	AA577440	AA577440 DNA encod	214	16	28.6	3420	4	AAH20728	AAH20728 Expressio
142	16	28.6	1968	5	AA582161	AA582161 DNA encod	215	16	28.6	3420	4	AAH20728	AAH20728 Expressio
143	16	28.6	1992	5	AA585142	AA585142 DNA encod	216	16	28.6	3427	2	AAO06304	AAO06304 Sequence
144	16	28.6	1992	10	ADP44788	ADP44788 De novo s	217	16	28.6	3431	10	ADE15907	ADE15907 Plasmid P
145	16	28.6	2016	5	AA572434	AA572434 DNA encod	218	16	28.6	3433	14	ADW44135	ADW44135 Sequence
146	16	28.6	2022	5	AA574778	AA574778 DNA encod	219	16	28.6	3440	2	AAQ06303	AAQ06303 Sequence
C 147	16	28.6	2082	13	ACN42317	ACN42317 Human dia	220	16	28.6	3462	4	AAH43178	AAH43178 PD56/RBS
148	16	28.6	2101	13	ADT77744	ADT77744 Yeast sel	221	16	28.6	3462	6	AAH43178	AAH43178 PD56/RBS
149	16	28.6	2101	13	ADT77744	ADT77744 Yeast sel	222	16	28.6	3462	6	AAH43178	AAH43178 PD56/RBS
150	16	28.6	2101	14	AE616999	AE616999 Yeast sel	223	16	28.6	3480	3	AA598011	AA598011 Expressio
151	16	28.6	2103	5	AA589976	AA589976 DNA encod	C 224	16	28.6	3501	5	AA589943	AA589943 DNA encod
152	16	28.6	2103	5	AA581425	AA581425 DNA encod	225	16	28.6	3519	3	AA598035	AA598035 Expressio
153	16	28.6	2106	5	AA589965	AA589965 DNA encod	C 226	16	28.6	3529	6	AAH40165	AAH40165 PD56/RBS
154	16	28.6	2154	5	AA569421	AA569421 DNA encod	227	16	28.6	3542	5	AA585900	AA585900 DNA encod
155	16	28.6	2159	4	AA160601	AA160601 Human pol	C 228	16	28.6	3558	3	AA575006	AA575006 Nucleotid
C 156	16	28.6	2167	6	ABL64405	ABL64405 Stomach c	229	16	28.6	3801	12	ADL72227	ADL72227 DNA beque
C 157	16	28.6	2175	14	AEBS3850	AEBS3850 Plasmid P	C 230	16	28.6	3803	2	AAQ03155	AAQ03155 Sequence
C 158	16	28.6	2175	14	AEBS3847	AEBS3847 Plasmid P	231	16	28.6	3817	10	ADD14893	ADD14893 Phage dls
C 159	16	28.6	2181	14	AEBS3851	AEBS3851 Plasmid P	232	16	28.6	3822	2	AAV13171	AAV13171 Complete
160	16	28.6	2191	10	ADP44787	ADP44787 De novo s	233	16	28.6	3833	1	AA591060	AA591060 Sequence
C 161	16	28.6	2346	5	AA577547	AA577547 DNA encod	234	16	28.6	3861	2	AAV13174	AAV13174 Complete
162	16	28.6	2436	5	AA591158	AA591158 DNA encod	235	16	28.6	3876	3	AA598037	AA598037 Expressio
163	16	28.6	2499	5	AA568213	AA568213 DNA encod	236	16	28.6	3879	3	AA598038	AA598038 Expressio
164	16	28.6	2499	5	AA589952	AA589952 DNA encod	237	16	28.6	3879	3	AA598031	AA598031 Expressio
165	16	28.6	2503	5	AA588792	AA588792 DNA encod	238	16	28.6	3879	3	AA598016	AA598016 Expressio



239	16	28.6	3879	3	AAA98036	Aaa98036	Expressio	312	16	28.6	4100	14	AEA43207	Aea43207	M. smegma
240	16	28.6	3879	3	AAA98017	Aaa98017	Expressio	313	16	28.6	4140	5	AAS69903	Aas69903	DNA encod
241	16	28.6	3879	3	AAA98015	Aaa98015	Expressio	314	16	28.6	4165	5	AAC55524	Aac55524	Donor pla
242	16	28.6	3885	3	AAA98013	Aaa98013	Expressio	315	16	28.6	4183	14	ADZ04225	Adz04225	BFDV modi
243	16	28.6	3888	2	AAV13175	Aav13175	Complete	316	16	28.6	4204	3	AAC55522	Aac55522	Donor pla
244	16	28.6	3888	2	AAA75008	Aaa75008	Nucleocid	317	16	28.6	4206	10	ADF79367	Adf79367	Transposo
245	16	28.6	3888	6	ABK15515	Abk15515	Chloromph	318	16	28.6	4208	3	AAC55523	Aac55523	Donor pla
246	16	28.6	3897	3	AAA98030	Aaa98030	Expressio	319	16	28.6	4245	8	ABZ70623	Abz70623	Donor pla
247	16	28.6	3900	3	AAA98019	Aaa98019	Expressio	320	16	28.6	4247	14	ADV00179	Adv00179	Recombina
248	16	28.6	3912	3	AAA98027	Aaa98027	Expressio	321	16	28.6	4338	14	ADM43610	Adm43610	PACKO-Bla
249	16	28.6	3912	3	AAA98018	Aaa98018	Expressio	322	16	28.6	4338	14	ADM47413	Adm47413	Protein b
250	16	28.6	3916	14	AEB47826	Aeb47826	Plasmid p	323	16	28.6	4338	14	ADY05018	Ady05018	Novel tra
251	16	28.6	3919	3	AAA98028	Aaa98028	Expressio	324	16	28.6	4349	13	AAV75007	Aav75007	Nucleocid
252	16	28.6	3927	3	AAA98026	Aaa98026	Expressio	325	16	28.6	4349	13	ADM50733	Adm50733	SARS coro
253	16	28.6	3927	3	AAA98032	Aaa98032	Expressio	326	16	28.6	4350	13	ADM23800	Adm23800	Expressio
254	16	28.6	3932	3	AAA98024	Aaa98024	Expressio	327	16	28.6	4368	3	AAA98020	Aaa98020	Expressio
255	16	28.6	3936	3	AAA98023	Aaa98023	Expressio	328	16	28.6	4380	2	AAA98022	Aaa98022	Expressio
256	16	28.6	3945	3	AAA98033	Aaa98033	Expressio	329	16	28.6	4411	2	AAV28088	Aav28088	Plasmid p
257	16	28.6	3946	4	AAH57537	Aah57537	Human bra	330	16	28.6	4416	5	AAH86058	Aah86058	DNA encod
258	16	28.6	3946	4	AAH57537	Aah57537	Human bra	331	16	28.6	4422	5	AAV72460	Aav72460	DNA encod
259	16	28.6	3955	2	AAV13173	Aav13173	Complete	332	16	28.6	4428	10	ABZ58768	Abz58768	Destinati
260	16	28.6	3957	2	AAA98034	Aaa98034	Expressio	333	16	28.6	4470	3	AAC55521	Aac55521	Donor pla
261	16	28.6	3976	2	AAQ25119	Aaq25119	Expressio	334	16	28.6	4470	10	ABZ58767	Abz58767	Destinati
262	16	28.6	3977	2	AAQ49223	Aaq49223	Plasmid p	335	16	28.6	4484	4	AAF63719	Aaf63719	Expressio
263	16	28.6	3977	2	AAO87691	Aao87691	Plasmid p	336	16	28.6	4491	6	AAI6712	Aai6712	Expressio
264	16	28.6	3977	2	AAO87692	Aao87692	Plasmid p	337	16	28.6	4500	6	ABK15516	Abk15516	Bicistron
265	16	28.6	3977	2	AAO87695	Aao87695	Plasmid p	338	16	28.6	4500	2	AAV13170	Aav13170	Complete
266	16	28.6	3977	2	AAO87706	Aao87706	Plasmid p	339	16	28.6	4504	3	AAC55541	Aac55541	atrr read
267	16	28.6	3977	2	AAO87701	Aao87701	Plasmid p	340	16	28.6	4626	2	AAT79498	Aat79498	Plasmid p
268	16	28.6	3977	2	AAO87683	Aao87683	Plasmid p	341	16	28.6	4627	10	ABZ58769	Abz58769	Destinati
269	16	28.6	3977	2	AAO87708	Aao87708	Plasmid p	342	16	28.6	4627	10	ABZ58770	Abz58770	Destinati
270	16	28.6	3977	2	AAO87685	Aao87685	Plasmid p	343	16	28.6	4702	13	ADM76384	Adm76384	SARS coro
271	16	28.6	3977	2	AAO87697	Aao87697	Plasmid p	344	16	28.6	4716	9	ADB87295	Adb87295	Plasmid p
272	16	28.6	3977	2	AAO87710	Aao87710	Plasmid p	345	16	28.6	4721	6	ABK15517	Abk15517	Bicistron
273	16	28.6	3977	2	AAO87686	Aao87686	Plasmid p	346	16	28.6	4755	6	AAI6713	Aai6713	Plasmid p
274	16	28.6	3977	2	AAO87698	Aao87698	Plasmid p	347	16	28.6	4758	14	ADV00180	Adv00180	Recombina
275	16	28.6	3977	2	AAO87711	Aao87711	Plasmid p	348	16	28.6	4765	12	ADP49313	Adp49313	Fusion pr
276	16	28.6	3977	2	AAO87702	Aao87702	Plasmid p	349	16	28.6	4765	12	ADP49315	Adp49315	Fusion pr
277	16	28.6	3977	2	AAO87707	Aao87707	Plasmid p	350	16	28.6	4773	14	ADV00181	Adv00181	Recombina
278	16	28.6	3977	2	AAO87709	Aao87709	Plasmid p	351	16	28.6	4777	14	ADV00182	Adv00182	Recombina
279	16	28.6	3977	2	AAO87712	Aao87712	Plasmid p	352	16	28.6	4810	4	ABL05868	AbL05868	Drosophi1
280	16	28.6	3977	2	AAO87703	Aao87703	Plasmid p	353	16	28.6	4813	14	ADM43608	Adm43608	PACKO-A18
281	16	28.6	3977	2	AAO87687	Aao87687	Plasmid p	354	16	28.6	4813	14	ADM43609	Adm43609	PACKO-A18
282	16	28.6	3977	2	AAO87699	Aao87699	Plasmid p	355	16	28.6	4813	14	ADM47412	Adm47412	Protein b
283	16	28.6	3977	2	AAO87688	Aao87688	Plasmid p	356	16	28.6	4813	14	ADY50516	Ady50516	Novel tra
284	16	28.6	3977	2	AAO87694	Aao87694	Plasmid p	357	16	28.6	4814	14	ADM43607	Adm43607	PACKO-A18
285	16	28.6	3977	2	AAO87696	Aao87696	Plasmid p	358	16	28.6	4814	14	ADY50517	Ady50517	Novel tra
286	16	28.6	3977	2	AAO87696	Aao87696	Plasmid p	359	16	28.6	4892	9	ADA50329	Ada50329	Plasmid v
287	16	28.6	3977	2	AAO87689	Aao87689	Plasmid p	360	16	28.6	4938	8	ABV75997	Abv75997	Donor vec
288	16	28.6	3977	2	AAO87704	Aao87704	Plasmid p	361	16	28.6	4939	3	AAC55525	Aac55525	Donor pla
289	16	28.6	3977	2	AAQ73431	Aaq73431	Plasmid p	362	16	28.6	5024	9	ACF06051	Acf06051	Plasmid p
290	16	28.6	3977	2	AAO87705	Aao87705	Plasmid p	363	16	28.6	5024	12	ADL18668	Adl18668	Plasmid p
291	16	28.6	3977	2	AAO87684	Aao87684	Plasmid p	364	16	28.6	5064	12	ADQ48539	Adq48539	Viral vec
292	16	28.6	3977	2	AAO87693	Aao87693	Plasmid p	365	16	28.6	5064	3	AAA98021	Aaa98021	Expressio
293	16	28.6	3977	2	AAO87700	Aao87700	Plasmid p	366	16	28.6	5069	14	ADZ59989	Adz59989	Expressio
294	16	28.6	3989	3	AAA98025	Aaa98025	Expressio	367	16	28.6	5096	2	AAQ83824	Aaq83824	Plasmid p
295	16	28.6	3991	1	AAH91061	Aah91061	Sequence	368	16	28.6	5100	5	AAS92584	Aas92584	DNA encod
296	16	28.6	3999	2	AAO2664	Aao2664	Sequence	369	16	28.6	5100	5	AAS89963	Aas89963	DNA encod
297	16	28.6	4003	2	AAO06305	Aao06305	Sequence	370	16	28.6	5109	8	ABZ69176	Abz69176	Vector co
298	16	28.6	4004	2	AAO06306	Aao06306	Sequence	371	16	28.6	5110	2	AAO83836	Aao83836	Plasmid p
299	16	28.6	4005	2	AAO40418	Aao40418	Sequence	372	16	28.6	5110	2	AAO83828	Aao83828	Plasmid p
300	16	28.6	4009	2	AAV13172	Aav13172	Complete	373	16	28.6	5110	2	AAO83835	Aao83835	Plasmid p
301	16	28.6	4010	9	ADA92560	Ada92560	Bam HI/Ba	374	16	28.6	5110	2	AAO83832	Aao83832	Plasmid p
302	16	28.6	4019	2	AAO2663	Aao2663	Vector pQ	375	16	28.6	5110	2	AAO83829	Aao83829	Plasmid p
303	16	28.6	4045	4	AAA91149	Aaa91149	Human pol	376	16	28.6	5110	2	AAO83834	Aao83834	Plasmid p
304	16	28.6	4055	4	AAI58815	Aai58815	Human pol	377	16	28.6	5110	2	AAO83825	Aao83825	Plasmid p
305	16	28.6	4055	4	AAI58815	Aai58815	DNA encod	378	16	28.6	5110	2	AAO83826	Aao83826	Plasmid p
306	16	28.6	4055	5	ADO99036	Ado99036	DNA encod	379	16	28.6	5110	2	AAO83830	Aao83830	Plasmid p
307	16	28.6	4055	5	ADO99036	Ado99036	DNA encod	380	16	28.6	5110	2	AAO83831	Aao83831	Plasmid p
308	16	28.6	4055	9	ADB48796	Adb48796	Novel hum	381	16	28.6	5110	2	AAO83833	Aao83833	Plasmid p
309	16	28.6	4055	9	ADB48796	Adb48796	Novel hum	382	16	28.6	5110	2	AAO83833	Aao83833	Plasmid p
310	16	28.6	4068	1	AAH80957	Aah80957	Plasmid p	383	16	28.6	5148	6	AAD27063	Aad27063	Plasmid p
311	16	28.6	4068	1	AAH90730	Aah90730	Sequence	384	16	28.6	5156	3	AAC55526	Aac55526	Donor pla



C 385	16	28.6	5161	10	ADH45226	Adh45226 Modified	458	16	28.6	6526	3	AAC55471	Aac55471 Destinati
386	16	28.6	5171	14	AEA96441	Aea96441 Plasmid p	459	16	28.6	6553	3	AAC55456	Aac55456 Destinati
387	16	28.6	5176	12	ADK18146	Adk18146 DNA of p	460	16	28.6	6607	14	ADZ03868	Adz03868 Plasmid p
388	16	28.6	5178	12	ADJ54094	Adj54094 pME27.1 D	461	16	28.6	6608	14	ADZ03870	Adz03870 Plasmid p
389	16	28.6	5178	14	ADZ55994	Adz55994 Plasmid p	462	16	28.6	6613	3	AAC55493	Aac55493 Destinati
390	16	28.6	5201	12	ADL72229	Adl72229 DNA seqe	463	16	28.6	6652	3	AAC55513	Aac55513 Destinati
391	16	28.6	5201	12	ADL72228	Adl72228 DNA seqe	464	16	28.6	6668	3	AAC55495	Aac55495 Destinati
392	16	28.6	5227	12	AAT79537	Aat79537 Plasmid p	465	16	28.6	6675	3	AAC55489	Aac55489 Destinati
C 393	16	28.6	5241	2	AAE62463	Aae62463 Modified	466	16	28.6	6708	3	AAC55475	Aac55475 Destinati
C 394	16	28.6	5241	2	AAE62464	Aae62464 Modified	467	16	28.6	6809	14	ADZ09260	Adz09260 DNA seqe
C 395	16	28.6	5241	2	AAE62465	Aae62465 Modified	468	16	28.6	6809	14	ADZ09368	Adz09368 DNA seqe
396	16	28.6	5262	12	AAV69927	Aav69927 Promoter	469	16	28.6	6809	14	ADZ09368	Adz09368 DNA seqe
397	16	28.6	5291	12	ADM78418	Adm78418 Newcastle	470	16	28.6	6809	14	ADZ09254	Adz09254 DNA seqe
C 398	16	28.6	5292	12	ADY93370	Ady93370 E. coli e	471	16	28.6	6823	3	AAC55459	Aac55459 Destinati
C 399	16	28.6	5300	14	ADY92618	Ady92618 DNA seqe	472	16	28.6	6876	5	AAS94032	Aas94032 DNA encod
400	16	28.6	5321	14	ADY92618	Ady92618 DNA seqe	473	16	28.6	6876	5	AAS94032	Aas94032 DNA encod
401	16	28.6	5362	14	ADV44285	Adv44285 pFosbeta	474	16	28.6	6961	3	AAC55510	Aac55510 Destinati
402	16	28.6	5362	14	ADV44286	Adv44286 pFosbeta	475	16	28.6	6961	3	AAC55461	Aac55461 Destinati
403	16	28.6	5375	12	AD134682	Ad134682 Nucleoid	476	16	28.6	6971	2	AAV26304	Aav26304 Sequence
404	16	28.6	5376	1	AAV90732	Aav90732 Sequence	477	16	28.6	7013	3	AAC55486	Aac55486 Destinati
405	16	28.6	5448	14	AAE15851	Aae15851 pectrepar	478	16	28.6	7026	2	AAV26303	Aav26303 Sequence
406	16	28.6	5454	14	AAE15850	Aae15850 pPR-GBP p	479	16	28.6	7055	2	AAV26303	Aav26303 Sequence
407	16	28.6	5517	6	ABK15518	Abk15518 Bictetron	480	16	28.6	7066	3	AAC55498	Aac55498 Destinati
408	16	28.6	5536	13	ADV34915	Adv34915 Vector pE	481	16	28.6	7114	3	AAC55631	Aac55631 Destinati
409	16	28.6	5558	12	ADL90419	Adl90419 Clostridi	482	16	28.6	7141	3	AAC55625	Aac55625 Destinati
410	16	28.6	5563	14	ABR31043	Ab31043 Plasmid D	483	16	28.6	7156	3	AAC55626	Aac55626 Destinati
411	16	28.6	5584	10	ABZ58766	Abz58766 Donor pla	484	16	28.6	7271	5	AAC55479	Aac55479 Destinati
412	16	28.6	5584	10	ABZ58766	Abz58766 Donor pla	485	16	28.6	7278	6	ABZ76589	Abz76589 Human ind
413	16	28.6	5587	14	ABR31042	Ab31042 Plasmid D	486	16	28.6	7278	6	ABZ76589	Abz76589 Human ind
C 414	16	28.6	5641	4	AAE30800	Aae30800 Vector p1	487	16	28.6	7326	5	AAE68517	Aae68517 DNA encod
C 415	16	28.6	5670	4	AAE30801	Aae30801 Vector p1	488	16	28.6	7336	1	AAE68517	Aae68517 DNA encod
C 416	16	28.6	5670	4	AAE30801	Aae30801 Vector p1	489	16	28.6	7336	1	AAE68517	Aae68517 DNA encod
C 417	16	28.6	5699	6	ABK15519	Abk15519 Bictetron	490	16	28.6	7341	12	ADQ48563	Adq48563 Viral vec
C 418	16	28.6	5740	8	ACC42351	Acc42351 Plasmid p	491	16	28.6	7341	12	ADQ48563	Adq48563 Viral vec
C 419	16	28.6	5776	14	ADZ68048	Adz68048 Selectabl	492	16	28.6	7437	14	ADZ09234	Adz09234 DNA seqe
C 420	16	28.6	5777	8	ABZ69181	Abz69181 Vector p1	493	16	28.6	7437	14	ADZ09234	Adz09234 DNA seqe
C 421	16	28.6	5793	8	AAE30798	Aae30798 Vector p1	494	16	28.6	7456	2	AAQ10686	Aaq10686 Plasmid p
C 422	16	28.6	5826	5	AAE30798	Aae30798 Vector p1	495	16	28.6	7481	14	ADZ09236	Adz09236 DNA seqe
C 423	16	28.6	5830	5	AAE30798	Aae30798 Vector p1	496	16	28.6	7487	8	AAV76000	Aav76000 Vector p1
C 424	16	28.6	5838	2	AAV28338	Aav28338 Plasmid p	497	16	28.6	7507	2	AAV76000	Aav76000 Vector p1
C 425	16	28.6	5838	2	AAZ22882	Aaz22882 Plasmid p	498	16	28.6	7519	14	ADZ09363	Adz09363 DNA seqe
C 426	16	28.6	5838	2	AAZ22882	Aaz22882 Plasmid p	499	16	28.6	7519	14	ADZ09362	Adz09362 DNA seqe
C 427	16	28.6	5848	5	AAE55481	Aae55481 Destinati	500	16	28.6	7544	3	AAC55627	Aac55627 Destinati
428	16	28.6	5848	5	AAE55481	Aae55481 Destinati	501	16	28.6	7559	3	AAC55628	Aac55628 Destinati
429	16	28.6	5925	5	AAE85841	Aae85841 DNA encod	502	16	28.6	7559	3	AAC55628	Aac55628 Destinati
430	16	28.6	5957	3	AAC55467	Aac55467 Destinati	503	16	28.6	7618	12	AD134678	Ad134678 Nucleoid
431	16	28.6	5957	3	AAC55464	Aac55464 Destinati	504	16	28.6	7618	12	AD134678	Ad134678 Nucleoid
432	16	28.6	5957	3	AAC55464	Aac55464 Destinati	505	16	28.6	7618	12	AD134678	Ad134678 Nucleoid
C 433	16	28.6	5986	6	ABZ40188	Abz40188 p243OR3	506	16	28.6	7675	14	AEA02105	Aea02105 Plasmid p
C 434	16	28.6	6025	3	AAE55469	Aae55469 Destinati	507	16	28.6	7783	2	AAZ26302	Aaz26302 Sequence
435	16	28.6	6035	5	AAE85839	Aae85839 DNA encod	508	16	28.6	7801	2	AAZ26302	Aaz26302 Sequence
436	16	28.6	6035	5	AAE85839	Aae85839 DNA encod	509	16	28.6	7801	2	AAZ26302	Aaz26302 Sequence
437	16	28.6	6038	13	ADW13055	Adw13055 L-glutam	510	16	28.6	7801	2	AAZ26302	Aaz26302 Sequence
438	16	28.6	6038	13	ADW13055	Adw13055 L-glutam	511	16	28.6	7801	2	AAZ26302	Aaz26302 Sequence
C 439	16	28.6	6043	11	ADM86629	Adm86629 pJFK4 pl	512	16	28.6	7935	12	ADQ48564	Adq48564 Viral vec
C 440	16	28.6	6071	4	AAE30799	Aae30799 Vector p1	513	16	28.6	7935	12	ADQ48564	Adq48564 Viral vec
441	16	28.6	6096	1	AAV70871	Aav70871 Plasmid p	514	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
442	16	28.6	6122	6	ABN84078	Abn84078 Plasmid p	515	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
443	16	28.6	6122	6	AAV41112	Aav41112 Plasmid p	516	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
444	16	28.6	6122	6	AAV41115	Aav41115 Plasmid p	517	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
445	16	28.6	6125	6	AAV41114	Aav41114 Plasmid p	518	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
446	16	28.6	6254	3	AAC55507	Aac55507 Destinati	519	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
447	16	28.6	6354	3	AAC55491	Aac55491 Destinati	520	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
448	16	28.6	6354	3	AAC55491	Aac55491 Destinati	521	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
449	16	28.6	6442	3	AAE28091	Aae28091 Plasmid p	522	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
450	16	28.6	6442	3	AAE28091	Aae28091 Plasmid p	523	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
451	16	28.6	6442	3	AAE28091	Aae28091 Plasmid p	524	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
452	16	28.6	6475	10	ABZ58765	Abz58765 Destinati	525	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
453	16	28.6	6501	6	AAE91168	Aae91168 DNA encod	526	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
454	16	28.6	6501	6	AAE91168	Aae91168 DNA encod	527	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
455	16	28.6	6501	12	ADK12499	Adk12499 Expressio	528	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
456	16	28.6	6510	5	AAE59435	Aae59435 DNA encod	529	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p
C 457	16	28.6	6525	8	ABV75999	Abv75999 Donor vec	530	16	28.6	8038	14	AEA02111	Aea02111 Plasmid p



531	16	28.6	8688	12	ADQ48556	Adq48556 Viral vec	c 604	16	28.6	67087	3	AAF22280	Aaf22280 BAC conta
532	16	28.6	8688	14	ADX82446	Adx82446 LentiVtru	605	16	28.6	75815	14	ADM44335	Adm44335 Chicken O
533	16	28.6	8724	5	AA888707	AA888707 DNA encod	606	16	28.6	75815	14	AE00969	Ae00969 DNA inser
534	16	28.6	8752	12	ADK51933	Adk51933 Novel rRN	607	16	28.6	75815	14	AE876922	Ae876922 Chicken O
535	16	28.6	8815	3	AA855630	AA855630 Destinat	608	16	28.6	77872	14	ADM44343	Adm44343 Ovomucoid
536	16	28.6	8849	3	AA889977	AA889977 DNA encod	609	16	28.6	77872	14	AE009977	Ae009977 Ovomucoid
537	16	28.6	8906	2	AAV32979	AAV32979 Tn7 targe	610	16	28.6	77872	14	AE876930	Ae876930 Chicken O
538	16	28.6	8906	6	AAV45061	AAV45061 Tn7 targe	611	16	28.6	83390	3	AAF22283	Aaf22283 BAC conta
539	16	28.6	8906	12	ADG46819	Adg46819 pER183 ta	612	16	28.6	92584	3	AAF22288	Aaf22288 BAC conta
540	16	28.6	8923	3	AA855504	AA855504 Destinat	613	16	28.6	92523	3	AAF22282	Aaf22282 BAC conta
541	16	28.6	9249	10	ADCA4959	Adc44959 Epstein-B	614	16	28.6	96593	9	ADA02600	Ada02600 Human RUN
542	16	28.6	9265	6	ABK87210	Abk87210 Synthetic	615	16	28.6	96593	10	AD872338	Ad872338 Human RUN
543	16	28.6	9320	12	ADQ48559	Adq48559 Viral vec	616	16	28.6	96593	10	AD895848	Ad895848 Human RUN
544	16	28.6	9320	14	ADM82449	Adm82449 LentiVtru	617	16	28.6	117754	11	ACM43866	AcM43866 Human gen
545	16	28.6	9332	12	ADM57433	Adm57433 T gondii	618	16	28.6	121001	3	AAF22284	Aaf22284 BAC conta
546	16	28.6	9425	6	ABK98630	Abk98630 Vector pE	619	16	28.6	165221	11	ACN44524	Acn44524 Mouse gen
547	16	28.6	9425	6	ACD13881	AcD13881 L. lactis	620	16	28.6	165799	14	AD213004	Ad213004 Murine ca
548	16	28.6	9437	6	ABK98601	Abk98601 Vector pE	621	16	28.6	177866	10	ADL13935	AdL13935 Osteoarth
549	16	28.6	9437	9	ACD13852	AcD13852 Xyl opara	622	16	28.6	183178	10	ADL13873	AdL13873 Osteoarth
550	16	28.6	9460	5	AA800466	AA800466 Plasmid p	623	16	28.6	218802	14	ADP98820	AdP98820 Human her
551	16	28.6	9484	6	ABK98633	Abk98633 Vector pI	624	16	28.6	19	2	AA779515	Aat779515 Cat gene
552	16	28.6	9484	6	ACD13884	AcD13884 L. lactis	625	16	28.6	19	2	AA779515	Aat779515 Cat gene
553	16	28.6	9652	6	ABQ76126	Abq76126 Plasmid p	626	16	28.6	19	2	AA779515	Aat779515 Cat gene
554	16	28.6	9725	3	AAA53873	AA53873 Expressio	627	16	28.6	29	2	AA779515	Aat779515 Cat gene
555	16	28.6	9732	3	AAA53879	AA53879 Expressio	628	16	28.6	33	10	ACCA2766	Acca2766 Histone H
556	16	28.6	9738	3	AAA53874	AA53874 Expressio	629	16	28.6	34	9	ACN62805	Acn62805 Chloamph
557	16	28.6	9772	14	ABE68189	AbE68189 pBind-RNA	630	16	28.6	34	9	ACN62804	Acn62804 Chloamph
558	16	28.6	9808	14	ADZ66224	Adz66224 Construct	631	16	28.6	265	14	ADVA2116	Adv42116 Flea test
559	16	28.6	9808	14	ABE80052	AbE80052 Vector pA	632	16	28.6	265	14	ADVA4213	Adv44213 Cat flea
560	16	28.6	9808	14	ABE72933	AbE72933 DNA seque	633	16	28.6	303	4	AAH72913	Aah72913 Human cer
561	16	28.6	9873	3	AAA53875	AA53875 Expressio	634	16	28.6	303	4	AAH72913	Aah72913 Human cer
562	16	28.6	9905	14	ADZ58434	Adz58434 Plasmid p	635	16	28.6	307	4	AAH70770	Aah70770 Human cer
563	16	28.6	9905	14	ADZ58435	Adz58435 Plasmid A	636	16	28.6	329	4	AAH69435	Aah69435 Human cer
564	16	28.6	10054	3	AAH53876	AA53876 Expressio	637	16	28.6	349	2	AAQ71580	Aaq71580 Mycobacte
565	16	28.6	10429	14	ADZ58430	Adz58430 Plasmid p	638	16	28.6	349	2	AAQ71580	Aaq71580 Mycobacte
566	16	28.6	10429	14	ADZ58436	Adz58436 Plasmid p	639	16	28.6	370	6	ABV96505	Abv96505 Human pan
567	16	28.6	10463	10	ADCA4958	Adc44958 LentiVtru	640	16	28.6	474	6	ABZ12431	Abz12431 Arbidops
568	16	28.6	10534	14	ABE88343	AbE88343 Plasmid p	641	16	28.6	477	3	AA852855	Aa852855 Arbidops
569	16	28.6	10580	12	AAO38104	AaO38104 Vector pE	642	16	28.6	482	4	AAI98742	Aai98742 Human exc
570	16	28.6	10903	12	ADK51929	Adk51929 Novel rRN	643	16	28.6	482	4	AA827189	Aa827189 CDNA enco
571	16	28.6	11120	5	AA886057	AA886057 DNA encod	644	16	28.6	482	4	ABK43482	Abk43482 DNA enco
572	16	28.6	11120	5	AA886057	AA886057 DNA encod	645	16	28.6	482	4	ABK43482	Abk43482 DNA enco
573	16	28.6	11180	7	ADZ75070	Adz75070 Binary p	646	16	28.6	482	5	AAI63138	Aai63138 Human kid
574	16	28.6	11241	6	ABO76125	AbO76125 Plasmid p	647	16	28.6	482	5	ADB93357	AdB93357 Human cDN
575	16	28.6	11241	12	ADH10182	AdH10182 E. coli-R	648	16	28.6	482	12	AD153869	Ad153869 CDNA enco
576	16	28.6	11713	3	AA855501	AA855501 Destinat	649	16	28.6	533	10	AD154186	Ad154186 CDNA enco
577	16	28.6	11918	12	ADK51930	Adk51930 Novel rRN	650	16	28.6	533	10	AD154186	Ad154186 CDNA enco
578	16	28.6	12288	3	AA855629	AA855629 Destinat	651	16	28.6	533	10	AD154186	Ad154186 CDNA enco
579	16	28.6	12464	3	AA855629	AA855629 Destinat	652	16	28.6	533	10	AD154186	Ad154186 CDNA enco
580	16	28.6	12495	12	ADDO5573	ADDO5573 Nucleotid	653	16	28.6	558	12	ACH87285	Ach87285 Human gen
581	16	28.6	12733	6	ABK98631	AbK98631 Vector pE	654	16	28.6	564	4	AAH42274	Aah42274 Nucleotid
582	16	28.6	12733	6	ABK98631	AbK98631 Vector pE	655	16	28.6	594	12	ACH73571	Ach73571 Human gen
583	16	28.6	12739	9	ABK98592	AbK98592 Vector pE	656	16	28.6	618	14	ADK55699	Adk55699 Fine chem
584	16	28.6	12739	9	ABK98592	AbK98592 Vector pE	657	16	28.6	649	13	ADOS5196	Ado55196 Novel can
585	16	28.6	12789	8	AB857536	Ab857536 Vector pK	658	16	28.6	651	13	ADRE1020	Adre1020 Cotton cd
586	16	28.6	13100	10	ACF89612	AcF89612 Recombina	659	16	28.6	651	13	ACN52274	Acn52274 Cotton an
587	16	28.6	13227	12	ADK51932	AdK51932 Novel rRN	660	16	28.6	655	14	ACLS4886	AcL54886 Human col
588	16	28.6	13274	6	ABK15666	AbK15666 Binary ve	661	16	28.6	700	4	AAH93269	Aah93269 Human inf
589	16	28.6	13274	12	ADK51931	AdK51931 Novel rRN	662	16	28.6	879	11	ACN44689	Acn44689 Mouse mRN
590	16	28.6	14000	10	ACF89611	AcF89611 Recombina	663	16	28.6	935	2	AAO93035	Aao93035 Wild toma
591	16	28.6	14468	8	ACG83500	AcG83500 Bacteri	664	16	28.6	966	2	AAQ93034	Aaq93034 Wild toma
592	16	28.6	16847	12	ADDO7464	Ado07464 Japanese	665	16	28.6	966	2	AAQ06186	Aaq06186 PR-P CDNA
593	16	28.6	18563	12	ADDO7466	Ado07466 Japanese	666	16	28.6	968	2	AAV62813	Aav62813 Tobacco P
594	16	28.6	18563	12	ADDO7466	Ado07466 Japanese	667	16	28.6	968	2	AAV62813	Aav62813 Tobacco P
595	16	28.6	18565	12	ADDO7467	Ado07467 Japanese	668	16	28.6	1004	6	ABX93063	Abx93063 C. annuum
596	16	28.6	18691	6	ABO82130	AbO82130 Acceptor	669	16	28.6	1065	12	ADP28881	Adp28881 Human sec
597	16	28.6	19038	12	ADDO7468	Ado07468 Japanese	670	16	28.6	1110	5	AA865579	Aa865579 Corn tryp
598	16	28.6	19038	12	ADDO7468	Ado07468 Japanese	671	16	28.6	1181	4	AAZ25121	Aaz25121 Corn tryp
599	16	28.6	19040	12	ADDO7470	Ado07470 Japanese	672	16	28.6	1182	4	AAZ25121	Aaz25121 Corn tryp
600	16	28.6	27413	11	ACN44832	Acn44832 Mouse gen	673	16	28.6	1182	10	ADA44791	Ada44791 Bacillus
601	16	28.6	34864	12	ADQ48537	Adq48537 Viral vec	674	16	28.6	1182	10	ADDO7641	Ado07641 B. subtili
602	16	28.6	36686	12	ADQ48533	Adq48533 Viral vec	675	16	28.6	1182	13	ADV65732	Adv65732 B. subtil
603	16	28.6	48000	4	AAF27996	Aaf27996 Human cal	676	16	28.6	1287	8	ACA38294	AcA38294 Prokaryot



677	15	26.8	1290	8	ACA040613	AcA040613	Prokaryot	c 750	15	26.8	96598	10	ADB95857	Ad95857	Mouse	NFK
678	15	26.8	1377	6	ABO68864	AbO68864	Listeria	751	15	26.8	110000	4	AA199682	AA199682	24	Continuation (25 o
679	15	26.8	1455	13	ADP41777	AdP41777	Bacterial	752	15	26.8	111252	4	AA199683	AA199683	24	Continuation (25 o
680	15	26.8	1494	9	ADA31315	AdA31315	DNA encod	753	15	26.8	111252	11	ACN44444	ACN44444	4	ACN44444 Mouse gen
681	15	26.8	1629	10	ADL24833	AdL24833	Intestina	754	15	26.8	127238	11	ACN44372	ACN44372	11	ACN44372 Mouse gen
682	15	26.8	1647	5	AA886231	Aa886231	DNA encod	755	15	26.8	127567	14	AEA61137	AEA61137	14	AEA61137 Human BCA
683	15	26.8	1661	10	ADBE96264	AdB96264	Human uri	756	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
684	15	26.8	1678	6	ABT07863	AbT07863	Human lun	757	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
685	15	26.8	1819	11	ADM07140	AdM07140	Aspergill	758	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
686	15	26.8	1835	4	AAK52883	AaK52883	Human pol	759	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
687	15	26.8	1873	4	AAK53184	AaK53184	Human pol	760	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
688	15	26.8	1921	10	ADBE96262	AdB96262	Human uri	761	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
689	15	26.8	1941	10	ADBE96263	AdB96263	Human uri	762	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
690	15	26.8	1954	5	AA886232	Aa886232	DNA encod	763	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
691	15	26.8	1986	12	ADDS5737	AdD55737	Thaleres	764	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
692	15	26.8	1986	12	ADDO1834	AdD01834	Thaleres	765	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
693	15	26.8	1986	12	ADDO1834	AdD01834	Thaleres	766	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
694	15	26.8	2024	6	ABK51222	AbK51222	Human kid	767	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
695	15	26.8	2145	4	AA44660	Aa44660	Novel pro	768	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
696	15	26.8	2145	4	AA44660	Aa44660	Novel pro	769	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
697	15	26.8	2182	11	ADM03360	AdM03360	Human CDN	770	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
698	15	26.8	2182	11	ADM03360	AdM03360	Human CDN	771	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
699	15	26.8	2183	4	AAK51899	AaK51899	Human pol	772	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
700	15	26.8	2290	13	ADK52531	AdK52531	Plant ful	773	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
701	15	26.8	2313	8	ABK63073	AbK63073	Human CDN	774	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
702	15	26.8	2373	2	AAQ45455	AaQ45455	Sequence	775	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
703	15	26.8	2503	13	ADK13669	AdK13669	Plant ful	776	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
704	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	777	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
705	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	778	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
706	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	779	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
707	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	780	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
708	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	781	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
709	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	782	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
710	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	783	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
711	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	784	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
712	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	785	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
713	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	786	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
714	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	787	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
715	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	788	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
716	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	789	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
717	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	790	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
718	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	791	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
719	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	792	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
720	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	793	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
721	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	794	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
722	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	795	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
723	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	796	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
724	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	797	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
725	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	798	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
726	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	799	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
727	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	800	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
728	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	801	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
729	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	802	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
730	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	803	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
731	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	804	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
732	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	805	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
733	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	806	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
734	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	807	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
735	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	808	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
736	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	809	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
737	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	810	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
738	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	811	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
739	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	812	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
740	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	813	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
741	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	814	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
742	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	815	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
743	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	816	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
744	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	817	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
745	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	818	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
746	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	819	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
747	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	820	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
748	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	821	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can
749	15	26.8	2570	11	ACN44445	ACN44445	Mouse mrn	822	15	26.8	1348101	12	ADQ97146	ADQ97146	12	ADQ97146 Human can



C 823	14	25.0	416	8	ABZ17807	Abz17807 S2 subclra	C 896	14	25.0	574	12	ACH75058	Ach75058 Human gen
C 824	14	25.0	417	5	ABV31525	Abv31525 Human pro	C 897	14	25.0	581	13	ADOS1593	Ados1593 Novel can
C 825	14	25.0	432	5	AAU02572	AAU02572 Human rep	C 898	14	25.0	586	13	AAZ24895	Aaz24895 Human sec
C 826	14	25.0	432	4	ABL97302	AbL97302 Human tes	C 899	14	25.0	587	12	ACH68403	Ach68403 Human gen
C 827	14	25.0	438	5	ABV01185	Abv01185 Human pro	C 900	14	25.0	589	14	ADZ60677	Adz60677 Rat g3225
C 828	14	25.0	446	12	ADL84604	AdL184604 DNA up-re	C 901	14	25.0	590	13	ACN48667	Acn48667 Cotton pr
C 829	14	25.0	446	12	ADL84603	AdL184603 DNA up-re	C 902	14	25.0	593	14	AAF74264	Aaf74264 Arabidops
C 830	14	25.0	455	4	AAH88547	AAH88547 Human pro	C 903	14	25.0	594	7	ADS72457	Ads72457 Human kid
C 831	14	25.0	455	4	ABA55123	AbA55123 Human pro	C 904	14	25.0	594	7	ADW41311	Adw41311 CDNA elev
C 832	14	25.0	455	4	ABA24869	AbA24869 Human foe	C 905	14	25.0	600	5	AAH67394	Aah67394 C glutami
C 833	14	25.0	455	4	AAK03385	AAK03385 Human brya	C 906	14	25.0	601	6	ABK16765	Abk16765 Human CDN
C 834	14	25.0	455	4	ABS28449	ABS28449 Human l1iv	C 907	14	25.0	601	14	ABO54743	Abos54743 Human ova
C 835	14	25.0	455	5	AAI03306	AAI03306 Probe #32	C 908	14	25.0	620	16	ABO54743	Abos54743 Human ova
C 836	14	25.0	455	6	ABS03368	ABs03368 Human gen	C 909	14	25.0	623	5	ABV01354	Abv01354 Human pro
C 837	14	25.0	456	8	ACA21695	ACa21695 Prokaryot	C 910	14	25.0	628	10	ADBE8618	Adbe8618 Toxicity-
C 838	14	25.0	461	4	AAI15320	AAI15320 Probe #52	C 911	14	25.0	628	10	ADBS3267	Adbs3267 Primary r
C 839	14	25.0	461	4	ABA46473	ABa46473 Human bre	C 912	14	25.0	628	12	ADM41425	Adm41425 Rat brain
C 840	14	25.0	462	5	ABV40494	ABv40494 Human pro	C 913	14	25.0	628	13	ADV41416	Adv41416 Rat cardi
C 841	14	25.0	464	2	AAI22418	AAI22418 Human gen	C 914	14	25.0	641	9	ACL23390	AcL23390 DNA clone
C 842	14	25.0	475	4	AAI12688	AAI12688 Probe #26	C 915	14	25.0	648	4	AAK93254	Aak93254 Human CDN
C 843	14	25.0	475	4	ABA54378	AbA54378 Human foe	C 916	14	25.0	648	12	ADL29681	AdL29681 5' end of
C 844	14	25.0	475	4	AAI34039	AAI34039 Probe #27	C 917	14	25.0	683	13	ABK62102	Abk62102 Rat beque
C 845	14	25.0	475	4	ABA43925	ABa43925 Human bre	C 918	14	25.0	691	13	ADRE4794	Adre4794 Cotton CD
C 846	14	25.0	475	4	ABA24157	ABa24157 Probe #26	C 919	14	25.0	693	10	ADBE09516	Adbe09516 Novel DNA
C 847	14	25.0	475	4	AAK28111	AAK28111 Human bon	C 920	14	25.0	705	2	AAV84211	Aav84211 Brugia ma
C 848	14	25.0	475	4	AAK02673	AAK02673 Human brya	C 921	14	25.0	705	2	AAV84212	Aav84212 Brugia ma
C 849	14	25.0	475	4	ABS27717	ABs27717 Human l1iv	C 922	14	25.0	716	4	AAZ27440	Aaz27440 CDNA enco
C 850	14	25.0	475	5	AAI02597	AAI02597 Probe #25	C 923	14	25.0	716	10	ADB933618	Adb93618 Human CDN
C 851	14	25.0	475	6	ABS02604	ABs02604 Human gen	C 924	14	25.0	717	6	ABL190828	AbL190828 Human pol
C 852	14	25.0	476	6	ABL19861	ABl19861 Drosophill	C 925	14	25.0	718	6	ABZ21431	AbZ21431 Corynebacc
C 853	14	25.0	477	3	AAC05768	AAc05768 Human sec	C 926	14	25.0	721	4	AAI96946	AAI96946 Human neu
C 854	14	25.0	478	9	ACH41779	ACH41779 Human foe	C 927	14	25.0	732	5	AA887113	AA887113 DNA enco
C 855	14	25.0	479	9	ACL23389	ACl23389 DNA clone	C 928	14	25.0	736	2	AAV84204	Aav84204 Brugia ma
C 856	14	25.0	494	12	ADN13352	ADn13355 Aspergill1	C 929	14	25.0	736	2	AAV84210	Aav84210 Brugia ma
C 857	14	25.0	497	10	ADG37365	ADg37365 Aspergill1	C 930	14	25.0	743	4	AAK91935	Aak91935 Human CDN
C 858	14	25.0	503	12	ACH67316	ACH67316 Human gen	C 931	14	25.0	743	4	AAK93345	Aak93345 Human CDN
C 859	14	25.0	504	9	ACH27987	ACH27987 Human adu	C 932	14	25.0	743	12	ADL29772	AdL29772 5' end of
C 860	14	25.0	509	4	ABK42776	ABk42776 Genomic 8	C 933	14	25.0	743	12	ADL28362	AdL28362 5' end of
C 861	14	25.0	509	4	ABK42250	ABk42250 Genomic 8	C 934	14	25.0	747	4	ABL09651	AbL09651 Drosophill
C 862	14	25.0	509	5	ABV10523	ABv10523 Human pro	C 935	14	25.0	747	10	AAU59914	Aau59914 Human kal
C 863	14	25.0	509	9	ADB60406	ADB60406 Connectiv	C 936	14	25.0	765	6	ABK54192	AbK54192 DNA enco
C 864	14	25.0	509	9	ADB60932	ADB60932 Connectiv	C 937	14	25.0	770	4	ABL17883	AbL17883 Drosophill
C 865	14	25.0	510	4	ABK41967	ABK41967 CDNA enco	C 938	14	25.0	771	13	ADS62117	AdS62117 Bacterial
C 866	14	25.0	510	9	ADB59634	ADB59634 Connectiv-	C 939	14	25.0	772	4	AAK93681	Aak93681 Human CDN
C 867	14	25.0	517	10	ADBE6364	ADbE6364 Toxicity-	C 940	14	25.0	772	12	ADL30108	AdL30108 3' end of
C 868	14	25.0	517	10	ADBS0863	ADbS0863 Primary r	C 941	14	25.0	783	5	AA565673	AA565673 DNA enco
C 869	14	25.0	519	12	ACH67751	ACH67751 Human gen	C 942	14	25.0	803	12	ADJ42505	Adj42505 Plant CDN
C 870	14	25.0	534	8	ACA01289	ACa01289 C. glutam	C 943	14	25.0	816	12	ADP28828	Adp28828 Human sec
C 871	14	25.0	535	4	AAK91915	AAK91915 Human CDN	C 944	14	25.0	819	14	AEA20721	Aea20721 Novel hum
C 872	14	25.0	535	4	AAK93946	AAK93946 Human CDN	C 945	14	25.0	840	2	AAK60906	AAK60906 Human CDN
C 873	14	25.0	535	12	ADL28342	ADl28342 5' end of	C 946	14	25.0	840	2	AAK60906	AAK60906 Human CDN
C 874	14	25.0	535	12	ADL30373	ADl30373 5' end of	C 947	14	25.0	840	2	AAK60906	AAK60906 Human CDN
C 875	14	25.0	540	4	ABA59922	ABa59922 Human foe	C 948	14	25.0	879	5	AA569877	AA569877 DNA enco
C 876	14	25.0	540	4	AAI39794	AAI39794 Probe #84	C 949	14	25.0	886	13	ADK35735	Adk35735 Plant ful
C 877	14	25.0	540	4	ABA28354	ABa28354 Probe #68	C 948	14	25.0	886	13	ADK35735	Adk35735 Plant ful
C 878	14	25.0	540	4	AAK34071	AAK34071 Human bon	C 950	14	25.0	894	3	AA524234	AA524234 Cotton CD
C 879	14	25.0	540	4	AAK08192	AAK08192 Human brya	C 951	14	25.0	906	4	AAK93936	AAK93936 Arabidops
C 880	14	25.0	540	4	ABS33872	ABs33872 Human l1iv	C 952	14	25.0	906	4	AAK93235	AAK93235 Human CDN
C 881	14	25.0	540	6	ABS08849	ABs08849 Human gen	C 953	14	25.0	906	4	AAK91977	AAK91977 Human CDN
C 882	14	25.0	541	6	ABN64838	ABn64838 Human can	C 954	14	25.0	906	12	ADL29662	AdL29662 5' end of
C 883	14	25.0	544	5	AAH98023	AAh98023 Murine 7-	C 955	14	25.0	906	12	ADL28404	AdL28404 5' end of
C 884	14	25.0	545	13	ADOS3091	Ados3091 Novel can	C 956	14	25.0	906	12	ADL30363	AdL30363 5' end of
C 885	14	25.0	546	4	AAI19220	AAI19220 Probe #91	C 957	14	25.0	914	2	AAQ32688	AAq32688 Luffin-g
C 886	14	25.0	546	4	ABA64228	ABa64228 Human foe	C 958	14	25.0	932	3	AA52430	AA52430 Arabidops
C 887	14	25.0	546	4	AAI44380	AAI44380 Probe #13	C 959	14	25.0	975	5	AAH67392	Aah67392 C glutami
C 888	14	25.0	546	4	ABA31373	ABa31373 Probe #98	C 960	14	25.0	1006	10	AD612102	Ad612102 Murine 11
C 889	14	25.0	546	4	AAK38426	AAK38426 Human bon	C 961	14	25.0	1032	10	ABZ66771	Abz66771 Corynebacc
C 890	14	25.0	546	4	AAK12706	AAK12706 Human brya	C 962	14	25.0	1065	13	ADP46020	Adp46020 Bacterial
C 891	14	25.0	546	4	ABS38019	ABs38019 Human l1iv	C 963	14	25.0	1069	9	ADA13516	Ada13516 Chlorotaph
C 892	14	25.0	546	4	ABS12484	ABs12484 Human gen	C 964	14	25.0	1074	14	AEC01871	Aec01871 Nucleotid
C 893	14	25.0	563	6	ACH39689	ACH39689 Human foe	C 965	14	25.0	1077	13	AD559800	Ad559800 Bacterial
C 894	14	25.0	568	14	ADY78433	Ady78433 Human CDN	C 966	14	25.0	1091	3	AAAY7671	AAaY7671 Human PRO
C 895	14	25.0	568	14	ADY78599	Ady78599 Human CDN	C 967	14	25.0	1091	3	AA58114	AA58114 Human PRO
C 896	14	25.0	574	12	ACH75058	Ach75058 Human gen	C 968	14	25.0	1091	3	AAA37075	AAA37075 Human PRO



c 969	14	25.0	1091	4	AAf54341
c 970	14	25.0	1091	9	ACD68378
c 971	14	25.0	1091	9	ACH04480
c 972	14	25.0	1091	9	ACD68024
c 973	14	25.0	1091	10	ADCL8062
c 974	14	25.0	1091	10	ADD70708
c 975	14	25.0	1091	10	ADD39785
c 976	14	25.0	1091	10	ADD70231
c 977	14	25.0	1091	10	ADD38352
c 978	14	25.0	1091	10	ADD39308
c 979	14	25.0	1091	10	ADD38831
c 980	14	25.0	1091	10	ADD40262
c 981	14	25.0	1091	10	ADE50483
c 982	14	25.0	1091	10	ADE20095
c 983	14	25.0	1091	10	ADE50006
c 984	14	25.0	1091	10	ADE21564
c 985	14	25.0	1091	10	ADFP2989
c 986	14	25.0	1091	10	ADPF5882
c 987	14	25.0	1091	10	ADH99386
c 988	14	25.0	1091	12	ADPE6566
c 989	14	25.0	1091	12	ADPF25877
c 990	14	25.0	1091	12	ADPF24776
c 991	14	25.0	1091	12	ADPF29512
c 992	14	25.0	1091	12	ADPE97043
c 993	14	25.0	1091	12	ADH03081
c 994	14	25.0	1091	12	ADH04035
c 995	14	25.0	1091	12	ADH03558
c 996	14	25.0	1091	12	ADH04512
c 997	14	25.0	1091	12	ADH61513
c 998	14	25.0	1091	12	ADL94712
c 999	14	25.0	1091	13	ADT94372
c1000	14	25.0	1095	11	ACH95859

## ALIGNMENTS

RESULT 1  
ID ADR48528 standard; DNA; 56 BP.  
XX  
AC ADR48528;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE capB target sequence #2.  
XX  
KM Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
XX PX01; PX02; target sequence; ds.  
XX  
OS Bacillus anthracis.  
XX  
PN WO2004070001-A2.  
XX  
PD 19-AUG-2004.  
XX  
PF 12-NOV-2003; 2003WO-US036240.  
XX  
PR 15-NOV-2002; 2002US-0426552P.  
XX PR 16-MAY-2003; 2003US-0471082P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;  
XX WPI; 2004-604428/58.  
XX  
DR WPI; 2004-604428/58.  
XX  
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis  
XX PT sequence; useful for detecting cutaneous and respiratory Bacillus anthrax  
XX PT infections.  
XX  
PS Claim 1; SEQ ID NO 26; 61bp; English.  
XX

CC The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a Bacillus  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of Bacillus anthracis  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids PX01 and PX02, without requiring handling of  
CC virulent Bacillus anthracis. The present sequence represents a capB  
CC target sequence.  
XX  
SQ Sequence 56 BP; 15 A; 12 C; 15 G; 14 T; 0 U; 0 Other;

Query Match 100.0%; Score 56; DB 13; Length 56;  
Best Local Similarity 100.0%; Pred. No. 1.2e-20;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTCGCGTGTATGTTGAATGCTCATCCGATCCAGGACGATGAGATTACAG 56  
DB 1 GCATTCGCGTGTATGTTGAATGCTCATCCGATCCAGGACGATGAGATTACAG 56

RESULT 2  
ID ADR48536 standard; DNA; 560 BP.  
XX  
AC ADR48536;  
XX  
DT 04-NOV-2004 (first entry)  
XX  
DE capB target sequence #3.  
XX  
KM Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
XX PX01; PX02; target sequence; ds.  
XX  
OS Bacillus anthracis.  
XX  
PN WO2004070001-A2.  
XX  
PD 19-AUG-2004.  
XX  
PF 12-NOV-2003; 2003WO-US036240.  
XX  
PR 15-NOV-2002; 2002US-0426552P.  
XX PR 16-MAY-2003; 2003US-0471082P.  
XX  
PA (GENP-) GEN-PROBE INC.  
XX  
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;  
XX WPI; 2004-604428/58.  
XX  
DR WPI; 2004-604428/58.  
XX  
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis  
XX PT sequence; useful for detecting cutaneous and respiratory Bacillus anthrax  
XX PT infections.  
XX  
PS Claim 1; SEQ ID NO 34; 61bp; English.  
XX  
SQ Sequence 560 BP; 181 A; 89 C; 131 G; 159 T; 0 U; 0 Other;



Query Match 100.0%; Score 56; DB 13; Length 560;  
 Best Local Similarity 100.0%; Pred. No. 1.1e-20;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTCCGTGGTATGTTGAATGCTCATCCGATCCAGAGCAATGAGATTACACG 56  
 DB 505 GCATTCCGTGGTATGTTGAATGCTCATCCGATCCAGAGCAATGAGATTACACG 560

## RESULT 3

ADR48515/c  
 ID ADR48515 standard; DNA; 29 BP.

AC ADR48515;

DT 04-NOV-2004 (first entry)

DE capB probe #5.

KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
 PX01; PX02; probe; ss.

OS Unidentified.

PN WO2004070001-A2.

PD 19-AUG-2004.

PF 12-NOV-2003; 2003WO-US036240.

PR 15-NOV-2002; 2002US-0426552P.

PR 16-MAY-2003; 2003US-0471082P.

XX (GENP-) GEN-PROBE INC.

PI Norman SA, Bungo JT, Hogan JT, Weisburg WG;

DR WPI; 2004-604428/58.

XX New oligonucleotides that hybridize specifically to a Bacillus anthracis  
 PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax  
 infections.

PS Claim 9; SEQ ID NO 13; 61bp; English.

XX The present invention relates to an oligonucleotide of 20-40 nucleotides  
 CC that specifically hybridizes to a sequence contained in a Bacillus  
 CC anthracis target sequence. The methods and compositions of the present  
 CC invention are useful for detecting the presence of Bacillus anthracis  
 CC nucleic acid in a sample, in particular for detecting cutaneous and  
 CC respiratory anthrax infections. Two synthetic genetic target sequences,  
 CC derived from pagA and capB gene sequences, were synthesized to provide  
 CC known standards for testing oligonucleotides for detection of the genes  
 CC carried by the plasmids pX01 and pX02, without requiring handling of  
 CC virulent Bacillus anthracis. The present sequence represents a capB  
 CC probe, used in the pX01 and pX02 detection kits.

XX Sequence 29 BP; 10 A; 7 C; 7 G; 5 T; 0 U; 0 Other;

Query Match 51.8%; Score 29; DB 13; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 7.6e-06;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 GCATTCCGTGGTATGTTGAATGCTCATCC 29  
 DB 29 GCATTCCGTGGTATGTTGAATGCTCATCC 1

## RESULT 4

ADR48516/c  
 ID ADR48516 standard; DNA; 27 BP.

AC ADR48516;

XX 04-NOV-2004 (first entry)

DE capB probe #6.

KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;  
 PX01; PX02; probe; ss.

OS Unidentified.

PN WO2004070001-A2.

PD 19-AUG-2004.

PF 12-NOV-2003; 2003WO-US036240.

PR 15-NOV-2002; 2002US-0426552P.

PR 16-MAY-2003; 2003US-0471082P.

XX (GENP-) GEN-PROBE INC.

PI Norman SA, Bungo JT, Hogan JT, Weisburg WG;

DR WPI; 2004-604428/58.

XX New oligonucleotides that hybridize specifically to a Bacillus anthracis  
 PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax  
 infections.

PS Claim 9; SEQ ID NO 14; 61bp; English.

XX The present invention relates to an oligonucleotide of 20-40 nucleotides  
 CC that specifically hybridizes to a sequence contained in a Bacillus  
 CC anthracis target sequence. The methods and compositions of the present  
 CC invention are useful for detecting the presence of Bacillus anthracis  
 CC nucleic acid in a sample, in particular for detecting cutaneous and  
 CC respiratory anthrax infections. Two synthetic genetic target sequences,  
 CC derived from pagA and capB gene sequences, were synthesized to provide  
 CC known standards for testing oligonucleotides for detection of the genes  
 CC carried by the plasmids pX01 and pX02, without requiring handling of  
 CC virulent Bacillus anthracis. The present sequence represents a capB  
 CC probe, used in the pX01 and pX02 detection kits.

XX Sequence 27 BP; 4 A; 8 C; 5 G; 10 T; 0 U; 0 Other;

Query Match 48.2%; Score 27; DB 13; Length 27;  
 Best Local Similarity 100.0%; Pred. No. 9.5e-05;  
 Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 GCATCCAGAGCAATGAGATTACACG 56  
 DB 27 GCATCCAGAGCAATGAGATTACACG 1

## RESULT 5

ADR4859/c  
 ID ADR4859 standard; DNA; 23 BP.

AC ADR4859;

DT 12-FEB-2004 (first entry)

DE Internal positive control related PCR primer BACPA4L SEQ ID NO:66.

KW internal positive control; IPC; probe; probe-based nucleic acid;

XX PCR primer; ss.

XX Synthetic.

XX WO2003075837-A2.

XX 18-SEP-2003.



PF 03-MAR-2003; 2003WO-US006347.  
 XX  
 PR 04-MAR-2002; 2002US-0361455P.  
 XX  
 PA (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.  
 XX  
 PI Hartman LJ, Norwood DA;  
 XX  
 DR WPI; 2003-756781/71.  
 XX  
 PT New nucleic acid molecule, useful as internal positive control in probe-  
 XX based nucleic acid assay such as TaqMan based assay.  
 XX  
 PS Example 3; SEQ ID NO 66; 56bp; English.  
 XX  
 CC The present invention describes an isolated nucleic acid molecule (1)  
 CC comprising the 548 base pair (bp) sequence of ABP44842, which is an  
 CC internal positive control (IPC) nucleic acid molecule. Also described:  
 CC (1) a probe comprising (1) and a label; (2) an assay using the probe; (3)  
 CC a kit for a probe-based nucleic acid assay comprising the isolated  
 CC nucleic acid molecule (1) packaged with instructions for use; and (4)  
 CC making an IPC nucleic acid molecule for a probe-based nucleic acid  
 CC molecule assay. The nucleic acid molecule (1) is useful as an IPC in  
 CC probe-based nucleic acid assay such as TaqMan (RTM) based assay. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 U; 0 Other;  
 XX  
 QY Query Match 41.1%; Score 23; DB 10; Length 23;  
 XX Best Local Similarity 100.0%; Pred. No. 0.015;  
 DB Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 7 CGTGTGATGTTGAATGCTCATCC 29  
 DB 23 CGTGTGATGTTGAATGCTCATCC 1  
 XX  
 RESULT 6  
 ID ABX61314 standard; DNA; 100 BP.  
 XX  
 AC ABX61314;  
 XX  
 DT 26-FEB-2003 (first entry)  
 XX  
 DE Arabidopsis thaliana polynucleotide #660.  
 XX  
 KW Thale cress; gene; ds; genetic manipulation; plant; biosynthesis;  
 KW genetic modification; environmental stress; disease resistance;  
 KW fungicide; insecticide; stress tolerance.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN US2002142319-A1.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 07-AUG-2001; 2001US-00924035.  
 XX  
 PR 13-AUG-1999; 99US-0148784P.  
 PR 11-AUG-2000; 2000US-00638258.  
 XX  
 PA (GORL/) GORLACH J.  
 PA (ANY/) AN Y.  
 PA (HAMI/) HAMILTON C M.  
 PA (PRIC/) PRICE J L.  
 PA (HARG/) HARGISS T R.  
 PA (YUY/) YU Y.  
 PA (RAME/) RAMEAKA J G.  
 PA (PAGE/) PAGE A.  
 PA (MATH/) MATHW A V.  
 PA (LEDF/) LEDFORD B L.  
 PA (WOES/) WOESSNER J P.

PA (HAAS/) HAAS W D.  
 PA (GARC/) GARCIA C A.  
 XX  
 PI Gorlach J, An Y, Hamilton CM, Price JL, Hargies TR, Yu Y;  
 PI Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;  
 PI Garcia CA;  
 XX  
 DR WPI; 2003-102509/09.  
 XX  
 PT Novel Arabidopsis thaliana nucleic acid useful for constructing a  
 PT transgenic plant with enhanced disease resistance and enhanced traits of  
 PT interest, as probes, and in diagnosis and screening purposes.  
 XX  
 PS Claim 1; Page 204; 277pp; English.  
 XX  
 CC The invention relates to Arabidopsis thaliana nucleic acid sequences. The  
 CC DNA sequences and the polypeptides they encode are useful for identifying  
 CC homologous or related genes, for producing compositions that modulate the  
 CC expression or function of the polypeptides, for mapping functional  
 CC regions of the protein, in diagnosis, for studying associated  
 CC physiological pathways, for genetic manipulation of cells, preferably  
 CC plant cells, in screening assays of various plant strains to determine  
 CC the strains that are capable of withstanding a particular disease or  
 CC environmental stress, for enhancing or inhibiting production of  
 CC biosynthetic products in plants and to create genetically modified and  
 CC transgenic organisms, such as plant cells and plants. Transgenic plants  
 CC are useful for introducing or improving disease resistance and stress  
 CC tolerance in plants, screening biologically active agents, such as  
 CC fungicides and insecticides, and for identifying factors involved in  
 CC biosynthetic pathways of nutritional, commercial or medicinal value.  
 CC Sequences ABX60655-ABX61554 represent Arabidopsis thaliana  
 CC polynucleotides of the invention  
 XX  
 SQ Sequence 100 BP; 51 A; 13 C; 13 G; 23 T; 0 U; 0 Other;  
 XX  
 QY Query Match 30.4%; Score 17; DB 10; Length 100;  
 XX Best Local Similarity 100.0%; Pred. No. 27;  
 DB Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 QY 12 TATGTTGAATGCTCATC 28  
 DB 23 TATGTTGAATGCTCATC 7  
 XX  
 RESULT 7  
 ID ABZ12232 standard; DNA; 201 BP.  
 XX  
 AC ABZ12232;  
 XX  
 DT 21-JAN-2003 (first entry)  
 XX  
 DE Arabidopsis thaliana stress regulated gene SEQ ID NO 37.  
 XX  
 KW Arabidopsis thaliana; plant; gene; stress; transgenic; ds.  
 XX  
 OS Arabidopsis thaliana.  
 XX  
 PN WO200216655-A2.  
 XX  
 PD 28-FEB-2002.  
 XX  
 PF 24-AUG-2001; 2001WO-US026685.  
 XX  
 PR 24-AUG-2000; 2000US-0227866P.  
 PR 26-JAN-2001; 2001US-0264647P.  
 PR 22-JUN-2001; 2001US-0300111P.  
 XX  
 PA (SCRI ) SCRIPS RES INST.  
 PA (SYGN ) SYNGENTA PARTICIPATIONS AG.  
 XX  
 PI Harper JF, Kreps J, Wang X, Zhu T;



DR WPI; 2002-304127/34.  
XX  
PT Identifying a stress condition to which a plant cell has been exposed and  
PT producing plants with increased tolerance to these abiotic stresses.  
XX  
PS Claim 144; SEQ ID NO 37; 577pp + Sequence Listing; English.  
XX  
CC The invention relates to identifying a stress condition to which a plant  
CC cell has been exposed, comprising: (a) contacting nucleic acid  
CC representative of expressed polynucleotides in the plant cell with an  
CC array or probes representative of the plant cell genome; and (b)  
CC characterizing a profile of expressed polynucleotides in the plant cell  
CC characteristic of a stress response. The method is useful in the  
CC production of transgenic plants, cells and seeds and in producing plants  
CC with increased tolerance to abiotic stress. The present sequence is that  
CC of an Arabidopsis thaliana stress regulated gene (AB212196-AB217574) used  
CC in methods of the invention. Note: The sequence data for this patent is  
CC not represented in the printed specification but is based on sequence  
CC information supplied to Derwent by the European Patent Office  
XX  
SQ Sequence 201 BP; 44 A; 30 C; 52 G; 75 T; 0 U; 0 Other;  
Query Match 30.4%; Score 17; DB 6; Length 201;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 TTCGGTGTATGTTGAA 20  
DB 161 TTCGGTGTATGTTGAA 177  
RESULT 8  
AB571886  
ID AB571886 standard; DNA; 500 BP.  
XX  
AC AB571886;  
XX  
DT 02-DEC-2002 (first entry)  
XX  
DE Human GTP-Rho binding protein 2 single-exon probe #27.  
XX  
XX Human; ss: GTP-Rho binding protein 2; GRBP2; chromosome 19q12; oncogene;  
KM tumour; liposarcoma; ichthyosis congenita III; probe;  
KM benign familial infantile convulsion; gene therapy.  
XX  
OS Homo sapiens.  
XX  
PN EP1231216-A2.  
XX  
PD 14-AUG-2002.  
XX  
PF 17-JAN-2002; 2002EP-00001026.  
XX  
PR 30-JAN-2001; 2001WO-US000663.  
PR 30-JAN-2001; 2001WO-US000664.  
PR 30-JAN-2001; 2001WO-US000665.  
PR 30-JAN-2001; 2001WO-US000666.  
PR 30-JAN-2001; 2001WO-US000667.  
PR 30-JAN-2001; 2001WO-US000668.  
PR 30-JAN-2001; 2001WO-US000669.  
PR 30-JAN-2001; 2001WO-US000670.  
PR 29-JUN-2001; 2001US-00895040.  
XX  
PA (ABOM-) ABOMICA INC.  
XX  
PI Shannon ME, JI Y;  
XX  
DR WPI; 2002-684026/74.  
XX  
PT Novel GTP-Rho binding protein 2 and nucleic acids encoding the protein,  
PT useful for the manufacture of a medicament for treating a disease  
PT associated with altered expression or activity of human GRBP2 protein.  
XX

PS Example 4; Page 63; 101pp; English.  
XX  
CC The invention relates to an isolated GTP-Rho binding protein 2 (GRBP2)  
CC polypeptide or a fragment of at least 6 amino acids or a sequence in  
CC which at least 95% of deviations from GRBP2 sequences are conservative  
CC substitutions. Also included are an isolated nucleic acid (GRBP2 NA)  
CC encoding GRBP2 comprising the full length cDNA or cDS, fragments or  
CC variants, GRBP2 vectors, host cells, antibodies, transgenic non-human  
CC animals modified to contain GRBP2 NA (or unable to express the endogenous  
CC orthologue of GRBP2), diagnosing a disease caused by a mutation in human  
CC GRBP2 or altered expression of GRBP2, anti-agonists of GRBP2, GRBP2  
CC microarrays, fusion proteins and screening for agents that modulate the  
CC expression of GRBP2 NA. GRBP2 is useful for identifying binding partners  
CC of GRBP2. GRBP2 NA and Ab are useful in therapy and in the  
CC manufacture of a medicament for the treatment or prevention of a disorder  
CC associated with increased or decreased expression or activity of human  
CC GRBP2 (e.g. tumour, liposarcoma, ichthyosis congenita III and benign  
CC familial infantile convulsion, all associated with the chromosomal  
CC location of GRBP2, 19q12). GRBP2 is useful as a standard in immunoassay  
CC specific for the protein, to be used in a therapeutic agent, as  
CC vaccines, to be and as antigens (e.g. for epitope mapping) or immunogens  
CC (e.g. for raising antibodies. GRBP2 NA is useful as hybridisation probes,  
CC to prime synthesis of nucleic acids, to prime first strand cDNA sequence  
CC on an mRNA template, and to drive in vivo expression of the proteins. The  
CC vector is useful for shuttling GRBP2 NA between host cells derived from  
CC disparate organisms, for inserting GRBP2 NA into host cell chromosome,  
CC for expressing sense or antisense RNA transcripts of GRBP2 NA in vitro or  
CC within a host cell, and for expressing GRBP2 alone or as fusions to  
CC heterologous polypeptides. The antibody is useful as an analytical  
CC reagent for detection and quantification of GRBP2 and as an immuno  
CC therapeutic agent and is useful for flow cytometric detection, for  
CC scanning laser cytometric detection, or for fluorescent immunoassay. The  
CC present sequence is a single exon probe for GRBP2  
XX  
SQ Sequence 500 BP; 127 A; 116 C; 114 G; 143 T; 0 U; 0 Other;  
Query Match 30.4%; Score 17; DB 6; Length 500;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 9 TGGTATGTTGAATGCTC 25  
DB 287 TGGTATGTTGAATGCTC 303  
RESULT 9  
AD061844  
ID AD061844 standard; DNA; 1743 BP.  
XX  
AC AD061844;  
XX  
DT 15-JUL-2004 (first entry)  
XX  
DE Transcription factor G1928 coding sequence, SEQ ID 311.  
XX  
XX Plant; transcription factor; transgenic plant; abiotic stress tolerance;  
KM osmotic stress tolerance; cold tolerance; heat tolerance;  
KM low nitrogen tolerance; low phosphate tolerance; fungal disease;  
KM glyophosphate resistance; flowering; fertility; seed development; ds.  
XX  
OS Arabidopsis thaliana.  
XX  
XX WO2004031349-A2.  
XX  
PN 15-APR-2004.  
XX  
PD 18-SEP-2003; 2003WO-US030292.  
XX  
PF 18-SEP-2002; 2002US-0411837P.  
XX  
PR 17-DEC-2002; 2002US-0434166P.  
XX  
PR 24-APR-2003; 2003US-0465809P.  
XX  
PA (MENDEL-) MENDEL BIOTECHNOLOGY INC.







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CC Revised record issued on 04-NOV-2004 : Correction to Feature table key
XX
SQ Sequence 9096 BP; 2269 A; 2092 C; 2243 G; 2491 T; 0 U; 1 Other;
Query Match      30.4%; Score 17; DB 2; Length 9096;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      8 GTGGTATGTTGAATGCT 24
Db      3452 GTGGTATGTTGAATGCT 3436

RESULT 11
ABD32930/c
XX ABD32930 standard; DNA; 36976 BP.
XX
AC ABD32930;
XX
DT 18-NOV-2004 (first entry)
XX
DE Human cancer-associated genomic DNA HD19-006.
XX
KW Human; ds; cancer-associated protein; gene; cytosstatic; cancer;
XX leukemia; lymphoma; CAP.
XX
OS Homo sapiens.
XX
PN WO2004074320-A2.
PD 02-SEP-2004.
PF 17-FEB-2004; 2004WO-US004730.
XX
PR 14-FEB-2003; 2003US-00367094.
PR 14-MAR-2003; 2003US-0038838.
PR 15-APR-2003; 2003US-00417375.
PR 13-JUN-2003; 2003US-00461862.
PR 15-SEP-2003; 2003US-00663431.
PR 15-DEC-2003; 2003US-00737318.
XX
PA (SAGR-) SAGRES DISCOVERY INC.
XX
PI Morris DW, Morris DW, Malandro MS;
XX
DR WPI; 2004-652914/63.
XX
PT New isolated cancer-associated polynucleotides and polypeptides useful
PT for diagnosing, preventing or treating cancers, especially lymphoma and
PT leukemia, or in screening for agents that modulate cancer.
XX
PS claim 16; seqid 650; 310p; English.
XX
XX The invention relates to an isolated nucleic acid comprising at least 10
CC contiguous nucleotides of any of the 233 polynucleotide sequences given
CC in the specification, or its complement. The nucleic acids encode cancer-
CC associated proteins. Also included are an expression vector comprising
CC the isolated nucleic acid cited above, a host cell comprising the above
CC recombinant nucleic acid or expression vector, a microarray for detecting
CC a cancer-associated (CA) nucleic acid comprising at least one probe
CC comprising at least 10 contiguous nucleotides of any of the above-
CC mentioned nucleotide sequences, an isolated polypeptide (encoded within
CC an open reading frame of a CA sequence selected from any of the 95
CC polynucleotide sequences as mentioned in the specification, or its
CC complement), an isolated antibody, (or its antigen binding fragment) that
CC binds to the above polypeptide, a hybridoma that produces the above
CC monoclonal antibody, a pharmaceutical composition comprising the above
CC antibody and a pharmaceutical excipient, a kit for detecting cancer
CC cells(comprising the antibody cited above, methods for diagnosing cancer
CC or for detecting the presence or absence of cancer cells in an
CC individual, a method for inhibiting growth of cancer cells in an
CC individual, a method for delivering a therapeutic agent to cancer cells
CC in an individual, an electronic library comprising the above
```

```
CC polynucleotide or polypeptide (or their fragments), methods of screening
CC for anticancer activity or for a bioactive agent capable of modulating
CC the activity of a CA protein (CAP), methods for detecting cancer
CC associated with expression of a polypeptide in a test cell sample, a
CC method for treating cancers and a method for inhibiting the expression of
CC CA gene in a cell. The composition and methods are useful for detecting,
CC diagnosing, preventing and treating cancers, especially lymphoma and
CC leukemia. These may also be used in screening for agents that modulate
CC cancer. The present sequence is a human CAP genomic sequence. Note: The
CC sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 36976 BP; 9745 A; 8625 C; 9013 G; 9593 T; 0 U; 0 Other;
Query Match      30.4%; Score 17; DB 13; Length 36976;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy      8 GTGGTATGTTGAATGCT 24
Db      21309 GTGGTATGTTGAATGCT 21293

RESULT 12
AA199682_28
Continuation (29 of 45) of AA199682 from base 2800001 (Mycobacterium tuberculosis str
WP Sequence split into 45 fragments LOCUS AA199682 Accession AA199682
WP      Fragment Name      Begin      End
WP      AA199682_00          1      110000
WP      AA199682_01        100001      210000
WP      AA199682_02        200001      310000
WP      AA199682_03        300001      410000
WP      AA199682_04        400001      510000
WP      AA199682_05        500001      610000
WP      AA199682_06        600001      710000
WP      AA199682_07        700001      810000
WP      AA199682_08        800001      910000
WP      AA199682_09        900001     1010000
WP      AA199682_10       1000001     1110000
WP      AA199682_11       1100001     1210000
WP      AA199682_12       1200001     1310000
WP      AA199682_13       1300001     1410000
WP      AA199682_14       1400001     1510000
WP      AA199682_15       1500001     1610000
WP      AA199682_16       1600001     1710000
WP      AA199682_17       1700001     1810000
WP      AA199682_18       1800001     1910000
WP      AA199682_19       1900001     2010000
WP      AA199682_20       2000001     2110000
WP      AA199682_21       2100001     2210000
WP      AA199682_22       2200001     2310000
WP      AA199682_23       2300001     2410000
WP      AA199682_24       2400001     2510000
WP      AA199682_25       2500001     2610000
WP      AA199682_26       2600001     2710000
WP      AA199682_27       2700001     2810000
WP      AA199682_28       2800001     2910000
WP      AA199682_29       2900001     3010000
WP      AA199682_30       3000001     3110000
WP      AA199682_31       3100001     3210000
WP      AA199682_32       3200001     3310000
WP      AA199682_33       3300001     3410000
WP      AA199682_34       3400001     3510000
WP      AA199682_35       3500001     3610000
WP      AA199682_36       3600001     3710000
WP      AA199682_37       3700001     3810000
WP      AA199682_38       3800001     3910000
WP      AA199682_39       3900001     4010000
WP      AA199682_40       4000001     4110000
WP      AA199682_41       4100001     4210000
WP      AA199682_42       4200001     4310000
WP      AA199682_43       4300001     4410000
```



WP AA19682\_44 440001 4411529

Query Match 30.4%; Score 17; DB 4; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTCATCCGATCCAGCA 39  
DB 22064 CTCATCCGATCCAGCA 22080

# RESULT 13

AA19683\_28  
Continuation (29 of 44) of AA19683 from base 2800001 (Mycobacterium tuberculosis strain  
WP Sequence split into 44 fragments LOCUS AA19683 Accession AA19683

WP	Fragment Name	Begin	End
WP	AA19683_00	1	110000
WP	AA19683_01	100001	210000
WP	AA19683_02	200001	310000
WP	AA19683_03	300001	410000
WP	AA19683_04	400001	510000
WP	AA19683_05	500001	610000
WP	AA19683_06	600001	710000
WP	AA19683_07	700001	810000
WP	AA19683_08	800001	910000
WP	AA19683_09	900001	1010000
WP	AA19683_10	1000001	1110000
WP	AA19683_11	1100001	1210000
WP	AA19683_12	1200001	1310000
WP	AA19683_13	1300001	1410000
WP	AA19683_14	1400001	1510000
WP	AA19683_15	1500001	1610000
WP	AA19683_16	1600001	1710000
WP	AA19683_17	1700001	1810000
WP	AA19683_18	1800001	1910000
WP	AA19683_19	1900001	2010000
WP	AA19683_20	2000001	2110000
WP	AA19683_21	2100001	2210000
WP	AA19683_22	2200001	2310000
WP	AA19683_23	2300001	2410000
WP	AA19683_24	2400001	2510000
WP	AA19683_25	2500001	2610000
WP	AA19683_26	2600001	2710000
WP	AA19683_27	2700001	2810000
WP	AA19683_28	2800001	2910000
WP	AA19683_29	2900001	3010000
WP	AA19683_30	3000001	3110000
WP	AA19683_31	3100001	3210000
WP	AA19683_32	3200001	3310000
WP	AA19683_33	3300001	3410000
WP	AA19683_34	3400001	3510000
WP	AA19683_35	3500001	3610000
WP	AA19683_36	3600001	3710000
WP	AA19683_37	3700001	3810000
WP	AA19683_38	3800001	3910000
WP	AA19683_39	3900001	4010000
WP	AA19683_40	4000001	4110000
WP	AA19683_41	4100001	4210000
WP	AA19683_42	4200001	4310000
WP	AA19683_43	4300001	4403765

Query Match 30.4%; Score 17; DB 4; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 CTCATCCGATCCAGCA 39  
DB 17517 CTCATCCGATCCAGCA 17533

RESULT 14  
ADQ31362/c  
ID ADQ31362 standard; DNA; 26 BP.

XX ADQ31362;

XX 07-OCT-2004 (first entry)

XX Human transferase PCR primer, SEQ ID 5.

XX Human; transferase; enzyme;

KW N-acetylglucosamine-6-O sulfate-specific beta 1;

KW 4-galactosyl transferase; beta 1; 4-galactosylation; PCR; primer; ss.

XX Homo sapiens.

PN WO2004058967-A1.

XX 15-JUL-2004.

XX 26-DEC-2003; 2003WO-JP016948.

XX 26-DEC-2002; 2002JP-00378727.

XX (NISC-) JAPAN SCI & TECHNOLOGY AGENCY.

XX Yamashita K, Seko A;

XX WPI; 2004-525884/50.

XX Beta 1,4-galactosylating glycan having N-acetylglucosamine-6-O sulfate

XX structure, useful in biosynthesis of sphingosine, involves reacting

XX PT glycan with N-acetylglucosamine 6-O sulfate-specific beta 1,4-galactosyl

XX transferase.

XX Disclosure; SEQ ID NO 5; 67pp; Japanese.

XX The present invention relates to a human transferase (ADQ31359) with N-

XX acetylglucosamine-6-O sulfate-specific beta 1,4-galactosyl transferase

XX activity. The transferase is useful for beta 1,4-galactosylating a glycan

XX (I) having N-acetylglucosamine-6-O sulfate structure to obtain

XX CC biosynthetic substances. The present sequence is the coding sequence for

XX CC the transferase of the invention. The present sequence is a PCR primer

XX used to illustrate the invention.

XX Sequence 26 BP; 5 A; 5 C; 9 G; 7 T; 0 U; 0 Other;

XX Query Match 28.6%; Score 16; DB 12; Length 26;

XX Best Local Similarity 100.0%; Pred. No. 1e+02;

XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 TGCTCATCCGATCCCA 36

DB 18 TGCTCATCCGATCCCA 3

RESULT 15

ABZ70624/c

ID ABZ70624 standard; DNA; 30 BP.

XX ABZ70624;

XX 23-MAY-2003 (first entry)

XX Plasmid pACYC184 p15A ori forward PCR primer.

XX Vector; pACYC184; origin of replication; p15A; mutagenesis; PCR; primer;

XX ss.

XX Escherichia coli.

XX WO2003008556-A2.

XX 30-JAN-2003.

XX 18-JUL-2002; 2002WO-US023089.



```
XX 18-JUN-2001; 2001US-0306344P.
PR
XX (EXPR-) EXPRESSIVE CONSTRUCTS INC.
XX
XX Sanders MC, Hamilton M;
XX
XX WPI, 2003-239326/23.
XX
XX New p15A origin of replication, useful in expressing and/or co-expressing
XX proteins, in purifying a cloned nucleic acid, and in converting a low
XX copy number plasmid into a more efficient high copy number plasmid.
XX
XX Disclousure; Page 5; 53pp; English.
XX
XX The present sequence is a forward primer for the pACYC184 plasmid origin
XX of replication (p15A ori). It includes an EcoRI site. The forward primer
XX and a reverse primer (see ABZ70625) containing an Hinarm site were used
XX to introduce random mutations into the p15A ori sequence. The 1.5 kb PCR
XX product was used with pACYC184 to create a plasmid library, which was
XX used to transform Escherichia coli BL21(DE3) cells. Transformed colonies
XX were screened for an operationally enhanced p15A ori, and plasmid pECT-
XX 073 was isolated, which has a copy number in E. coli BL21(DE3) about 4.47
XX -fold higher than that of pACYC184. Sequencing of the p15A ori of pECT-
XX 073 (see ABZ70621) revealed 10 base substitutions compared with the
XX native sequence. The mutated (enhanced) p15A ori sequence can be used to
XX convert a low copy number plasmid to a high copy number plasmid useful
XX for more efficient cloning, DNA and RNA purification, protein expression
XX and co-expression
XX
XX Sequence 30 BP; 8 A; 7 C; 9 G; 6 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 16; DB 8; Length 30;
XX Best Local Similarity 100.0%; Pred. No. 1e+02;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 17 TGAATGCTCATCCGGA 32
XX |||||
XX 25 TGAATGCTCATCCGGA 10
XX
XX RESULT 16
XX ABT17495
XX ID ABT17495 standard; DNA; 40 BP.
XX
XX AC ABT17495;
XX
XX 10-APR-2003 (first entry)
XX
XX DE Selection by avidity capture related PCR primer #18.
XX
XX KW Selection avidity capture; SAC; interaction; covalent binding;
XX ionic binding; hydrogen-binding; Van der Waal's binding; PCR; primer; ss.
XX
XX OS Unidentified.
XX
XX PN WO2002103363-A2.
XX
XX 27-DEC-2002.
XX
XX 18-JUN-2002; 2002WO-GB002839.
XX
XX 18-JUN-2001; 2001GB-00014856.
XX
XX (MEDI-) MEDICAL RES COUNCIL.
XX PA (DWIL/) DE WILDT R.
XX PA (TOML/) TOMLINSON I.
XX
XX De Wildt R, Tomlinson I, Holliger P;
XX WPI; 2003-167561/16.
XX
XX Selecting first and second molecules according to their interaction
XX
```

```
PT comprises allowing the first and second molecules to interact such that a
PT complex comprising each of the first and second molecules in multivalent
PT form is generated.
XX
XX Example; Page 28; 60pp; English.
XX
XX The invention relates to a novel selection avidity capture (SAC) method
XX for selecting first and second molecules according to an interaction
XX between the first and second molecules. This method comprises allowing
XX the first and second molecules to interact, such that a complex of the
XX first and second molecules in multivalent form is generated. The novel
XX method is useful for selecting first and second molecules according to
XX their interaction, thus identifying interactions between a wide variety
XX of different types of molecules, e.g. binding or association through
XX covalent binding, ionic binding, hydrogen-binding, Van der Waal's
XX binding, or other types of reversible or irreversible association. This
XX polynucleotide sequence represents a PCR primer relating to the SAC
XX method of the invention
XX
XX Sequence 40 BP; 11 A; 8 C; 11 G; 10 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 16; DB 8; Length 40;
XX Best Local Similarity 100.0%; Pred. No. 99;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 17 TGAATGCTCATCCGGA 32
XX |||||
XX 5 TGAATGCTCATCCGGA 20
XX
XX RESULT 17
XX AAC05090/C
XX ID AAC05090 standard; cDNA; 158 BP.
XX
XX AC AAC05090;
XX
XX 06-OCT-2000 (first entry)
XX
XX DE Human secreted protein 5' EST, SEQ ID NO: 9165.
XX
XX KW Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
XX gene therapy; chromosome mapping; ss.
XX
XX OS Homo sapiens.
XX
XX PN EP1033401-A2.
XX
XX 06-SEP-2000.
XX
XX 21-FEB-2000; 2000EP-00200610.
XX
XX 26-FEB-1999; 99US-0122487P.
XX
XX (GEST ) GENSET.
XX
XX Dumas Milne Edwards J, Duclert A, Giordano J;
XX WPI; 2000-500381/45.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
XX obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
XX diagnostic, forensic, gene therapy and chromosome mapping procedures.
XX
XX Claim 1; SEQ ID NO 9165; 71pp + Sequence listing; English.
XX
XX The present sequence is one of a large number of 5' ESTs derived from
XX mRNAs encoding secreted proteins. No ORF has yet been conclusively
XX identified within the present sequence. The 5' ESTs were prepared from
XX total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
XX sequences usually correspond mainly to the 3' untranslated region (UTR)
XX of the mRNA because they are often obtained from oligo-dT primed cDNA
XX libraries. Such ESTs are not well suited for isolating cDNA sequences
XX derived from the 5' ends of mRNAs and even in those cases where longer
XX
```



CC cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. CC They are used to obtain upstream regulatory sequences and to design expression and secretion vectors

CC Sequence 158 BP; 47 A; 41 C; 31 G; 38 T; 0 U; 1 Other;

Query Match 28.6%; Score 16; DB 3; Length 158;  
Best Local Similarity 100.0%; Pred. No. 95;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 TGCTCATCCGATCCA 36  
DB 50 TGCTCATCCGATCCA 35

RESULT 18  
AAT69648  
ID AAT69648 standard; DNA; 202 BP.  
AC AAT69648;  
DT 20-FEB-1998 (first entry)  
XX  
DE Amplification strand for determination of telomerase activity.  
XX  
XX Telomerase; substrate; primer; detection; 5'-region; retrovirus;  
KM long terminal repeat 2; LTR-2; diagnosis; tumour; screening;  
KM effector compound; PCR; amplification strand; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT primer\_bind 1..37  
FT /tag= b  
FT /note= "primer TB-1-ST binding site"  
FT primer\_bind 1..18  
FT /tag= a  
FT /note= "primer PI binding site"  
FT primer\_bind 61..80  
FT /tag= c  
FT /note= "primer TB-CAT binding site"  
FT primer\_bind 158..202  
FT /tag= d  
FT /note= "primer TE-ACT-ST binding site"  
FT primer\_bind 177..202  
FT /tag= e  
FT /note= "primer TB-ACT binding site"  
XX  
PN DB19644302-A1.  
XX  
XX 05-JUN-1997.  
XX  
XX 24-OCT-1996; 96DE-01044302.  
XX  
XX 28-NOV-1995; 95DE-01044317.  
XX  
XX (BOEP ) BOEHRINGER MANNHEIM GMBH.  
XX  
XX Emrich T, Leyling H, Hinzpeter M, Karl G;  
XX WPI, 1997-299542/28.  
XX  
XX Measuring telomerase activity, useful for tumour diagnosis and compound  
PT screening - by extending substrate primer, followed by amplification and  
PT immobilising product for detection.  
XX  
XX Example; Fig 5; 21pp; German.  
XX  
XX The present sequence is an amplification strand, which can be used in a  
CC novel method for the quantitative determination of telomerase activity by

CC PCR. The method comprises adding to a test sample a 1st primer, that  
CC serves as telomerase substrate, and nucleoside triphosphate (dNTP) and  
CC incubating to allow primer extension by the telomerase, amplifying the  
CC extension product, immobilising the amplification product (AP) on a solid  
CC phase and qualitative and/or quantitative detection of AP, where the  
CC substrate primer is preferably from the 5'-region of the long terminal  
CC repeat 2 (LTR-2) sequence of a retrovirus. The method can be used to  
CC diagnose tumours and screen compounds for effector activity.  
CC Immobilisation of AP provides a signal that is reproducibly  
CC representative of telomerase activity, eliminates the need for gel  
CC electrophoretic separation and provides high sensitivity. Radioactive  
CC labels are not required and the method can be automated for routine use.  
CC Specific detection is achieved by proper choice of hybridisation  
CC conditions, without separation of the telomerase extension product. A  
CC specific signal is generated by 1-10 cell equivalents, but for tumour  
CC analysis 10-1000 ng of tissue is usually used  
XX  
SQ Sequence 202 BP; 46 A; 46 C; 55 G; 55 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 2; Length 202;  
Best Local Similarity 100.0%; Pred. No. 94;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
DB 28 TGAATGCTCATCCGGA 43

RESULT 19  
AAQ37002  
ID AAQ37002 standard; DNA; 219 BP.  
XX  
XX AAQ37002;  
AC  
XX 25-MAR-2003 (revised)  
DT 18-JUN-1993 (first entry)  
XX  
DE CAT 1-73 coding sequence.  
XX  
XX Human; proinsulin; vector; pUC19; pPINS; CAT; pUC-CAT-proinsulin;  
KM insulin analogue; type I; type II; diabetes; ss.  
XX  
OS Synthetic.  
XX  
PN WO9303174-A1.  
XX  
XX 18-FEB-1993.  
PD  
XX 31-JUL-1992; 92WO-US006451.  
XX  
XX 08-AUG-1991; 91US-00741938.  
PR 30-JUL-1992; 92US-00918953.  
XX  
XX (SCIO-) SCIOS INC.  
XX (Pfiz ) PFIZER INC.  
XX  
XX Andy RJ, Larson ER;  
XX WPI, 1993-076530/09.  
XX P-PSDB; AAR32366.  
XX  
XX New hepato selective and peripheral selective human insulin analogues -  
PT and their corresp. DNA, for treatment of type I and type II diabetes.  
XX  
XX Disclosure; Fig 2a; 58pp; English.  
XX  
XX The sequence given encodes amino acids 1-73 of CAT. This sequence was  
CC used in the construction of proinsulin analogues. The sequences in  
CC AAQ36996-7001 are oligonucleotides which can be combined to form a gene  
CC which codes for human proinsulin. The resulting cDNA coding for  
CC proinsulin was inserted into plasmid vector pUC19 and digested with KpnI  
CC and HindIII. This resulted in the formation of the vector pPINS. This CAT  
CC fragment was inserted into pPINS to give a plasmid which contained DNA



CC sequences which coded for amino acids 1-73 of CAT, an 8 amino acid linker  
 CC sequence and human proinsulin (see AAQ37003). This plasmid, pUC-CAT-  
 CC proinsulin, could be used in the formation of insulin analogues which may  
 CC be used in the treatment of types I and II diabetes. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)

XX  
 SQ Sequence 219 BP; 69 A; 49 C; 39 G; 62 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 2; Length 219;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
 |||||  
 Db 200 TGAATGCTCATCCGGA 215

# RESULT 20

AAQ03560  
 ID AAQ03560 standard; DNA; 226 BP.

XX  
 AC AAQ03560;

XX  
 DT 30-JUL-1990 (first entry)

XX  
 DE Restriction site and function map of pCHNFI42.

XX  
 KW CAT; hybrid protein; Atrial Natriuretic Peptide; ds.

XX  
 OS Synthetic.

XX  
 PN WO9001540-A.

XX  
 PD 22-FEB-1990.

XX  
 PF 09-AUG-1989; 89WO-US003417.

XX  
 PR 11-AUG-1988; 88US-00231224.

XX  
 PA (CALB-) CALIF BIOTECHN INC.

XX  
 PI H111ker S, White R;

XX  
 DR WPI; 1990-083499/11.

XX  
 PT Heterologous protein expression in prokaryotic host - using 3' truncated  
 PT chloramphenicol acetyl-transferase gene to stably express hybrid protein.

XX  
 PS Example; Fig 21; 67pp; English.

CC Site-specific mutagenesis was used to substitute Tyr and Ser codons for  
 CC residues 16 and 31, respectively, of the CAT gene. One or more codons may  
 CC be altered to eliminate potential chemical cleavage sites. The expression  
 CC vector pCHNFI42 encodes a 99 amino acid CAT-hmNP hybrid protein. See also  
 CC AAQ03557 to AAQ05366; and AAN94767

XX  
 SQ Sequence 226 BP; 73 A; 50 C; 37 G; 66 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 2; Length 226;  
 Best Local Similarity 100.0%; Pred. No. 94;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
 |||||  
 Db 202 TGAATGCTCATCCGGA 217

# RESULT 21

AAQ04767  
 ID AAQ04767 standard; DNA; 315 BP.

XX  
 AC AAQ04767;

DT 30-JUL-1990 (first entry)

XX  
 DE Sequence encoding CAT-GLP-1 hybrid protein.

XX  
 KW CAT; hybrid protein; GLP-1 protein; ss.

XX  
 OS Synthetic.

XX  
 FH Key Location/Qualifiers

XX  
 FT CDS 1..222

XX  
 FT /tag= a

XX  
 FT /product= "CAT(1-73)"

XX  
 FT CDS 223..315

XX  
 FT /tag= b

XX  
 FT /product= "GLP-1(7-37)"

XX  
 PN WO9001540-A.

XX  
 PD 22-FEB-1990.

XX  
 PF 09-AUG-1989; 89WO-US003417.

XX  
 PR 11-AUG-1988; 88US-00231224.

XX  
 PA (CALB-) CALIF BIOTECHN INC.

XX  
 PI H111ker S, White R;

XX  
 DR WPI; 1990-083499/11.

XX  
 P-PSDB; AAR05446.

XX  
 PT Heterologous protein expression in prokaryotic host - using 3' truncated  
 PT chloramphenicol acetyl-transferase gene to stably express hybrid protein.

XX  
 PS Example; Fig 4B; 67pp; English.

XX  
 CC First 73 amino acids encoding the amino terminus of the CAT protein  
 CC joined in-frame to the synthetic GLP-1 gene preceded by a Met codon.  
 CC (Cyanogen bromide cleavage site.) See also AAQ03557 to AAQ03566

XX  
 SQ Sequence 315 BP; 89 A; 73 C; 65 G; 88 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 2; Length 315;  
 Best Local Similarity 100.0%; Pred. No. 93;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
 |||||  
 Db 200 TGAATGCTCATCCGGA 215

RESULT 22  
 AAS67496  
 ID AAS67496 standard; cDNA; 324 BP.

XX  
 AC AAS67496;

XX  
 DT 13-FEB-2002 (first entry)

XX  
 DE DNA encoding novel human diagnostic protein #3300.

XX  
 KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
 KW food supplement; medical imaging; diagnostic; genetic disorder; ss.

XX  
 OS Homo sapiens.

XX  
 PN WO200175067-A2.

XX  
 PD 11-OCT-2001.

XX  
 PF 30-MAR-2001; 2001WO-US008631.

XX  
 PR 31-MAR-2000; 2000US-00540217.



```

PR 23-AUG-2000; 2000US-00649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX P-PSDB; ABG03309.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity.
XX
XX Claim 1; SEQ ID NO 3300; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)
XX sequences. (I) is useful as hybridisation probes, polymerase chain
XX reaction (PCR) primers, oligomers, and for chromosome and gene mapping,
XX and in recombinant production of (II). The polynucleotides are also used
XX in diagnostics as expressed sequence tags for identifying expressed
XX genes. (II) is useful in gene therapy techniques to restore normal
XX activity of (II) or to treat disease states involving (II). (II) is
XX useful for generating antibodies against it, detecting or quantitating a
XX polypeptide in tissue, as molecular weight markers and as a food
XX supplement. (II) and its binding partners are useful in medical imaging
XX of sites expressing (II). (I) and (II) are useful for treating disorders
XX involving aberrant protein expression or biological activity. The
XX polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic
XX coding sequences of the invention. Note: The sequence data for this
XX patent did not appear in the printed specification, but was obtained in
XX electronic format directly from WIPO at
XX ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 324 BP; 90 A; 86 C; 73 G; 75 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 16; DB 5; Length 324;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 17 TGAATGCTCATCCGGA 32
XX |||||
XX Db 191 TGAATGCTCATCCGGA 206
XX
XX RESULT 23
XX AAI84591
XX ID AAI84591 standard; cDNA; 350 BP.
XX
XX AC AAI84591;
XX
XX DT 06-NOV-2001 (first entry)
XX
XX DE Human polynucleotide SEQ ID NO 4651.
XX
XX KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX tissue growth factor; immunomodulatory; cancer; leukaemia;
XX nervous system disorders; arthritis; inflammation; ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200164835-A2.
XX
XX PD 07-SEP-2001.
XX
XX PF 26-FEB-2001; 2001MO-US004927.
XX
XX PR 28-FEB-2000; 2000US-00515126.

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PR 18-MAY-2000; 2000US-0057409.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-514838/56.
XX
XX P-PSDB; AAO04660.
XX
XX Isolated nucleic acids and polypeptides, useful for preventing diagnosing
XX and treating e.g. leukemia, inflammation and immune disorders.
XX
XX Claim 1; SEQ ID NO 4651; 139pp + Sequence Listing; English.
XX
XX The invention relates to human polynucleotides (AAI79941-AAI93641) and
XX the encoded proteins (AAO00010-AAO13910) that exhibit activity relating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoiesis regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activin/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation. Note: The sequence data for this patent did not form part
XX of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
XX SQ Sequence 350 BP; 105 A; 73 C; 74 G; 98 T; 0 U; 0 Other;
XX
XX Query Match 28.6%; Score 16; DB 4; Length 350;
XX Best Local Similarity 100.0%; Pred. No. 93;
XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 17 TGAATGCTCATCCGGA 32
XX |||||
XX Db 230 TGAATGCTCATCCGGA 245
XX
XX RESULT 24
XX AAO03563
XX ID AAO03563 standard; DNA; 396 BP.
XX
XX AC AAO03563;
XX
XX DT 30-JUL-1990 (first entry)
XX
XX DE Sequence encoding CAT-A4-751i hybrid protein.
XX
XX KW CAT; hybrid protein; A4-751i protein; ss.
XX
XX OS Synthetic.
XX
XX FH Key Location/Qualifiers
XX FT CDS 1..225
XX FT /tag= a
XX FT /product= "CAT"
XX FT /note= "first 73 codons encoding amino terminus."
XX FT CDS 226..396
XX FT /tag= b
XX FT /product= "A4-761i protein"
XX
XX PN WO9001540-A.
XX
XX PD 22-FEB-1990.
XX
XX PF 09-AUG-1989; 89WO-US003417.
XX
XX PR 11-AUG-1988; 88US-00231224.
XX
XX PA (CALB-) CALIF BIOTECH INC.
XX
XX PI Hilleker S, White R;

```



XX WPI: 1990-083499/11.  
DR P-PSDB: AAR05445.  
XX  
PT Heterologous protein expression in prokaryotic host - using 3' truncated  
PT chloramphenicol acetyl-transferase gene to stably express hybrid protein.  
XX  
PS Example; Fig 4A; 67pp; English.  
XX  
CC First 73 codons encoding the amino terminus of the CAT protein joined in-  
CC frame to synthetic A4-7511 gene preceded by a chemical cleavage site  
CC (hydroxylamine) encoded by Asn-Gly. See also AAQ03557 to AAQ05366; and  
CC AAQ04767  
XX  
SQ Sequence 396 BP; 106 A; 92 C; 93 G; 105 T; 0 U; 0 Other;  
Query Match 28.6%; Score 16; DB 2; Length 396;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGAATGCTCATCCGGA 32  
Db 200 TGAATGCTCATCCGGA 215  
RESULT 25  
AAS71671/c  
ID AAS71671 standard; cDNA; 405 BP.  
XX  
AC AAS71671;  
XX  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #7475.  
XX  
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KM food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
XX Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI: 2001-639362/73.  
DR P-PSDB: ABG07484.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 7475; 103pp; English.  
XX  
XX The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probes, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
CC and in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging

CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AAS64197-AAS94564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 405 BP; 99 A; 90 C; 93 G; 123 T; 0 U; 0 Other;  
Query Match 28.6%; Score 16; DB 5; Length 405;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGAATGCTCATCCGGA 32  
Db 185 TGAATGCTCATCCGGA 170  
RESULT 26  
AAT61810  
ID AAT61810 standard; RNA; 414 BP.  
XX  
AC AAT61810;  
XX  
DT 07-NOV-1997 (first entry)  
XX  
DE T7 RNA sequence CIRC.  
XX  
KM Ribonuclease; diagnosis; therapy; ss.  
XX  
OS Synthetic.  
XX  
PN JP09019289-A.  
XX  
PD 21-JAN-1997.  
XX  
PF 05-JUL-1995; 95JP-00192475.  
XX  
PR 05-JUL-1995; 95JP-00192475.  
XX  
PA (NISR) JAPAN TOBACCO INC.  
XX  
XX WPI: 1997-139608/13.  
XX  
PT Ribonuclease specifically cleaving hybridised RNA section - useful in  
PT genetic engineering, and in diagnosis and therapy.  
XX  
PS Example 31; Page 16; 19pp; Japanese.  
XX  
CC The present sequence was used in the development of a ribonuclease, which  
CC specifically recognises and cleaves a hybridised section of a 1st and 2nd  
CC RNA chain at the 3'-terminal of the 1st chain, or at a section located 1  
CC to 3 nucleotides from it, where at least 5 contiguous nucleotides from  
CC the 5'-terminal of the 2nd RNA chain are hybridised to the 1st RNA chain.  
CC The ribonuclease has an optimum pH of 7.0 to 7.5, an optimum temperature  
CC of 50 to 60 degrees C, a molecular weight of 100 kDa as determined by  
CC molecular sieve chromatography and an isoelectric point of 4.5 as  
CC determined by chromatofocusing. The ribonuclease can be used to  
CC specifically cleave RNA at an arbitrary site, useful in genetic  
CC engineering and diagnosis and therapy  
XX  
SQ Sequence 414 BP; 120 A; 87 C; 91 G; 0 T; 116 U; 0 Other;  
Query Match 28.6%; Score 16; DB 2; Length 414;  
Best Local Similarity 75.0%; Pred. No. 92;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGAATGCTCATCCGGA 32



Db :|||||:|||||  
230 UGAAGCCTCAUCCGGA 245

RESULT 27  
AA577936/c  
ID AA577936 standard; cDNA; 496 BP.  
XX  
AC AA577936;  
DT 13-FEB-2002 (first entry)  
XX  
DE DNA encoding novel human diagnostic protein #13740.  
XX  
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;  
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200175067-A2.  
XX  
PD 11-OCT-2001.  
XX  
PF 30-MAR-2001; 2001WO-US008631.  
XX  
PR 31-MAR-2000; 2000US-00540217.  
PR 23-AUG-2000; 2000US-00649167.  
XX  
PA (HYSE-) HYSEQ INC.  
XX  
PI Drmanac RT, Liu C, Tang YT;  
XX  
DR WPI; 2001-639362/73.  
DR P-ESDB; ABG13749.  
XX  
PT New isolated polynucleotide and encoded polypeptides, useful in  
PT diagnostics, forensics, gene mapping, identification of mutations  
PT responsible for genetic disorders or other traits and to assess  
PT biodiversity.  
XX  
PS Claim 1; SEQ ID NO 13740; 103bp; English.  
XX  
SS The invention relates to isolated polynucleotide (I) and polypeptide (II)  
CC sequences. (I) is useful as hybridisation probe, polymerase chain  
CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping.  
CC in recombinant production of (II). The polynucleotides are also used  
CC in diagnostics as expressed sequence tags for identifying expressed  
CC genes. (I) is useful in gene therapy techniques to restore normal  
CC activity of (II) or to treat disease states involving (II). (II) is  
CC useful for generating antibodies against it, detecting or quantitating a  
CC polypeptide in tissue, as molecular weight markers and as a food  
CC supplement. (II) and its binding partners are useful in medical imaging  
CC of sites expressing (II). (I) and (II) are useful for treating disorders  
CC involving aberrant protein expression or biological activity. The  
CC polypeptide and polynucleotide sequences have applications in  
CC diagnostics, forensics, gene mapping, identification of mutations  
CC responsible for genetic disorders or other traits to assess biodiversity  
CC and to produce other types of data and products dependent on DNA and  
CC amino acid sequences. AA564197-AA594564 represent novel human diagnostic  
CC coding sequences of the invention. Note: The sequence data for this  
CC patent did not appear in the printed specification, but was obtained in  
CC electronic format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences  
XX  
SQ Sequence 496 BP; 98 A; 127 C; 90 G; 181 T; 0 U; 0 Other;

Query Match 28 6%; Score 16; DB 5; Length 496;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGGA 32  
|||||  
DB 39 TGAATGCTCATCCGGA 24

RESULT 28  
AAQ72699  
ID AAQ72699 standard; DNA; 497 BP.  
XX  
AC AAQ72699;  
XX  
DT 07-JUN-1995 (first entry)  
XX  
DE pGm/E.14 CRNA promoter-CAT antisense expression system fragment.  
XX  
KW Constitutive promoter element; CPE; promoter; soybean; CRNA; antisense;  
KW CRNA methionine initiator; chloramphenicol acetyl transferase; CAT;  
KW plant; inactivate; expression; ss.  
XX  
OS Glycine max.  
XX  
PN US5354854-A.  
XX  
PD 11-OCT-1994.  
XX  
PF 07-NOV-1991; 91US-00790199.  
XX  
PR 07-NOV-1991; 91US-00790199.  
XX  
PA (UMOR ) UNIV MISSOURI.  
XX  
PI Folk WR, Bourque JR;  
XX  
DR WPI; 1994-324604/40.  
XX  
PT Suppressing foreign gene expression in plants - by transcribing  
PT anti-sense DNA fused to the promoter of CRNA methionine initiator gene.  
XX  
PS Disclosure; Col 11-14; 14pp; English.  
XX  
SS The nucleotide sequence across and surrounding the constitutive promoter  
CC element (CPE) of the soybean CRNA methionine initiator (CRNA met1) linked  
CC to a fragment from the chloramphenicol acetyl transferase (CAT) gene in  
CC plasmid pGm/E.14. A series of plasmids with differing sites of inserted  
CC CAT gene fragments were generated (AAQ72698-700 and AAQ74277). The  
CC plasmid pGm/E.14 is generated by digesting pBLCAT3, a CAT containing  
CC plasmid, with XhoI and EcoRI to generate a 256 bp fragment from the 5'  
CC end of the CAT gene. This is placed into the XhoI and end-filled HindIII  
CC site in the CRNA-met1 coding sequence. The CAT fragment is placed in  
CC reversed orientation to the CRNA-met1. This allows expression of an  
CC antisense CAT fragment by RNA polIII. This reduces the expression of CAT  
CC by 50% in carrot protoplasts harbouring a plasmid with the CAT gene under  
CC control of the CamV 35S promoter. The system allows antisense (AS) genes  
CC under the control of the CPE to be expressed in all plant tissues. The AS  
CC gene should be able to suppress specific gene expression and thus  
CC inactivate a wide variety of genes  
XX  
SQ Sequence 497 BP; 132 A; 94 C; 111 G; 160 T; 0 U; 0 Other;

Query Match 28 6%; Score 16; DB 2; Length 497;  
Best Local Similarity 100.0%; Pred. No. 92;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGGA 32  
|||||  
DB 242 TGAATGCTCATCCGGA 257

RESULT 29  
ABK30710  
ID ABK30710 standard; cDNA; 561 BP.  
XX  
AC ABK30710;  
XX

DT 07-AUG-2003 (revised)  
DT 23-APR-2002 (first entry)



XX Plant dwarfing/stunting related cDNA seq ID 124.  
 XX  
 DE Plant; ss; dwarfism; stunting; EST; expressed sequence tag;  
 KW transgenic plant; plant metabolism.  
 KM  
 XX Nicotiana benthamiana.  
 OS  
 XX MO200208410-A2.  
 PN  
 XX 31-JAN-2002.  
 PD  
 XX 20-JUL-2001; 2001WO-US023120.  
 PF  
 XX 20-JUL-2000; 2000US-0219809P.  
 PR 20-JUL-2000; 2000US-0219810P.  
 XX  
 PA (DOMC ) DOM CHEM CO.  
 PA (REDD/) REDDY S A.  
 PA (LARR/) LARRINUA M I.  
 PA (RUEG/) RUEGGER M.  
 PA (WGL/) WEGLARZ T.  
 PA (BLAK/) BLAKESLEE B.  
 PA (ORIE/) ORIEDO V B J.  
 PA (SAVI/) SAVICKAS J P.  
 PA (MCCR/) MCCREARY A D.  
 PA (MILL/) MILLER A B.  
 PA (POGU/) POGUR P G.  
 PA (DELL/) DELLA-CIOPPA R G.  
 PA (WOLF/) WOLFE M G.  
 PA (ZHEN/) ZHENG W.  
 PA (GACH/) GACHOTTE D.  
 PA (GROS/) GROSLLEY R.  
 PA (PELL/) PELL R.  
 XX  
 XX Reddy SA, Larrinua MI, Ruegger M, Weglarz T, Blakeslee B;  
 PI Oriedo VBJ, Savickas JP, McCreary AD, Miller AB, Pogue PG;  
 PI Della-Cioppa RG, Wolfe MG, Zheng W, Gachotte D, Grosley R, Pell R;  
 PI  
 XX WPI; 2002-164823/21.  
 DR  
 XX Polynucleotide and amino acid sequences identified in one or more  
 PT metabolic pathways that lead to dwarfism and stunting in plants, useful  
 PT in agriculture to create dwarf varieties of any plant species.  
 XX  
 XX Example 10; Fig 1; 717pp; English.  
 PS  
 XX The invention relates to polynucleotide and amino acid sequences  
 CC identified in one or more metabolic pathways that lead to dwarfism and  
 CC stunting in plants. Also included are vectors comprising the  
 CC polynucleotides, transgenic plants (including the seed and leaf)  
 CC transected with the polynucleotides or vectors, a process for altering  
 CC the metabolism of a plant comprising providing the above vector and a  
 CC plant, and transecting the plant with the vector under conditions such  
 CC that the metabolism of the plant is altered by expression of the isolated  
 CC nucleic acid from the vector, e.g. such that a stunting phenotype in an  
 CC industrial plant is produced and a process for the characterisation of  
 CC fractionated biological samples, comprising (a) providing one or more  
 CC fractionated biological samples, reference samples, a gas chromatography  
 CC apparatus, a mass spectroscopy apparatus or data analysis software and  
 CC (b) treating the fractionated biological samples and the reference  
 CC samples with the gas chromatography apparatus to generate chromatographic  
 CC data corresponding to the fractionated biological samples and the  
 CC reference samples, (c) treating the fractionated biological samples and  
 CC the reference samples with the mass spectroscopy apparatus to generate  
 CC spectroscopic data corresponding to the fractionated biological samples  
 CC and the reference samples and (d) processing the chromatographic and the  
 CC spectroscopic data with the data analysis software. The nucleic acid and  
 CC the vector are useful for altering the metabolism of a plant and for  
 CC stunting a plant. The nucleic acids are useful in agriculture to create  
 CC dwarf varieties of any plant species. The present sequence is a plant  
 CC EST, expressed sequence tag, isolated from a cDNA library and related to  
 CC stunting/dwarfism. (Updated on 07-AUG-2003 to correct OS field.)

XX SQ Sequence 561 BP; 140 A; 129 C; 140 G; 152 T; 0 U; 0 Other;  
 XX  
 XX Query Match 28.6%; Score 16; DB 6; Length 561;  
 XX Best Local Similarity 100.0%; Pred. No. 91;  
 XX Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 36 AGAGCAATGAGAAAT 51  
 DB 492 AGAGCAATGAGAAAT 507  
 XX  
 XX RESULT 30  
 XX AAQ15266  
 XX ID AAQ15266 standard; DNA; 657 BP.  
 XX  
 XX AAQ15266;  
 XX AC  
 XX 25-MAR-2003 (revised)  
 XX DT 16-MAR-1992 (first entry)  
 XX  
 XX SP-C from pC149SP-C insert.  
 DE  
 XX Alveolar surfactant protein; CAT; fusion protein; SP-5; ss.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX Key Location/Qualifiers  
 XX CDS 90..653  
 XX FT /\*tag= a  
 XX FT /label= fusion\_protein  
 XX FT 90..536  
 XX FT /\*tag= b  
 XX FT /label= CAT  
 XX FT 537..548  
 XX FT /\*tag= c  
 XX FT /label= linker  
 XX FT 549..657  
 XX FT /\*tag= d  
 XX FT /label= SP-C  
 XX  
 XX WO9118015-A.  
 XX  
 XX 28-NOV-1991.  
 XX  
 XX 17-MAY-1990; 90US-00524360.  
 XX  
 XX 17-MAY-1990; 90US-00524360.  
 XX  
 XX 17-MAY-1990; 90US-00524360.  
 XX  
 XX (CALD ) CALIFORNIA BIOTECHNOLOGY INC.  
 XX  
 XX Benson BJ, White RT, Schilling JW, Buckley DI, Scarborough RM;  
 PI WPI; 1991-369185/50.  
 XX P-PSDB; AARI5612.  
 DR  
 XX New alveolar surfactant protein analogues - used for treating respiratory  
 PT distress syndrome, pneumonia and bronchitis.  
 PT  
 XX Disclosure; Fig 9; 67pp; English.  
 PS  
 XX An amino acid sequence of a 187 residue fusion protein encoded by pC149SP  
 CC -C is a slight modification of the sequence shown in AAQ15265. In plasmid  
 CC pC149SP-C, the 149 amino acids of CAT are joined to 35 amino acids of SP-  
 CC 5 through a linker of 3 amino acids. The SP-5 comprises 18.7% of the  
 CC total fusion. To construct pC149SP-C, a portion of the CAT segment of  
 CC pC210SP-C extending from the DdeI site at nucleotide 523 (AAQ15265) to  
 CC the EcoRI site at nucleotide 728 was removed and replaced by a set of two  
 CC complementary oligonucleotides. See also AARI5602-7, AAQ15262-63 and  
 CC AAQ15265-66. (Updated on 25-MAR-2003 to correct PA field.)  
 CC  
 XX Sequence 657 BP; 178 A; 146 C; 142 G; 191 T; 0 U; 0 Other;



Query Match 28.6%; Score 16; DB 2; Length 657;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGGA 32  
 |||||  
 DB 289 TGAATGCTCATCCGGA 304

RESULT 31  
 AAQ49262  
 ID AAQ49262 standard; DNA; 657 BP.  
 XX  
 AC AAQ49262;  
 XX  
 DT 04-MAY-1994 (first entry)  
 XX  
 DE Vector derived from pBR325.  
 XX  
 KW pBR325; nonnatural amino acid; iso-accepting tRNA; kit; synthesis;  
 KM protein synthesis; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN JP05236987-A.  
 XX  
 PD 17-SEP-1993.  
 XX  
 PF 20-AUG-1991; 91JP-00208321.  
 XX  
 PR 20-AUG-1991; 91JP-00208321.  
 XX  
 PA (NITO) NIPPON SANSO KK.  
 XX  
 DR WPI; 1993-330594/42.  
 XX  
 PT Non-natural aminoacid-contg. protein prepn. - comprises combining iso-  
 PT accepting tRNA corresponding to specific codon and non-natural aminoacid  
 PT using non-cellular protein synthetic system, etc.  
 XX  
 PS Disclosure; Page 8; 9pp; Japanese.  
 XX  
 CC The sequence is used to synthesise nonnatural amino acid-containing  
 CC proteins. This is done by combining iso-accepting tRNA corresponding to a  
 CC specific codon and a nonnatural amino acid, by using a noncellular  
 CC protein synthetic system  
 CC  
 SQ Sequence 657 BP; 174 A; 144 C; 151 G; 188 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 2; Length 657;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGGA 32  
 |||||  
 DB 200 TGAATGCTCATCCGGA 215

RESULT 32  
 ABL61148  
 ID ABL61148 standard; DNA; 658 BP.  
 XX  
 AC ABL61148;  
 XX  
 DT 18-SEP-2002 (first entry)  
 XX  
 DE CAT reporter DNA fragment.  
 XX  
 KW Alpha-SMA; smooth muscle actin; screening; smooth muscle cell; reporter;  
 KW myofibroblast; gene therapy; chloramphenicol-acetyltransferase; CAT; ds.  
 XX  
 OS Unidentified.

PN EP1172375-A1.  
 XX  
 PD 16-JAN-2002.  
 XX  
 PF 22-DEC-2000; 2000EP-00128446.  
 XX  
 PR 11-JUL-2000; 2000DE-01033633.  
 XX  
 PR 31-OCT-2000; 2000DE-01053879.  
 XX  
 PA (ODEN/) ODENTHAL M.  
 XX  
 PI Odenthal M, Jung D;  
 XX  
 DR WPI; 2002-149590/20.  
 XX  
 PT New nucleic acid containing regulatory region of the smooth muscle actin  
 PT gene, useful e.g. for manipulating gene expression in smooth muscle  
 PT cells.  
 XX  
 PS Disclosure; Page 23; 44pp; German.  
 XX  
 CC This invention describes a novel nucleic acid (I) comprising: (i) at  
 CC least one functional region (Ia) from the regulatory region of the alpha-  
 CC smooth muscle actin (SMA) gene and (ii) at least one additional  
 CC functional sequence (Ib) operably linked to (Ia). The products of the  
 CC invention can be used for preparing genetically modified eukaryotic cells  
 CC or organisms, for isolation and screening of smooth muscle cells,  
 CC myofibroblasts or related cells, and for manipulation of gene expression  
 CC and/or cell function in smooth muscle cell or myofibroblasts.  
 CC particularly for gene therapy. Component (Ia) provides cell-type or  
 CC differentiation-specific expression or modulation of genes. This sequence  
 CC represents a chloramphenicol-acetyltransferase (CAT) DNA fragment which  
 CC can be used as a reporter molecule under the control of the alpha-SMA  
 CC described in the invention  
 CC  
 SQ Sequence 658 BP; 174 A; 144 C; 152 G; 188 T; 0 U; 0 Other;

Query Match 28.6%; Score 16; DB 6; Length 658;  
 Best Local Similarity 100.0%; Pred. No. 91;  
 Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGGA 32  
 |||||  
 DB 200 TGAATGCTCATCCGGA 215

RESULT 33  
 ADF79371  
 ID ADF79371 standard; DNA; 658 BP.  
 XX  
 AC ADF79371;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Chloramphenicol resistance gene coding sequence.  
 XX  
 KW Transposon TnRIBD; genome deletion; non-essential gene;  
 KW chloramphenicol resistance; gene; selectable marker; ds.  
 XX  
 OS Chimeric.  
 OS Escherichia coli.  
 XX  
 FT Key 1.658 Location/Qualifiers  
 FT CDS /\*tag= a  
 FT /\*gene= "Cmr"  
 XX  
 PN WO2003089639-A1.  
 XX  
 PD 30-OCT-2003.  
 XX  
 PF 18-APR-2003; 2003WO-KR000798.



PR 20-APR-2002; 2002KR-00021811.  
XX (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
PA Kim S, Sung B, Yu B, Kim J, Lee W, Lee C, Lee J;  
XX WPI; 2003-854122/79.  
DR  
XX New transposon, useful for developing a mutant strain with deletion of an  
PT optional part of the chromosome, and for identifying non-essential genes  
PT for growth of microorganisms.  
XX  
PS Claim 1; SEQ ID NO 5; 47bp; English.  
XX  
CC The present sequence is the coding sequence of the chloramphenicol  
CC resistance gene. The coding sequence was obtained by PCR and used in the  
CC construction of transposon TnRIBD ADF79367, providing a positive  
CC selectable marker. A claimed method for developing a mutant microbial  
CC strain with deletion of an optional part of the chromosome involves  
CC inserting transposon TnRIBD into an optional site, identifying the  
CC insertion site, and deleting the parts of the chromosome on the left and  
CC right hand sides of the insertion site using a transposase expression  
CC vector. A claimed method for identifying non-essential genes for growth  
CC involves constructing a new mutant strain by deleting an optional part of  
CC the genome, identifying the genes in the deleted part, and investigating  
CC the survival of the mutant strain. The methods can be used to develop  
CC novel strains of *Escherichia coli* and other microorganisms.  
XX  
SQ Sequence 658 BP; 176 A; 143 C; 151 G; 188 T; 0 U; 0 Other;  
Query Match 28.6%; Score 16; DB 10; Length 658;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGAATGCTCATCCGGA 32  
Db 200 TGAATGCTCATCCGGA 215  
RESULT 34  
ADY03530  
ID ADY03530 standard; DNA; 658 BP.  
XX  
AC ADY03530;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Histidine operon deletion-related chloramphenicol resistance gene (Cmr).  
XX  
KW genetically engineered microorganism; chloramphenicol-resistance; ds.  
XX  
OS Unidentified.  
XX  
PN KR2004036371-A.  
XX  
PD 30-APR-2004.  
XX  
PF 24-OCT-2002; 2002KR-00065351.  
XX  
PR 24-OCT-2002; 2002KR-00065351.  
XX  
PA (KOAD ) KOREA ADV INST SCI & TECHNOLOGY.  
XX  
FI Kim JM, Kim SC, Lee CH, Lee JH, Lee WS, Sung BH, Yoo BJ;  
XX WPI; 2004-589890/57.  
XX  
DR  
XX Linear DNA fragment for developing mutated microorganism of which  
PT specific region in chromosome.  
XX  
PS Claim 2; SEQ ID NO 5; 42bp; Korean.  
XX  
CC The invention relates to a novel linear DNA fragment for developing a

CC mutated microorganism in which a specific region within a chromosome is  
CC removed. Also disclosed is a method for preparing the microorganism. The  
CC current sequence is that of the *Escherichia coli* K12 MG1655 histidine  
CC operon deletion-related chloramphenicol resistance gene (Cmr) of the  
CC invention.  
XX  
SQ Sequence 658 BP; 176 A; 143 C; 151 G; 188 T; 0 U; 0 Other;  
Query Match 28.6%; Score 16; DB 13; Length 658;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 17 TGAATGCTCATCCGGA 32  
Db 200 TGAATGCTCATCCGGA 215  
RESULT 35  
AAV28374  
ID AAV28374 standard; cDNA; 660 BP.  
XX  
AC AAV28374;  
XX  
DT 30-JUL-1998 (first entry)  
XX  
DE *Escherichia coli* CAT protein encoding cDNA.  
XX  
KW CAT gene; conjugative transfer; intraorganellar; expression vector;  
KW donor microbe; gene therapy; ss.  
XX  
OS *Escherichia coli*.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..660  
FT /\*tag= a  
FT /product= "CAT protein"  
XX  
FN JP10075793-A.  
XX  
PD 24-MAR-1998.  
XX  
PF 06-SEP-1996; 96JP-00255378.  
XX  
PR 06-SEP-1996; 96JP-00255378.  
XX  
PA (MITK ) MITSUI TOATSU CHEM INC.  
XX  
DR WPI; 1998-244365/22.  
XX P-PSDB; AAW56687.  
XX  
FT Conjugative transfer intraorganellar expression vector - and conjugatively  
PT transferring vector from donor microbe carrying to eukaryote, used in  
PT gene therapy.  
XX  
PS Example; Page 16-17; 24pp; Japanese.  
XX  
CC This cDNA encodes the *Escherichia coli* CAT protein. The invention  
CC provides a conjugative transfer intraorganellar expression vector  
CC containing a replication starting point functioned by organelle, a  
CC replication starting point functioned by the donor microbe, a selective  
CC marker gene functioned by organelle, a selective marker gene functioned  
CC by the donor microbe, a desired foreign gene functioned by organelle and  
CC oriT sequence required for the conjugative transfer between prokaryote  
CC and eukaryote. The vector can be conjugatively transferred from donor  
CC microbe carrying the vector to a eukaryote (which is a host cell) using  
CC tra gene and mob gene to introduce the vector to the organelle present in  
CC the eukaryote. This conjugative transfer intraorganellar expression vector  
CC can be used in the gene therapy. The CAT gene was converted to  
CC translation codon for mitochondria by site-specific mutation  
XX  
SQ Sequence 660 BP; 175 A; 146 C; 151 G; 188 T; 0 U; 0 Other;  
Query Match 28.6%; Score 16; DB 2; Length 660;



Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 200 TGAATGCTCATCCGGA 215

## RESULT 36

AAH02154  
ID AAH02154 standard; DNA; 660 BP.

AC AAH02154;

DT 24-JUN-2001 (first entry)

DE Escherichia coli nucleotide sequence SEQ ID NO:2147.

KW Species specific; genus specific; family specific; probe; detection;  
KW identification; algal; archaeal; bacterial; fungal; parasitical;  
KW microorganism; diagnosis; translation elongation factor Tu; toxin;  
KW translation elongation factor G; RecA recombinase; resistance;  
KW catalytic subunit of proton-translocating ATPase; antimicrobial; vaccine;  
KW primer; ds.

OS Escherichia coli.

PN WO200123604-A2.

PD 05-APR-2001.

PF 28-SEP-2000; 2000WO-CA001150.

PR 28-SEP-1999; 99CA-02283458.

PR 19-MAY-2000; 2000CA-02307010.

PA (INFE-) INFECTIO DIAGNOSTIC (IDI) INC.

PI Bergeron MG, Bolesnot M, Huletsky A, Menard C, Ouellette M;  
PI Picard FJ, Roy PH;

DR WPI; 2001-245006/25.

PT Nucleic acid sequences are used to generate universal probes and primers  
PT which can be used to identify and detect the presence of algal, archaeal,  
PT bacterial, fungal and parasitical species in a test sample.

PS Disclosure; Page 1512; 1580pp; English.

XX The present invention describes a method for generating a repository of  
XX nucleic acids of tuf, fus, atpD and/or recA genes from which probes  
XX and/or primers are derived. The method comprises amplifying the nucleic  
XX acids of determined algal, archaeal, bacterial, fungal and parasitical  
XX species with a combination of defined primer pairs. The method can be  
XX used for producing probes and/or primers for detecting one or more  
XX related microorganisms e.g. algae, archaea, bacteria, fungi and  
XX parasites, for universal detection and for specific and ubiquitous  
XX detection and identification of an algal, archaeal, bacterial, fungal and  
XX parasitical species, genus, family and group. A nucleic acid (I) obtained  
XX using the method of the invention can be used for the universal detection  
XX of any bacterium, fungus or parasite in a sample and for the detection of  
XX at least one antimicrobial agent resistance gene or at least one toxin  
XX gene. Hexa nucleic acids are used for the specific and ubiquitous  
XX detection and for identification of Streptococcus pneumoniae. (I) can be  
XX used to design a therapeutic agent which is effective against  
XX microorganisms. Microbial species or genus or family or phylum or group  
XX which can be detected include Abiotrophia adiacens, Bordetella sp.,  
XX Corynebacterium sp., Enterobacteriaceae group, Escherichia coli,  
XX Mycobacteriaceae family, Pseudomonads group, Streptococcus sp., Neisseria  
XX gonorrhoeae and Staphylococcus sp. Using DNA based tests provides faster  
XX results than substrate specificity tests as results can be determined in  
XX an hour and improved accuracy is also achieved. AAH00010 to AAH002304  
XX represent nucleotide sequences and primers/probes which are given in the

CC exemplification of the present invention

XX Sequence 660 BP; 176 A; 145 C; 151 G; 188 T; 0 U; 0 Other;

Qy Query Match 28.6%; Score 16; DB 4; Length 660;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 200 TGAATGCTCATCCGGA 215

## RESULT 37

AD036313  
ID AD036313 standard; DNA; 660 BP.

AC AD036313;

DT 26-AUG-2004 (first entry)

DE Intracellular antibody isolation-related CAM gene #85.

KW Intracellular antibody; neutralise; interaction; protein ligand; cell;  
KW transformed yeast clone; expression; CAM; gene; ds.

OS Unidentified.

PN WO2004046192-A2.

PD 03-JUN-2004.

PF 21-NOV-2003; 2003WO-IT000764.

PR 21-NOV-2002; 2002IT-RM000588.

PA (LAVL-) LAV LINE GENOMICS SPA.

PI Visintin M, Cattaneo A;

DR WPI; 2004-431953/40.

PT Isolating intracellular antibodies able to neutralize an interaction  
PT between a known protein ligand x and a known protein ligand y inside a  
PT cell comprises selecting transformed yeast clones by inducing the  
PT expression of both ligands.

PS Disclosure; Page 55; 93pp; English.

XX This invention relates to a novel method of isolating intracellular  
XX antibodies able to neutralise an interaction between a known protein  
XX ligand x and a known protein ligand y inside a cell. The method comprises  
XX selecting transformed yeast clones by inducing the expression of both  
XX ligand x and ligand y. The method is useful for isolating intracellular  
XX antibodies able to neutralise an interaction between a known protein  
XX ligand x and a known protein ligand y inside a cell. The present sequence  
XX is that of a gene which is related to the method of the invention.

XX Sequence 660 BP; 176 A; 143 C; 151 G; 190 T; 0 U; 0 Other;

Qy Query Match 28.6%; Score 16; DB 12; Length 660;  
Best Local Similarity 100.0%; Pred. No. 91;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
| | | | | | | | | | | | | | | | | | | | | |  
Db 200 TGAATGCTCATCCGGA 215

RESULT 38  
ADZ39850  
ID ADZ39850 standard; DNA; 660 BP.  
XX



AC	ADZ39850;
XX	
DT	30-JUN-2005 (first entry)
XX	
DE	Chloramphenicol acetyltransferase (CAT) coding sequence - SEQ ID 2.
XX	
KW	protein engineering; protein solubilization; gene; ds;
KM	chloramphenicol acetyltransferase; CAT.
XX	
OS	unidentified.
XX	
PN	JP2005095079-A.
PD	
XX	
PP	14-APR-2005.
XX	
PF	25-SEP-2003; 2003JP-00333932.
XX	
PR	25-SEP-2003; 2003JP-00333932.
XX	
PA	(DOKU-) DOKURITSU GYOSEI HOJIN RIKAGAKU KENKYUSH.
DR	WI; 2005-299480/31.
XX	
PT	Synthesizing C-terminal defective protein, involves translating 3' terminal deleted RNA obtained by performing RNA transcription using template DNA, RNA polymerase and substance capable of stopping RNA transcription.
XX	
PS	Example 1; SEQ ID NO 2; 19pp; Japanese.
XX	
CC	The invention comprises a method of synthesizing a C-terminal defective protein, the method involves obtaining 3' terminal deleted RNA through CC RNA transcription, and obtaining C-terminal defective protein by CC translating the obtained 3' terminal deleted RNA. The method of the CC invention is useful for synthesizing C-terminal defective protein, the preparing soluble protein, and for determining solubilization domain. The CC present DNA sequence represents a chloramphenicol acetyltransferase (CAT) coding sequence.
XX	
SQ	Sequence 660 BP; 176 A; 145 C; 151 G; 188 T; 0 U; 0 Other;
Query Match	28.6%; Score 16; DB 14; Length 660;
Best Local Similarity	100.0%; Pred. No. 91;
Matches 16; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	17 TGAATGCTCATCCGA 32       200 TGAATGCTCATCCGA 215
DB	
RESULT 39	
AAN90107	
ID	AAN90107 standard; DNA; 662 BP.
XX	
AC	AAN90107;
XX	
DT	25-MAR-2003 (revised)
DT	19-JAN-1991 (first entry)
XX	
DE	Sequence of BamHI/HindIII insert of pCI49SP-C which encodes a CAT-SP-5 fusion protein.
XX	
KW	Alveolar surfactant protein; respiratory distress syndrome; pneumonia;
KM	bronchitis; therapy; ss.
XX	
OS	Homo sapiens.
XX	
FH	Key Location/Qualifiers
FT	CDS 95..658
FT	/tag= a
FT	misc_feature complement(551..574)
FT	/tag= b
FT	/note= "to obtain modified sequences encoding hsp-5

[illegible]



PT New isolated polynucleotide and encoded polypeptides, useful in  
 PT diagnostics, forensics, gene mapping, identification of mutations  
 PT responsible for genetic disorders or other traits and to assess  
 PT biodiversity.

PS Claim 1; SEQ ID NO 11630; 103bp; English.

XX  
 CC The invention relates to isolated polynucleotide (I) and polypeptide (II)  
 CC sequences. (I) is useful as hybridisation probes, polymerase chain  
 CC reaction (PCR) primers, oligomers, and for chromosome and gene mapping,  
 CC and in recombinant production of (II). The polynucleotides are also used  
 CC in diagnostics as expressed sequence tags for identifying expressed  
 CC genes. (I) is useful in gene therapy techniques to restore normal  
 CC activity of (II) or to treat disease states involving (II). (II) is  
 CC useful for generating antibodies against it, detecting or quantitating a  
 CC polypeptide in tissue, as molecular weight markers and as a food  
 CC supplement. (II) and its binding partners are useful in medical imaging  
 CC of sites expressing (II). (I) and (II) are useful for treating disorders  
 CC involving aberrant protein expression or biological activity. The  
 CC polypeptide and polynucleotide sequences have applications in  
 CC diagnostics, forensics, gene mapping, identification of mutations  
 CC responsible for genetic disorders or other traits to assess biodiversity  
 CC and to produce other types of data and products dependent on DNA and  
 CC amino acid sequences. AA664197-AA694564 represent novel human diagnostic  
 CC coding sequences of the invention. Note: The sequence data for this  
 CC patent did not appear in the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences

XX Sequence 666 BP; 172 A; 151 C; 152 G; 191 T; 0 U; 0 Other;

SO Query Match

28.6%; Score 16; DB 5; Length 666;

Best Local Similarity 100.0%; Pred. No. 91;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 17 TGAATGCTCATCCGA 32

DB 467 TGAATGCTCATCCGA 452

Search completed: April 11, 2006, 16:26:23  
 Job time : 96.0231 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 18:10:11 ; Search time 22.7298 Seconds  
(without alignments) 4379.433 Million cell updates/sec

Title: US-10-712-654-26

Perfect score: 56

Sequence: 1 gcattccgtgtatgttgaa.....ggagcatgagattacacg 56

Scoring table: OLIGO\_NUC

Searched: 1303057 seqs, 888780828 residues

Word size : 1

Total number of hits satisfying chosen parameters: 2605320

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database : Issued Patents NA:\*

1: /cgm2\_6/ptodata/1/ina/1\_COMB.seq:\*  
2: /cgm2\_6/ptodata/1/ina/5\_COMB.seq:\*  
3: /cgm2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
4: /cgm2\_6/ptodata/1/ina/6B\_COMB.seq:\*  
5: /cgm2\_6/ptodata/1/ina/H\_COMB.seq:\*  
6: /cgm2\_6/ptodata/1/ina/PCRTUS\_COMB.seq:\*  
7: /cgm2\_6/ptodata/1/ina/PP\_COMB.seq:\*  
8: /cgm2\_6/ptodata/1/ina/RE\_COMB.seq:\*  
9: /cgm2\_6/ptodata/1/ina/backfile1.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	30.4	601	3	US-09-949-016-91323
2	17	30.4	601	3	US-09-949-016-91324
3	17	30.4	9096	3	US-09-147-119-5
4	17	30.4	15936	3	US-09-147-119-1
5	17	30.4	18650	3	US-09-949-016-14366
6	17	30.4	4403765	3	US-09-103-840A-2
7	17	30.4	4411529	3	US-09-103-840A-1
8	16	28.6	158	3	US-09-513-999C-9165
9	16	28.6	202	3	US-08-973-857-16
10	16	28.6	457	2	US-08-039-364-17
11	16	28.6	457	2	US-09-158-710-17
12	16	28.6	497	2	US-07-790-199-2
13	16	28.6	510	2	US-07-918-953-7
14	16	28.6	510	2	US-08-081-661-7
15	16	28.6	601	3	US-09-949-016-180092
16	16	28.6	660	3	US-09-949-016-180093
17	16	28.6	660	3	US-09-193-707-7
18	16	28.6	723	2	US-07-790-199-3
19	16	28.6	723	2	US-07-790-199-3
20	16	28.6	741	3	US-08-264-042-1
21	16	28.6	741	3	US-08-264-042-2
22	16	28.6	768	3	US-08-264-042-3
23	16	28.6	768	3	US-09-489-039A-4076
24	16	28.6	781	3	US-09-363-970-3

25	16	28.6	1750	3	US-10-001-052-41	Sequence 41, Appli
26	16	28.6	1824	3	US-09-930-329-1	Sequence 1, Appli
27	16	28.6	1825	2	US-08-176-414B-1	Sequence 1, Appli
28	16	28.6	1825	2	US-08-336-724-1	Sequence 1, Appli
29	16	28.6	3225	3	US-09-358-856C-2	Sequence 2, Appli
30	16	28.6	3249	2	US-08-507-455-4	Sequence 4, Appli
31	16	28.6	3400	3	US-09-793-372-1	Sequence 1, Appli
32	16	28.6	3462	3	US-09-744-373-10	Sequence 10, Appli
33	16	28.6	3462	3	US-10-394-058-10	Sequence 10, Appli
34	16	28.6	3801	3	US-09-640-882-1	Sequence 1, Appli
35	16	28.6	3803	2	US-07-623-953-1	Sequence 1, Appli
36	16	28.6	3822	3	US-07-640-476-1	Sequence 1, Appli
37	16	28.6	3822	3	US-08-675-566-8	Sequence 8, Appli
38	16	28.6	3861	3	US-08-675-566-11	Sequence 11, Appli
39	16	28.6	3881	3	US-09-744-016A-15	Sequence 15, Appli
40	16	28.6	3955	3	US-08-675-566-10	Sequence 10, Appli
41	16	28.6	3975	3	US-09-744-016A-13	Sequence 13, Appli
42	16	28.6	3977	2	US-07-794-400-2	Sequence 2, Appli
43	16	28.6	3977	2	US-07-794-400-2	Sequence 2, Appli
44	16	28.6	3977	2	US-07-794-400-13	Sequence 13, Appli
45	16	28.6	3977	2	US-08-041-648-1	Sequence 1, Appli
46	16	28.6	3977	2	US-08-217-529-1	Sequence 1, Appli
47	16	28.6	3977	2	US-08-397-470-2	Sequence 2, Appli
48	16	28.6	3977	2	US-08-397-470-13	Sequence 13, Appli
49	16	28.6	4009	3	US-08-675-566-9	Sequence 9, Appli
50	16	28.6	4045	3	US-09-809-517A-37	Sequence 37, Appli
51	16	28.6	4055	3	US-09-620-312D-706	Sequence 706, App
52	16	28.6	4055	3	US-09-620-312D-706	Sequence 706, App
53	16	28.6	4245	2	US-08-929-967-4	Sequence 4, Appli
54	16	28.6	4411	2	US-08-929-967-5	Sequence 5, Appli
55	16	28.6	4491	3	US-09-837-863-23	Sequence 23, Appli
56	16	28.6	4503	3	US-08-675-566-7	Sequence 7, Appli
57	16	28.6	4755	3	US-09-837-863-24	Sequence 24, Appli
58	16	28.6	5096	2	US-08-106-433A-3	Sequence 3, Appli
59	16	28.6	5110	2	US-08-106-433A-4	Sequence 4, Appli
60	16	28.6	5110	2	US-08-106-433A-5	Sequence 5, Appli
61	16	28.6	5110	2	US-08-106-433A-6	Sequence 6, Appli
62	16	28.6	5110	2	US-08-106-433A-7	Sequence 7, Appli
63	16	28.6	5110	2	US-08-106-433A-8	Sequence 8, Appli
64	16	28.6	5110	2	US-08-106-433A-9	Sequence 9, Appli
65	16	28.6	5110	2	US-08-106-433A-10	Sequence 10, Appli
66	16	28.6	5110	2	US-08-106-433A-11	Sequence 11, Appli
67	16	28.6	5110	2	US-08-106-433A-12	Sequence 12, Appli
68	16	28.6	5110	2	US-08-106-433A-13	Sequence 13, Appli
69	16	28.6	5110	2	US-08-106-433A-14	Sequence 14, Appli
70	16	28.6	5201	3	US-09-640-882-2	Sequence 2, Appli
71	16	28.6	5201	3	US-09-640-882-2	Sequence 2, Appli
72	16	28.6	5241	3	US-08-809-513A-1	Sequence 1, Appli
73	16	28.6	5241	3	US-08-809-513A-2	Sequence 2, Appli
74	16	28.6	5241	3	US-09-298-367B-5	Sequence 5, Appli
75	16	28.6	5498	3	US-09-744-016A-29	Sequence 29, Appli
76	16	28.6	5525	3	US-09-744-016A-20	Sequence 20, Appli
77	16	28.6	5525	3	US-09-744-016A-32	Sequence 32, Appli
78	16	28.6	5525	3	US-09-744-016A-32	Sequence 32, Appli
79	16	28.6	5555	3	US-09-744-016A-17	Sequence 17, Appli
80	16	28.6	5557	3	US-09-744-016A-26	Sequence 26, Appli
81	16	28.6	5611	3	US-09-744-016A-26	Sequence 26, Appli
82	16	28.6	5641	3	US-09-630-911A-13	Sequence 13, Appli
83	16	28.6	5670	3	US-09-630-911A-14	Sequence 14, Appli
84	16	28.6	5677	2	US-07-623-953-4	Sequence 4, Appli
85	16	28.6	5740	3	US-09-921-380-3	Sequence 3, Appli
86	16	28.6	5826	3	US-09-630-911A-11	Sequence 11, Appli
87	16	28.6	5838	2	US-08-850-880-3	Sequence 3, Appli
88	16	28.6	5838	2	US-08-944-916-3	Sequence 3, Appli
89	16	28.6	5838	2	US-08-814-877-3	Sequence 3, Appli
90	16	28.6	5838	2	US-09-272-432A-3	Sequence 3, Appli
91	16	28.6	6043	3	US-09-630-929-4	Sequence 4, Appli
92	16	28.6	6071	3	US-09-630-931A-12	Sequence 12, Appli
93	16	28.6	6363	2	US-08-929-967-6	Sequence 6, Appli
94	16	28.6	6501	3	US-09-767-515-1	Sequence 1, Appli
95	16	28.6	6501	3	US-09-767-515-2	Sequence 2, Appli
96	16	28.6	6971	3	US-09-495-880A-31	Sequence 31, Appli
97	16	28.6	7055	3	US-09-495-880A-18	Sequence 18, Appli



C 98	16	28.6	7326	9	5304637-21	Patent No. 5304637	171	15	26.8	968	2	US-08-161-271A-12	Sequence 12, Appl
C 99	16	28.6	7336	2	US-08-418-085-3	Sequence 3, Appl	172	15	26.8	968	2	US-08-449-315-12	Sequence 12, Appl
C 100	16	28.6	7336	3	US-09-099-011A-3	Sequence 3, Appl	173	15	26.8	968	2	US-08-444-803-12	Sequence 12, Appl
C 101	16	28.6	7336	3	US-08-470-369-21	Sequence 21, Appl	174	15	26.8	968	2	US-08-449-043-12	Sequence 12, Appl
C 102	16	28.6	7336	3	US-09-098-877B-3	Sequence 3, Appl	175	15	26.8	968	2	US-08-456-265A-12	Sequence 12, Appl
C 103	16	28.6	7339	3	US-08-675-566-13	Sequence 13, Appl	176	15	26.8	968	2	US-08-455-416-12	Sequence 12, Appl
C 104	16	28.6	7507	2	US-08-975-763-1	Sequence 1, Appl	177	15	26.8	968	2	US-08-455-244-12	Sequence 12, Appl
C 105	16	28.6	7566	2	US-08-232-016-23	Sequence 23, Appl	178	15	26.8	968	2	US-08-454-876-12	Sequence 12, Appl
C 106	16	28.6	7639	2	US-08-232-016-22	Sequence 22, Appl	179	15	26.8	968	2	US-08-457-364-12	Sequence 12, Appl
C 107	16	28.6	7783	3	US-09-495-880A-3	Sequence 3, Appl	180	15	26.8	968	2	US-08-456-262-12	Sequence 12, Appl
C 108	16	28.6	7811	2	US-08-549-680A-5	Sequence 5, Appl	181	15	26.8	968	2	US-08-456-240-12	Sequence 12, Appl
C 109	16	28.6	8066	3	US-09-027-169-5	Sequence 5, Appl	182	15	26.8	968	2	US-08-455-726-12	Sequence 12, Appl
C 110	16	28.6	9652	3	US-10-007-527A-7	Sequence 7, Appl	183	15	26.8	968	2	US-08-971-217-12	Sequence 12, Appl
C 111	16	28.6	9737	3	US-09-479-122-22	Sequence 22, Appl	184	15	26.8	968	3	US-09-350-600-12	Sequence 12, Appl
C 112	16	28.6	9737	3	US-09-479-122-23	Sequence 23, Appl	185	15	26.8	968	3	US-09-906-234-12	Sequence 12, Appl
C 113	16	28.6	9737	3	US-09-479-122-28	Sequence 28, Appl	186	15	26.8	1494	3	US-09-328-352-2602	Sequence 2602, Ap
C 114	16	28.6	9737	3	US-09-484-997-22	Sequence 22, Appl	187	15	26.8	1678	3	US-10-002-344A-8	Sequence 8, Appl
C 115	16	28.6	9737	3	US-09-484-997-23	Sequence 23, Appl	188	15	26.8	2373	2	US-08-445-586-1	Sequence 1, Appl
C 116	16	28.6	9737	3	US-09-484-997-28	Sequence 28, Appl	189	15	26.8	3420	3	US-09-513-505-1	Sequence 1, Appl
C 117	16	28.6	9737	3	US-09-481-355-22	Sequence 22, Appl	190	15	26.8	3478	3	US-09-513-505-3	Sequence 3, Appl
C 118	16	28.6	9737	3	US-09-481-355-23	Sequence 23, Appl	191	15	26.8	4156	3	US-10-104-047-321	Sequence 321, App
C 119	16	28.6	9737	3	US-09-481-355-28	Sequence 28, Appl	192	15	26.8	14485	3	US-09-876-216-3	Sequence 3, Appl
C 120	16	28.6	9737	3	US-09-481-282-22	Sequence 22, Appl	193	15	26.8	14485	3	US-10-359-076-3	Sequence 3, Appl
C 121	16	28.6	9737	3	US-09-481-282-23	Sequence 23, Appl	194	15	26.8	22067	3	US-09-820-001-3	Sequence 3, Appl
C 122	16	28.6	9737	3	US-09-481-282-28	Sequence 28, Appl	195	15	26.8	22067	3	US-10-003-302-3	Sequence 3, Appl
C 123	16	28.6	9737	3	US-09-455-659A-22	Sequence 22, Appl	196	15	26.8	130563	3	US-09-949-016-12273	Sequence 12273, A
C 124	16	28.6	9737	3	US-09-455-659A-23	Sequence 23, Appl	197	15	26.8	133379	3	US-09-949-016-16050	Sequence 16050, A
C 125	16	28.6	9737	3	US-09-455-659A-28	Sequence 28, Appl	198	15	26.8	133030	3	US-09-949-016-14896	Sequence 14896, A
C 126	16	28.6	9737	3	US-09-484-996-22	Sequence 22, Appl	199	15	26.8	176677	3	US-09-949-016-13444	Sequence 13444, A
C 127	16	28.6	9737	3	US-09-484-996-23	Sequence 23, Appl	200	15	26.8	285986	3	US-09-949-016-12287	Sequence 12287, A
C 128	16	28.6	9737	3	US-09-484-996-28	Sequence 28, Appl	201	14	25.0	32	2	US-07-872-644-33	Sequence 33, Appl
C 129	16	28.6	9737	3	US-09-479-123-22	Sequence 22, Appl	202	14	25.0	32	2	US-08-297-494-33	Sequence 33, Appl
C 130	16	28.6	9737	3	US-09-479-123-23	Sequence 23, Appl	203	14	25.0	32	2	US-08-297-510-33	Sequence 33, Appl
C 131	16	28.6	9737	3	US-09-479-123-28	Sequence 28, Appl	204	14	25.0	32	2	US-08-479-532-33	Sequence 33, Appl
C 132	16	28.6	9737	3	US-09-484-317A-22	Sequence 22, Appl	205	14	25.0	32	2	US-08-455-525-33	Sequence 33, Appl
C 133	16	28.6	9737	3	US-09-484-317A-23	Sequence 23, Appl	206	14	25.0	32	2	US-08-455-525-33	Sequence 33, Appl
C 134	16	28.6	9737	3	US-09-484-317A-28	Sequence 28, Appl	207	14	25.0	32	2	US-09-139-491-33	Sequence 33, Appl
C 135	16	28.6	9737	3	US-09-276-820A-22	Sequence 22, Appl	208	14	25.0	32	3	US-09-883-825-33	Sequence 33, Appl
C 136	16	28.6	9737	3	US-09-276-820A-23	Sequence 23, Appl	209	14	25.0	32	6	PCR-US92-03222-33	Sequence 3, Appl
C 137	16	28.6	9737	3	US-09-276-820A-28	Sequence 28, Appl	210	14	25.0	47	3	US-09-349-644-8	Sequence 8, Appl
C 138	16	28.6	9811	3	US-09-479-122-24	Sequence 24, Appl	211	14	25.0	64	3	US-09-349-644-7	Sequence 7, Appl
C 139	16	28.6	9811	3	US-09-479-122-24	Sequence 24, Appl	212	14	25.0	121	3	US-09-513-999C-15121	Sequence 15121, A
C 140	16	28.6	9811	3	US-09-481-355-24	Sequence 24, Appl	213	14	25.0	226	3	US-10-131-827-8445	Sequence 8445, Ap
C 141	16	28.6	9811	3	US-09-481-355-24	Sequence 24, Appl	214	14	25.0	323	3	US-09-513-999C-2299	Sequence 2299, Ap
C 142	16	28.6	9811	3	US-09-455-659A-24	Sequence 24, Appl	215	14	25.0	399	3	US-09-621-976-681	Sequence 681, App
C 143	16	28.6	9811	3	US-09-484-996-24	Sequence 24, Appl	216	14	25.0	477	3	US-09-513-999C-8843	Sequence 8843, Ap
C 144	16	28.6	9811	3	US-09-479-123-24	Sequence 24, Appl	217	14	25.0	601	3	US-09-949-016-28341	Sequence 28341, A
C 145	16	28.6	9811	3	US-09-479-123-24	Sequence 24, Appl	218	14	25.0	601	3	US-09-949-016-47339	Sequence 47339, A
C 146	16	28.6	9811	3	US-09-276-820A-24	Sequence 24, Appl	219	14	25.0	601	3	US-09-949-016-47340	Sequence 47340, A
C 147	16	28.6	10060	3	US-09-479-122-25	Sequence 25, Appl	220	14	25.0	601	3	US-09-949-016-66403	Sequence 66403, A
C 148	16	28.6	10060	3	US-09-484-997-25	Sequence 25, Appl	221	14	25.0	601	3	US-09-949-016-73995	Sequence 73995, A
C 149	16	28.6	10060	3	US-09-481-355-25	Sequence 25, Appl	222	14	25.0	601	3	US-09-949-016-74101	Sequence 74101, A
C 150	16	28.6	10060	3	US-09-481-355-25	Sequence 25, Appl	223	14	25.0	601	3	US-09-949-016-88136	Sequence 88136, A
C 151	16	28.6	10060	3	US-09-481-282-25	Sequence 25, Appl	224	14	25.0	601	3	US-09-949-016-89306	Sequence 89306, A
C 152	16	28.6	10060	3	US-09-455-659A-25	Sequence 25, Appl	225	14	25.0	601	3	US-09-949-016-108352	Sequence 108352, A
C 153	16	28.6	10060	3	US-09-479-123-25	Sequence 25, Appl	226	14	25.0	601	3	US-09-949-016-108353	Sequence 108353, A
C 154	16	28.6	10060	3	US-09-484-317A-25	Sequence 25, Appl	227	14	25.0	601	3	US-09-949-016-134074	Sequence 134074, A
C 155	16	28.6	10060	3	US-09-276-820A-25	Sequence 25, Appl	228	14	25.0	601	3	US-09-949-016-134075	Sequence 134075, A
C 156	16	28.6	10580	2	US-08-196-259-1	Sequence 1, Appl	229	14	25.0	601	3	US-09-949-016-156747	Sequence 156747, A
C 157	16	28.6	11241	3	US-10-007-527A-6	Sequence 6, Appl	230	14	25.0	601	3	US-09-949-016-143011	Sequence 143011, A
C 158	16	28.6	11241	3	US-10-055-001B-13	Sequence 13, Appl	231	14	25.0	601	3	US-09-949-016-154483	Sequence 154483, A
C 159	16	28.6	100928	3	US-09-949-016-16326	Sequence 16326, A	232	14	25.0	601	3	US-09-949-016-16327	Sequence 16327, A
C 160	16	28.6	19	3	US-09-495-880A-1	Sequence 1, Appl	233	14	25.0	601	3	US-09-949-016-166748	Sequence 166748, A
C 161	16	28.6	29	3	US-08-898-234-4	Sequence 4, Appl	234	14	25.0	601	3	US-09-949-016-166748	Sequence 166748, A
C 162	16	28.6	34	3	US-09-288-971-1	Sequence 1, Appl	235	14	25.0	601	3	US-09-949-016-168835	Sequence 168835, A
C 163	16	28.6	34	3	US-09-288-971-2	Sequence 2, Appl	236	14	25.0	601	3	US-09-949-016-168835	Sequence 168836, A
C 164	16	28.6	349	2	US-08-275-225-10	Sequence 10, Appl	237	14	25.0	601	3	US-09-949-016-190569	Sequence 190569, A
C 165	16	28.6	439	2	US-08-644-729-27	Sequence 27, Appl	238	14	25.0	601	3	US-09-949-016-190570	Sequence 190570, A
C 166	16	28.6	601	3	US-09-949-016-115305	Sequence 115305, A	239	14	25.0	601	3	US-09-949-016-134419	Sequence 134419, A
C 167	16	28.6	601	3	US-09-949-016-153457	Sequence 153457, A	240	14	25.0	601	3	US-09-949-016-194570	Sequence 194570, A
C 168	16	28.6	700	3	US-09-735-271-1281	Sequence 1281, Ap	241	14	25.0	601	3	US-09-949-016-205089	Sequence 205089, A
C 169	16	28.6	935	2	US-08-162-475A-3	Sequence 3, Appl	242	14	25.0	601	3	US-09-949-016-205090	Sequence 205090, A
C 170	16	28.6	966	2	US-08-162-475A-1	Sequence 1, Appl	243	14	25.0	705	3	US-08-862-54A-11	Sequence 11, Appl



244	14	25.0	705	3	US-08-862-540-12	Sequence 12, Appl	C 317	14	25.0	26257	3	US-09-949-016-16791	Sequence 16791, A
C 245	14	25.0	705	3	US-09-633-043-11	Sequence 11, Appl	C 318	14	25.0	31035	3	US-09-949-016-17272	Sequence 17272, A
C 246	14	25.0	705	3	US-09-633-043-12	Sequence 12, Appl	C 319	14	25.0	31035	3	US-09-949-016-17272	Sequence 17272, A
C 247	14	25.0	736	3	US-08-862-540-8	Sequence 8, Appl	C 320	14	25.0	32010	3	US-09-949-016-13127	Sequence 13127, A
C 248	14	25.0	736	3	US-08-862-540-10	Sequence 10, Appl	C 321	14	25.0	36023	3	US-09-949-016-15577	Sequence 15577, A
C 249	14	25.0	736	3	US-09-633-043-8	Sequence 8, Appl	C 322	14	25.0	39949	3	US-09-949-016-14210	Sequence 14210, A
C 250	14	25.0	736	3	US-09-633-043-10	Sequence 10, Appl	C 323	14	25.0	43985	3	US-08-742-185-101	Sequence 101, App
C 251	14	25.0	765	3	US-09-813-453B-48	Sequence 48, Appl	C 324	14	25.0	44798	3	US-09-949-016-16334	Sequence 16334, A
C 252	14	25.0	840	3	US-09-244-111-5	Sequence 5, Appl	C 325	14	25.0	50000	3	US-09-146-053-3	Sequence 3, Appl
C 253	14	25.0	900	3	US-09-949-016-3102	Sequence 3102, Ap	C 326	14	25.0	52661	3	US-09-949-016-17191	Sequence 17191, A
C 254	14	25.0	940	3	US-09-771-161A-34	Sequence 34, Appl	C 327	14	25.0	56516	2	US-08-996-306-1	Sequence 1, Appl
C 255	14	25.0	951	3	US-09-771-161A-35	Sequence 35, Appl	C 328	14	25.0	56516	3	US-09-338-007-1	Sequence 1, Appl
C 256	14	25.0	1068	3	US-09-949-016-2280	Sequence 2280, Ap	C 329	14	25.0	56516	3	US-09-218-207-1	Sequence 1, Appl
C 257	14	25.0	1074	3	US-09-949-016-1077	Sequence 1077, Ap	C 330	14	25.0	56520	3	US-09-338-007-179	Sequence 179, App
C 258	14	25.0	1091	3	US-10-012-231A-193	Sequence 193, App	C 331	14	25.0	56520	3	US-09-218-207-179	Sequence 179, App
C 259	14	25.0	1091	3	US-10-015-389A-193	Sequence 193, App	C 332	14	25.0	56976	3	US-09-949-016-17466	Sequence 17466, A
C 260	14	25.0	1091	3	US-10-006-768A-193	Sequence 193, App	C 333	14	25.0	61462	3	US-09-949-016-17522	Sequence 17522, A
C 261	14	25.0	1091	3	US-10-015-671A-193	Sequence 193, App	C 334	14	25.0	67899	3	US-09-949-016-15432	Sequence 15432, A
C 262	14	25.0	1091	3	US-10-015-393A-193	Sequence 193, App	C 335	14	25.0	67902	3	US-09-949-016-11870	Sequence 11870, A
C 263	14	25.0	1091	3	US-10-011-833A-193	Sequence 193, App	C 336	14	25.0	69842	3	US-09-949-016-15339	Sequence 15339, A
C 264	14	25.0	1091	3	US-10-006-041A-193	Sequence 193, App	C 337	14	25.0	69842	3	US-09-949-016-12435	Sequence 12435, A
C 265	14	25.0	1091	3	US-10-012-064A-193	Sequence 193, App	C 338	14	25.0	69813	3	US-09-949-016-13905	Sequence 13905, A
C 266	14	25.0	1095	3	US-09-489-039A-1654	Sequence 1654, Ap	C 339	14	25.0	69813	3	US-09-949-016-13906	Sequence 13906, A
C 267	14	25.0	1096	3	US-09-771-161A-33	Sequence 33, Appl	C 340	14	25.0	69833	3	US-09-949-016-12861	Sequence 12861, A
C 268	14	25.0	1206	3	US-09-248-796A-1612	Sequence 1612, Ap	C 341	14	25.0	72278	3	US-09-949-016-16113	Sequence 16113, A
C 269	14	25.0	1242	3	US-09-068-132-1	Sequence 1, Appl	C 342	14	25.0	76985	3	US-09-949-016-12416	Sequence 12416, A
C 270	14	25.0	1242	3	US-09-068-132-2	Sequence 2, Appl	C 343	14	25.0	76986	3	US-09-949-016-13120	Sequence 13120, A
C 271	14	25.0	1242	3	US-10-018-730A-1	Sequence 1, Appl	C 344	14	25.0	83665	3	US-09-949-016-16395	Sequence 16395, A
C 272	14	25.0	1320	3	US-09-328-352-242	Sequence 242, App	C 345	14	25.0	87591	3	US-09-949-016-12115	Sequence 12115, A
C 273	14	25.0	1402	3	US-09-246-451A-1	Sequence 1, Appl	C 346	14	25.0	87611	3	US-09-949-016-16139	Sequence 16139, A
C 274	14	25.0	1581	3	US-09-323-195A-16	Sequence 16, Appl	C 347	14	25.0	91588	3	US-09-949-016-15702	Sequence 15702, A
C 275	14	25.0	1596	3	US-09-323-195A-19	Sequence 19, Appl	C 348	14	25.0	92344	3	US-09-949-016-16882	Sequence 16882, A
C 276	14	25.0	1633	3	US-09-396-154-46	Sequence 46, Appl	C 349	14	25.0	94873	3	US-09-949-016-14217	Sequence 14217, A
C 277	14	25.0	1705	3	US-09-364-220-15	Sequence 15, Appl	C 350	14	25.0	100863	3	US-09-949-016-17031	Sequence 17031, A
C 278	14	25.0	1930	3	US-09-106-872A-21	Sequence 21, Appl	C 351	14	25.0	101349	3	US-09-949-016-17433	Sequence 17433, A
C 279	14	25.0	2032	3	US-09-191-593-5	Sequence 5, Appl	C 352	14	25.0	101674	3	US-09-949-016-12033	Sequence 12033, A
C 280	14	25.0	2032	3	US-09-191-593-5	Sequence 5, Appl	C 353	14	25.0	101674	3	US-09-949-016-12033	Sequence 12033, A
C 281	14	25.0	2032	3	US-09-715-036-5	Sequence 5, Appl	C 354	14	25.0	101951	3	US-09-949-016-15668	Sequence 15668, A
C 282	14	25.0	2041	3	US-09-106-872A-23	Sequence 23, Appl	C 355	14	25.0	105733	3	US-09-949-016-13060	Sequence 13060, A
C 283	14	25.0	2270	3	US-09-789-582A-1	Sequence 1, Appl	C 356	14	25.0	106450	3	US-09-949-016-13873	Sequence 13873, A
C 284	14	25.0	2436	3	US-09-441-340-31	Sequence 31, Appl	C 357	14	25.0	107941	3	US-09-949-016-14206	Sequence 14206, A
C 285	14	25.0	2495	3	US-09-620-312D-272	Sequence 272, Appl	C 358	14	25.0	109378	3	US-09-949-016-12391	Sequence 12391, A
C 286	14	25.0	2730	3	US-09-789-599A-1	Sequence 1, Appl	C 359	14	25.0	110243	3	US-09-949-016-13668	Sequence 13668, A
C 287	14	25.0	2803	3	US-09-949-016-2464	Sequence 2464, Ap	C 360	14	25.0	117838	3	US-09-949-016-17595	Sequence 17595, A
C 288	14	25.0	2923	3	US-09-619-353-9	Sequence 9, Appl	C 361	14	25.0	125192	3	US-09-949-016-14110	Sequence 14120, A
C 289	14	25.0	3107	3	US-09-949-016-1300	Sequence 1300, Ap	C 362	14	25.0	128175	3	US-09-949-016-16268	Sequence 16268, A
C 290	14	25.0	3116	2	US-08-449-645A-14	Sequence 14, Appl	C 363	14	25.0	129327	3	US-09-949-016-12257	Sequence 12257, A
C 291	14	25.0	3116	2	US-08-702-367A-14	Sequence 14, Appl	C 364	14	25.0	129327	3	US-09-949-016-15368	Sequence 15368, A
C 292	14	25.0	3116	6	PCT-US95-04681-14	Sequence 14, Appl	C 365	14	25.0	131254	3	US-09-949-016-13734	Sequence 13734, A
C 293	14	25.0	3348	2	US-08-222-616-34	Sequence 34, Appl	C 366	14	25.0	136264	3	US-09-949-016-12756	Sequence 12756, A
C 294	14	25.0	3348	3	US-08-446-648-34	Sequence 34, Appl	C 367	14	25.0	136265	3	US-09-949-016-13001	Sequence 13001, A
C 295	14	25.0	3348	3	US-09-982-610-34	Sequence 34, Appl	C 368	14	25.0	139049	3	US-09-949-016-17030	Sequence 17030, A
C 296	14	25.0	3348	6	PCT-US95-04228-34	Sequence 34, Appl	C 369	14	25.0	141454	3	US-09-949-016-12055	Sequence 12055, A
C 297	14	25.0	3506	3	US-09-091-899-9	Sequence 9, Appl	C 370	14	25.0	141455	3	US-09-949-016-17190	Sequence 17190, A
C 298	14	25.0	4237	3	US-09-949-016-649	Sequence 649, App	C 371	14	25.0	150394	3	US-09-949-016-13042	Sequence 13042, A
C 299	14	25.0	5247	3	US-09-949-016-14844	Sequence 14844, A	C 372	14	25.0	157032	3	US-09-949-016-16502	Sequence 16502, A
C 300	14	25.0	5787	3	US-09-774-528-217	Sequence 217, App	C 373	14	25.0	157337	3	US-09-949-016-16182	Sequence 16182, A
C 301	14	25.0	6002	3	US-10-120-988-217	Sequence 217, App	C 374	14	25.0	157336	3	US-09-949-016-12831	Sequence 12831, A
C 302	14	25.0	6002	3	US-09-949-016-13696	Sequence 13696, A	C 375	14	25.0	157337	3	US-09-949-016-14378	Sequence 14378, A
C 303	14	25.0	6663	3	US-09-335-011-15	Sequence 15, Appl	C 376	14	25.0	157337	3	US-09-949-002-1338	Sequence 1338, App
C 304	14	25.0	7223	3	US-09-335-011-8	Sequence 8, Appl	C 377	14	25.0	157337	3	US-09-949-002-1338	Sequence 1338, App
C 305	14	25.0	7408	3	US-09-115-475-13	Sequence 13, Appl	C 378	14	25.0	218940	3	US-09-949-016-17539	Sequence 17539, A
C 306	14	25.0	79798	3	US-09-949-016-14022	Sequence 14022, A	C 379	14	25.0	221958	3	US-09-949-016-13875	Sequence 13875, A
C 307	14	25.0	9801	3	US-09-949-016-12819	Sequence 12819, A	C 380	14	25.0	221958	3	US-09-949-016-12713	Sequence 12713, A
C 308	14	25.0	9980	3	US-09-998-716-26	Sequence 26, Appl	C 381	14	25.0	221958	3	US-09-949-016-15498	Sequence 15498, A
C 309	14	25.0	10523	3	US-09-453-702B-13	Sequence 13, Appl	C 382	14	25.0	222452	3	US-09-949-016-12968	Sequence 12968, A
C 310	14	25.0	10523	3	US-10-114-170-13	Sequence 13, Appl	C 383	14	25.0	224288	3	US-09-949-002-687	Sequence 687, App
C 311	14	25.0	15206	3	US-09-949-016-13585	Sequence 13585, A	C 384	14	25.0	224288	3	US-09-949-016-17272	Sequence 17272, A
C 312	14	25.0	15206	3	US-09-949-016-13586	Sequence 13586, A	C 385	14	25.0	224288	3	US-09-949-002-841	Sequence 841, App
C 313	14	25.0	19861	3	US-09-949-016-14498	Sequence 14498, A	C 386	14	25.0	227863	3	US-09-949-016-13404	Sequence 13404, A
C 314	14	25.0	21862	3	US-09-949-016-17319	Sequence 17319, A	C 387	14	25.0	246240	2	US-08-724-394A-20	Sequence 20, Appl
C 315	14	25.0	23925	3	US-09-949-016-11797	Sequence 11797, A	C 388	14	25.0	246240	2	US-08-724-394A-21	Sequence 21, Appl
C 316	14	25.0	23929	3	US-09-949-016-11301	Sequence 13301, A	C 389	14	25.0	246240	2	US-08-724-394A-22	Sequence 22, Appl



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C 395	14	25.0	258775	3	US-09-949-016-16435	Sequence 16435, A
C 396	14	25.0	258775	3	US-09-949-016-15779	Sequence 15779, A
C 397	14	25.0	265038	3	US-09-949-016-13187	Sequence 13187, A
C 398	14	25.0	265748	3	US-09-949-016-13188	Sequence 13188, A
C 399	14	25.0	300598	3	US-09-949-016-11868	Sequence 11868, A
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C 403	14	25.0	343352	3	US-09-949-016-14543	Sequence 14543, A
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C 405	14	25.0	421118	3	US-09-949-016-12557	Sequence 12557, A
C 406	14	25.0	421883	3	US-09-214-808-1	Sequence 40, Appl
C 407	14	25.0	536165	3	US-09-617-871-40	Sequence 60108, A
C 408	13	23.2	19	3	US-09-396-196G-60108	Sequence 62142, A
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C 538	13	23.2	601	3	US-09-949-016-174559	Sequence 174559,	611	13	23.2	933	3	US-09-369-247-26	Sequence 26, Appl
C 539	13	23.2	601	3	US-09-949-016-174560	Sequence 174560,	612	13	23.2	933	3	US-10-062-548-26	Sequence 26, Appl
C 540	13	23.2	601	3	US-09-949-016-174561	Sequence 174561,	c 613	13	23.2	937	3	US-09-270-767-1745	Sequence 1745, Ap
541	13	23.2	601	3	US-09-949-016-174977	Sequence 174977,	c 614	13	23.2	937	3	US-09-270-767-17027	Sequence 17027, A
542	13	23.2	601	3	US-09-949-016-174980	Sequence 174980,	615	13	23.2	951	3	US-09-248-796A-4727	Sequence 4727, Ap
543	13	23.2	601	3	US-09-949-016-175003	Sequence 175003,	616	13	23.2	953	3	US-09-270-767-19660	Sequence 21960, A
C 544	13	23.2	601	3	US-09-949-016-185774	Sequence 185774,	617	13	23.2	954	3	US-09-134-000C-1257	Sequence 1257, Ap
545	13	23.2	601	3	US-09-949-016-188634	Sequence 188634,	c 618	13	23.2	958	3	US-09-442-013-7	Sequence 7, Appl
546	13	23.2	601	3	US-09-949-016-188683	Sequence 188683,	619	13	23.2	978	3	US-09-489-039A-1168	Sequence 1168, Ap
547	13	23.2	601	3	US-09-949-016-188732	Sequence 188732,	c 620	13	23.2	978	3	US-09-252-991A-7255	Sequence 7255, Ap
548	13	23.2	601	3	US-09-949-016-188781	Sequence 188781,	c 621	13	23.2	989	2	US-08-874-460-1	Sequence 1, Appl
C 549	13	23.2	601	3	US-09-949-016-189410	Sequence 189410,	622	13	23.2	989	2	US-09-272-162-1	Sequence 1, Appl
C 550	13	23.2	601	3	US-09-949-016-189496	Sequence 189496,	623	13	23.2	1001	3	US-09-641-638-168	Sequence 168, Ap
C 551	13	23.2	601	3	US-09-949-016-189949	Sequence 189949,	624	13	23.2	1001	3	US-09-641-638-169	Sequence 169, Ap
C 552	13	23.2	601	3	US-09-949-016-189950	Sequence 189950,	625	13	23.2	1001	3	US-09-671-317-43	Sequence 43, Appl
C 553	13	23.2	601	3	US-09-949-016-192865	Sequence 192865,	c 626	13	23.2	1001	3	US-09-671-317-43	Sequence 43, Appl
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555	13	23.2	601	3	US-09-949-016-192957	Sequence 192957,	628	13	23.2	1001	3	US-10-170-097-168	Sequence 168, Ap
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559	13	23.2	601	3	US-09-949-016-193235	Sequence 193235,	632	13	23.2	1047	3	US-09-902-540-2626	Sequence 2626, Ap
560	13	23.2	601	3	US-09-949-016-193328	Sequence 193328,	633	13	23.2	1056	3	US-09-949-016-2265	Sequence 2265, Ap
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C 564	13	23.2	601	3	US-09-949-002-3363	Sequence 3363, Ap	c 637	13	23.2	1177	3	US-09-949-016-1953	Sequence 4953, Ap
C 565	13	23.2	601	3	US-09-949-002-3364	Sequence 3364, Ap	c 638	13	23.2	1177	3	US-09-949-016-1954	Sequence 4954, Ap
C 566	13	23.2	601	3	US-09-949-002-3365	Sequence 3365, Ap	c 639	13	23.2	1177	3	US-09-949-016-1955	Sequence 4955, Ap
C 567	13	23.2	601	3	US-09-949-002-4187	Sequence 4187, Ap	c 640	13	23.2	1184	3	US-09-533-559-8261	Sequence 5261, Ap
C 568	13	23.2	601	3	US-09-949-002-4617	Sequence 4617, Ap	c 641	13	23.2	1200	3	US-09-598-401C-36	Sequence 36, Appl
C 569	13	23.2	601	3	US-09-949-002-4618	Sequence 4618, Ap	642	13	23.2	1203	3	US-09-434-774-9	Sequence 9, Appl
C 570	13	23.2	601	3	US-09-949-002-4619	Sequence 4619, Ap	c 643	13	23.2	1203	3	US-08-680-395-7	Sequence 7, Appl
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C 577	13	23.2	637	3	US-09-270-767-4879	Sequence 4879, Ap	c 650	13	23.2	1348	3	US-09-949-016-1967	Sequence 5767, Ap
C 578	13	23.2	637	3	US-09-270-767-20161	Sequence 20161, A	c 651	13	23.2	1364	3	US-09-949-016-164	Sequence 464, Ap
579	13	23.2	645	3	US-09-533-559-6856	Sequence 6856, Ap	c 652	13	23.2	1365	3	US-09-134-001C-1601	Sequence 1601, Ap
C 580	13	23.2	672	3	US-09-134-001C-580	Sequence 580, Ap	c 653	13	23.2	1380	3	US-09-489-847-125	Sequence 125, Ap
C 581	13	23.2	672	3	US-09-252-991A-15450	Sequence 15450, A	654	13	23.2	1395	3	US-08-957-302A-3	Sequence 3, Appl
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C 583	13	23.2	704	3	US-09-533-559-7728	Sequence 7728, Ap	656	13	23.2	1404	2	US-08-727-548-1	Sequence 1, Appl
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C 585	13	23.2	732	3	US-09-134-000C-2779	Sequence 2779, Ap	c 658	13	23.2	1476	3	US-09-270-767-1584	Sequence 584, Ap
C 586	13	23.2	733	3	US-09-533-559-5922	Sequence 5922, Ap	c 659	13	23.2	1476	3	US-09-270-767-15866	Sequence 15866, A
C 587	13	23.2	738	3	US-09-949-016-4678	Sequence 4678, Ap	c 660	13	23.2	1476	3	US-09-248-796A-8230	Sequence 8230, Ap
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C 590	13	23.2	745	3	US-09-614-124B-1284	Sequence 1284, Ap	c 663	13	23.2	1539	3	US-09-248-796A-1083	Sequence 1083, Ap
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C 593	13	23.2	745	3	US-10-017-754-1284	Sequence 1284, Ap	c 666	13	23.2	1630	3	US-09-270-767-1000	Sequence 4000, Ap
C 594	13	23.2	745	3	US-09-651-563-1284	Sequence 1284, Ap	c 667	13	23.2	1630	3	US-09-270-767-19282	Sequence 19282, A
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598	13	23.2	784	3	US-09-270-767-10238	Sequence 10238, A	c 671	13	23.2	1722	3	US-09-252-991A-15428	Sequence 15428, A
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602	13	23.2	820	2	US-08-460-507-1	Sequence 1, Appl	c 675	13	23.2	1771	3	US-10-104-044-1543	Sequence 1543, Ap
603	13	23.2	835	3	US-08-957-302A-9	Sequence 9, Appl	c 676	13	23.2	1776	3	US-09-583-110-152	Sequence 152, Ap
604	13	23.2	835	3	US-09-542-403-9	Sequence 9, Appl	c 677	13	23.2	1791	3	US-09-107-433-1960	Sequence 1960, Ap
605	13	23.2	876	3	US-09-522-752-10	Sequence 10, Appl	c 678	13	23.2	1827	3	US-09-602-787A-29	Sequence 29, Appl
606	13	23.2	879	3	US-09-522-752-8	Sequence 8, Appl	c 679	13	23.2	1845	4	US-09-605-703B-253	Sequence 253, Ap
607	13	23.2	882	3	US-09-270-767-25620	Sequence 25620, A	680	13	23.2	1945	2	US-08-525-742-5	Sequence 5, Appl
608	13	23.2	894	3	US-09-248-796A-1443	Sequence 1443, Ap	c 681	13	23.2	2003	3	US-09-148-545-109	Sequence 109, Ap



C 682	13	23.2	2003	3	US-09-621-011-109
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C 685	13	23.2	2053	3	US-09-833-129-18
C 686	13	23.2	2070	3	US-09-148-545-51
C 687	13	23.2	2070	3	US-09-621-011-51
C 688	13	23.2	2072	3	US-09-833-129-31
C 689	13	23.2	2147	3	US-09-949-016-5050
C 690	13	23.2	2171	3	US-09-022-655-575
C 691	13	23.2	2210	3	US-09-016-434-1177
C 692	13	23.2	2210	3	US-10-166-199-1
C 693	13	23.2	2219	3	US-10-104-047-1917
C 694	13	23.2	2240	3	US-09-489-847-84
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964	13	23.2	99304	3	US-09-949-016-15440	Sequence 15440, A
965	13	23.2	101472	3	US-09-949-016-15861	Sequence 15861, A
966	13	23.2	102758	3	US-09-949-016-12447	Sequence 12447, A
967	13	23.2	103730	3	US-09-949-016-13058	Sequence 13058, A
C 967	13	23.2	104428	3	US-09-949-016-12737	Sequence 12737, A
968	13	23.2	104428	3	US-09-949-016-13814	Sequence 13814, A
969	13	23.2	104429	3	US-09-326-402C-1	Sequence 1, Appl1
C 970	13	23.2	106746	3	US-09-326-402C-12	Sequence 12, Appl1
C 971	13	23.2	106746	3	US-09-949-016-12060	Sequence 12060, A
C 972	13	23.2	106929	3	US-09-949-016-16618	Sequence 16618, A
C 973	13	23.2	106929	3	US-09-949-016-16618	Sequence 16618, A



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C 974 13 23.2 107458 3 US-09-949-016-15687 A Sequence 15687, A
C 975 13 23.2 109690 3 US-09-949-016-13525 A Sequence 13525, A
976 13 23.2 112623 3 US-09-949-016-13374 A Sequence 14374, A
977 13 23.2 113100 3 US-09-949-016-12245 A Sequence 12245, A
C 978 13 23.2 116592 3 US-09-818-512-3 Sequence 3, Appl1
C 979 13 23.2 116592 3 US-10-354-065-3 Sequence 15996, A
980 13 23.2 118382 3 US-09-949-016-15996 A Sequence 15996, A
981 13 23.2 118382 3 US-09-949-016-15997 A Sequence 15997, A
982 13 23.2 118899 3 US-09-791-105B-32 Sequence 32, Appl
983 13 23.2 119801 3 US-09-949-016-13453 A Sequence 13453, A
C 984 13 23.2 121384 3 US-09-949-016-16944 A Sequence 16944, A
C 985 13 23.2 124264 3 US-09-949-016-16396 A Sequence 16396, A
986 13 23.2 124280 3 US-09-949-016-15921 A Sequence 15921, A
987 13 23.2 124701 3 US-09-949-016-11817 A Sequence 11817, A
988 13 23.2 124701 3 US-09-949-016-15439 A Sequence 15439, A
C 989 13 23.2 126237 3 US-09-949-016-16674 A Sequence 16674, A
C 990 13 23.2 126237 3 US-09-949-016-16675 A Sequence 16675, A
991 13 23.2 127280 3 US-09-949-016-14857 A Sequence 14857, A
C 992 13 23.2 129899 3 US-09-949-016-14684 A Sequence 14684, A
993 13 23.2 132266 3 US-09-949-016-14860 A Sequence 14860, A
994 13 23.2 132456 3 US-09-949-016-13750 A Sequence 13750, A
C 995 13 23.2 134008 3 US-09-949-016-13841 A Sequence 13841, A
996 13 23.2 134987 3 US-09-949-016-15348 A Sequence 15348, A
997 13 23.2 134987 3 US-09-949-016-15349 A Sequence 15349, A
998 13 23.2 134987 3 US-09-949-016-15350 A Sequence 15350, A
999 13 23.2 134987 3 US-09-949-016-15507 A Sequence 15507, A
1000 13 23.2 134987 3 US-09-949-016-15508 A Sequence 15508, A
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## ALIGNMENTS

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RESULT 1
US-09-949-016-91323/c
; Sequence 91323, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91323
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91323

Query Match 30.4%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTATGTGAATGCT 24
Db 372 GTGGTATGTGAATGCT 356

RESULT 2
US-09-949-016-91324/c
; Sequence 91324, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 91324
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-91324

Query Match 30.4%; Score 17; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 GTGGTATGTGAATGCT 24
Db 210 GTGGTATGTGAATGCT 194

RESULT 3
US-09-147-119-5/c
; Sequence 5, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
; APPLICANT: KURTH, Ruth
; APPLICANT: BAIER, Michael
; APPLICANT: BANNERT, No. 6338844bert
; APPLICANT: METZNER, Karin
; APPLICANT: WERNER, Albrecht
; TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH
; CODE FOR POLYPEPTIDES WITH II-16 ACTIVITY, PROCESS FOR THE
; TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Nikaido, Marmelestein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,119
; FILING DATE: HERewith
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/01753
; FILING DATE: 10-APR-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: DE 196 14 099.4
; FILING DATE: 10-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: WONG, King L.
; REGISTRATION NUMBER: 37,500
; REFERENCE/DOCKET NUMBER: P1614-8068
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 638-5000
; TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9096 base pairs
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;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 1..338
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 339..663
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 664..832
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 833..2870
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 2871..2972
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 2973..5224
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 5225..5483
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 5484..5737
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 5738..5863
;   FEATURE:
;   NAME/KEY: intron
;   LOCATION: 5864..7926
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 7927..9096
;   FEATURE:
;   NAME/KEY: -
;   LOCATION: 356
;   OTHER INFORMATION: /product= "N means between 1 -
;   OTHER INFORMATION: about 6 bp"
;
; US-09-147-119-5
;
; Query Match      30.4%; Score 17; DB 3; Length 9096;
; Best Local Similarity 100.0%; Pred. No. 4.2;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      8 GTGGTATGTGAATGCT 24
; Db      3452 GTGGTATGTGAATGCT 3436
;
; RESULT 4
; US-09-147-119-1/c
; Sequence 1, Application US/09147119
; Patent No. 6338844
; GENERAL INFORMATION:
;   APPLICANT: KURTH, Ruth
;   APPLICANT: BAIRER, Michael
;   APPLICANT: BANNER, No. 6338844bert
;   APPLICANT: METZNER, Karin
;   APPLICANT: WERNER, Albrecht
;   TITLE OF INVENTION: GENOMIC NUCLEIC ACIDS, cDNA AND mRNA WHICH
;   TITLE OF INVENTION: CODE FOR POLYPEPTIDES WITH IL-16 ACTIVITY, PROCESS FOR THE
;   TITLE OF INVENTION: PRODUCTION THEREOF AND THEIR USE
;   NUMBER OF SEQUENCES: 7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Nikaido, Mamelestein, Murray & Oram LLP
;   STREET: 655 Fifteenth St., NW
;   CITY: Washington
;   STATE: DC
;   COUNTRY: USA

```

```

;
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/09/147, 119
;   FILING DATE: HERWITH
; CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/EP97/01753
;   FILING DATE: 10-APR-1996
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: DE 196 14 099.4
;   FILING DATE: 10-APR-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Wong, King L.
;   REGISTRATION NUMBER: 37,500
;   REFERENCE/DOCKET NUMBER: P1614-8068
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (202) 638-5000
;   TELEFAX: (202) 638-4810
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 15936 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: double
;   TOPOLOGY: linear
; MOLECULE TYPE: DNA
;
; FEATURE:
;   NAME/KEY: exon
;   LOCATION: 3100..3238
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 5540..6635
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 7504..7672
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 9711..9812
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 12065..12323
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 12578..12703
;   FEATURE:
;   NAME/KEY: exon
;   LOCATION: 14767..15936
;
; US-09-147-119-1
;
; Query Match      30.4%; Score 17; DB 3; Length 15936;
; Best Local Similarity 100.0%; Pred. No. 4.2;
; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
;
; QY      8 GTGGTATGTGAATGCT 24
; Db      10292 GTGGTATGTGAATGCT 10276
;
; RESULT 5
; US-09-949-016-1436/c
; Sequence 14366, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
;   APPLICANT: VENTER, J. Craig et al.
;   TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
;   TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
;   FILE REFERENCE: C1001307
;   CURRENT APPLICATION NUMBER: US/09/949, 016
;   CURRENT FILING DATE: 2000-04-14

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;; PRIOR APPLICATION NUMBER: 60/241,755
;; PRIOR FILING DATE: 2000-10-20
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FASTSEQ for Windows Version 4.0
;; SEQ ID NO: 14366
;; LENGTH: 18650
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-14366

Query Match          30.4%; Score 17; DB 3; Length 18650;
Best Local Similarity 100.0%; Pred. No. 4.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GTGCTATGTTGAATGCT 24
Db      11005 GTGCTATGTTGAATGCT 10969

RESULT 6
US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match          30.4%; Score 17; DB 3; Length 4403765;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTCATCCGATCCAGCA 39
Db      2817517 CTCATCCGATCCAGCA 2817533

RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
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;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 1
;; LENGTH: 4411529
;; TYPE: DNA
;; ORGANISM: Mycobacterium tuberculosis
;; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match          30.4%; Score 17; DB 3; Length 4411529;
Best Local Similarity 100.0%; Pred. No. 4.3;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 CTCATCCGATCCAGCA 39
Db      2822064 CTCATCCGATCCAGCA 2822080

RESULT 8
US-09-513-999C-9165/C
; Sequence 9165, Application US/09513999C
; Patent No. 6783961
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Duclet, A.Y.
; APPLICANT: Giordano, J.Y.
; TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.
; FILE REFERENCE: 59, US2, REG
; CURRENT APPLICATION NUMBER: US/09/513,999C
; CURRENT FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/122,487
; PRIOR FILING DATE: 1999-02-26
; NUMBER OF SEQ ID NOS: 36681
; SOFTWARE: Patent.pm
; SEQ ID NO: 9165
; LENGTH: 158
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 7
; OTHER INFORMATION: v=a or c or g
US-09-513-999C-9165

Query Match          28.6%; Score 16; DB 3; Length 158;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TGCTATCCGATCCCA 36
Db      50 TGCTATCCGATCCCA 35

RESULT 9
US-08-973-857-16
; Sequence 16, Application US/08973857
; Patent No. 6221584
; GENERAL INFORMATION:
; APPLICANT: EMRICH, Thomas
; APPLICANT: LEYING, Hermann
; APPLICANT: HINZPETER, Mathias
; APPLICANT: KARL, Gerlinde
; TITLE OF INVENTION: METHOD FOR THE DETECTION OF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Nikaïdo, Marmelstein, Murray & Oram LLP
; STREET: 655 Fifteenth St., NW
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005-5701
; COMPUTER READABLE FORM:
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MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/973,857  
FILING DATE: 29-DEC-1997  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/EP96/05245  
FILING DATE: 11-AUG-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19544317.9  
FILING DATE: 28-NOV-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19644302.4  
FILING DATE: 24-OCT-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Berman, Richard J.  
REGISTRATION NUMBER: 39,107  
REFERENCE/DOCKET NUMBER: P564-7031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 638-5000  
TELEFAX: (202) 638-4810  
INFORMATION FOR SEQ ID NO: 16:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 202 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-973-857-16

Query Match 28.6%; Score 16; DB 3; Length 202;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 28 TGAATGCTCATCCGGA 43

RESULT 10  
US-08-039-364-17  
Sequence 17, Application US/08039364  
Patent No. 5811393  
GENERAL INFORMATION:  
APPLICANT: Klagsbrun, Michael  
APPLICANT: Abraham, Judith A.  
APPLICANT: Higashiyama, Shigeki  
APPLICANT: Beener, Gail F.  
TITLE OF INVENTION: HEPARIN BINDING MITOGEN WITH  
TITLE OF INVENTION: HOMOLOG TO EPIDERMAL GROWTH FACTOR  
TITLE OF INVENTION:  
NUMBER OF SEQUENCES: 18  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: U.S.A.  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb  
COMPUTER: IBM PS/2 Model 502 or 55SX  
OPERATING SYSTEM: MS-DOS (Version 5.0)  
SOFTWARE: WordPerfect (Version 5.1)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/039,364  
FILING DATE: 15 JUN 1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/598,082  
FILING DATE: 16 OCT 1990

ATTORNEY/AGENT INFORMATION:  
NAME: Freeman, John W.  
REGISTRATION NUMBER: 29,066  
REFERENCE/DOCKET NUMBER: 05162/002002  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (617) 542-5070  
TELEFAX: (617) 542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 457 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-039-364-17

Query Match 28.6%; Score 16; DB 2; Length 457;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 203 TGAATGCTCATCCGGA 218

RESULT 11  
US-09-158-710-17  
Sequence 17, Application US/09158710  
Patent No. 6235884  
GENERAL INFORMATION:  
APPLICANT: Klagsbrun, Michael  
APPLICANT: Abraham, Judith A.  
APPLICANT: Higashiyama, Shigeki  
APPLICANT: Beener, Gail F.  
TITLE OF INVENTION: HEPARIN BINDING MITOGEN WITH HOMOLOG TO EPIDERMAL  
TITLE OF INVENTION: GROWTH FACTOR (EGF)  
FILE REFERENCE: 05162/002003  
CURRENT APPLICATION NUMBER: US/09/158,710  
CURRENT FILING DATE: 1998-09-22  
EARLIER APPLICATION NUMBER: US 08/039,364  
EARLIER FILING DATE: 1993-06-15  
EARLIER APPLICATION NUMBER: US 07/598,082  
EARLIER FILING DATE: 1990-10-16  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastsEQ for Windows Version 3.0  
SEQ ID NO 17  
LENGTH: 457  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (4) ... (450)  
US-09-158-710-17

Query Match 28.6%; Score 16; DB 3; Length 457;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 203 TGAATGCTCATCCGGA 218

RESULT 12  
US-07-790-199-2  
Sequence 2, Application US/07790199  
Patent No. 5354854  
GENERAL INFORMATION:  
APPLICANT: Bourque, June E.  
APPLICANT: Folk, William R.  
TITLE OF INVENTION: EXPRESSION SYSTEM FOR USE IN PLANTS TO  
TITLE OF INVENTION: SUPPRESS FOREIGN EXPRESSION AND METHOD  
NUMBER OF SEQUENCES: 4



```

CORRESPONDENCE ADDRESS:
ADDRESS: Reising, Ethnington, Barnard, Perry & Milton
STREET: P.O. Box 4390
CITY: Troy
STATE: Michigan
COUNTRY: U.S.A.
ZIP: 48099

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/790,199
FILING DATE: 19920403
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: 91UMC039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 497 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
ANTI-SENSE: YES
ORIGINAL SOURCE:
ORGANISM: Glycine max
FEATURE:
NAME/KEY: prim transcripct
LOCATION: 275..347
NAME/KEY: prim transcripct
LOCATION: 276..347
US-07-790-199-2

Query Match      28.6%; Score 16; DB 2; Length 497;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
      |||
      242 TGAATGCTCATCCGGA 257

RESULT 13
US-07-918-953-7
; Sequence 7, Application US/07918953
; Patent No. 5268453
; GENERAL INFORMATION:
; APPLICANT: ANDY, ROBIN J.
; APPLICANT: LARSON, ERIC R.
; TITLE OF INVENTION: TISSUE-SELECTIVE INSULIN ANALOGS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304-1018
; TELEPHONE: (415) 494-0792
; TELEFAX: (415) 494-0792
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/918,953
; FILING DATE: 19920730
```

```

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BOZICEVIC, KARL
REGISTRATION NUMBER: 28,807
REFERENCE/DOCKET NUMBER: 21900-2027420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-0792
TELEFAX: (415) 494-0792
TELEX: 706141
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 510 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..510
OTHER INFORMATION:
US-07-918-953-7

Query Match      28.6%; Score 16; DB 2; Length 510;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
      |||
      200 TGAATGCTCATCCGGA 215

RESULT 14
US-08-081-661-7
; Sequence 7, Application US/08081661
; Patent No. 5446020
; GENERAL INFORMATION:
; APPLICANT: ANDY, ROBIN J.
; APPLICANT: LARSON, ERIC R.
; TITLE OF INVENTION: TISSUE-SELECTIVE INSULIN ANALOGS
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/081,661
; FILING DATE: 23-JUN-1993
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/918,953
; FILING DATE: 30-JUL-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BOZICEVIC, KARL
; REGISTRATION NUMBER: 28,807
; REFERENCE/DOCKET NUMBER: 21900-2027420
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-0792
; TELEFAX: (415) 494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 510 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
```



MOLECULE TYPE: CDNA  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..510  
OTHER INFORMATION:  
US-08-081-661-7

Query Match 28.6%; Score 16; DB 2; Length 510;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
|||||  
Db 200 TGAATGCTCATCCGGA 215

RESULT 15  
US-09-949-016-180092  
Sequence 180092, Application US/09949016  
Patent No. 6812339

GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CLO01307  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 180092  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-180092

Query Match 28.6%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GATCCAGAGCAATGA 46  
|||||  
Db 82 GATCCAGAGCAATGA 97

RESULT 16  
US-09-949-016-180093  
Sequence 180093, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
FILE REFERENCE: CLO01307  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 180093  
LENGTH: 601  
TYPE: DNA  
ORGANISM: Human

US-09-949-016-180093

Query Match 28.6%; Score 16; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 31 GATCCAGAGCAATGA 46  
|||||  
Db 349 GATCCAGAGCAATGA 364

RESULT 17  
US-09-193-707-7  
Sequence 7, Application US/09193707  
Patent No. 6524792

GENERAL INFORMATION:  
APPLICANT: Renner, Wolfgang A.  
APPLICANT: Orberger, Georg H.  
APPLICANT: Koller, Daniel  
APPLICANT: Bailey, James E.  
TITLE OF INVENTION: EXPRESSION CLONING PROCESSES FOR THE DISCOVERY,  
TITLE OF INVENTION: CHARACTERIZATION AND ISOLATION OF GENES ENCODING POLYPEPTIDES  
FILE REFERENCE: 8358-0005-999  
CURRENT FILING DATE: 1998-11-17  
CURRENT APPLICATION NUMBER: US/09/193,707  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 7  
LENGTH: 660  
TYPE: DNA  
ORGANISM: Escherichia coli  
US-09-193-707-7

Query Match 28.6%; Score 16; DB 3; Length 660;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
|||||  
Db 200 TGAATGCTCATCCGGA 215

RESULT 18  
US-07-790-199-3  
Sequence 3, Application US/07790199  
Patent No. 5354854

GENERAL INFORMATION:  
APPLICANT: Bourque, June E.  
APPLICANT: Folk, William R.  
TITLE OF INVENTION: EXPRESSION SYSTEM FOR USE IN PLANTS TO  
TITLE OF INVENTION: SUPPRESS FOREIGN EXPRESSION AND METHOD  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reising, Ethington, Barnard, Perry & Milton  
STREET: P.O. Box 4390  
CITY: Troy  
STATE: Michigan  
COUNTRY: U.S.A.  
ZIP: 48099  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/790,199  
FILING DATE: 19920403  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kohn, Kenneth I.  
REGISTRATION NUMBER: 30,955  
REFERENCE/DOCKET NUMBER: 91UMC039



TELECOMMUNICATION INFORMATION:  
TELEPHONE: (313) 689-3554  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 672 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ANTI-SENSE: YES  
ORIGINAL SOURCE:  
ORGANISM: Glycine max  
FEATURE:  
NAME/KEY: prim\_transcript  
LOCATION: 451..522  
US-07-790-199-3

Query Match 28.6%; Score 16; DB 2; Length 672;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
|||||  
DB 242 TGAATGCTCATCCGGA 257

RESULT 19  
5223425-12  
PATENT NO. 5223425  
APPLICANT: FLIER, JEFFREY S.; SPIEGELMAN, BRUCE M.; ROSEN,  
BARRY M.; WHITE, TYLER R.  
TITLE OF INVENTION: DNA ENCODING HUMAN ADIPIN WITH COMPLEMENT  
ID ACTIVITY  
NUMBER OF SEQUENCES: 19  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/277,963  
FILING DATE: 30-NOV-1988  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 34,203  
FILING DATE: 02-APR-1987  
SEQ ID NO: 12  
LENGTH: 723  
5223425-12

Query Match 28.6%; Score 16; DB 9; Length 723;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
|||||  
DB 200 TGAATGCTCATCCGGA 215

RESULT 20  
US-08-264-042-1  
SEQUENCE 1, Application US/08264042  
PATENT NO. 6316004  
GENERAL INFORMATION:  
APPLICANT: Vladimir G. Lunin  
APPLICANT: Olga V. Sergienko  
APPLICANT: Marat-Vladimir L. Khodun  
APPLICANT: Leila B. Bader  
APPLICANT: Vladimir A. Karpov  
APPLICANT: Thomas J. Tikhonenko  
TITLE OF INVENTION: Chimeric Somatostatin Containing Protein  
TITLE OF INVENTION: And Encoding DNA, Plasmids Of Expression, Method For  
TITLE OF INVENTION: Preparing Chimeric Protein, Strain-Products, Immunogenic  
TITLE OF INVENTION: Composition, Method For Increasing The Productivity  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Thomas J. Tikhonenko  
STREET: Karetny ryad, 5/10

CITY: Moscow  
STATE: Russia  
COUNTRY: Russian Federation  
ZIP: 103006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH, 1.44 MB  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,042  
FILING DATE: 22 - June - 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SU-93031156 and SU-9303157  
FILING DATE: 22 - June - 1993 (both applications)  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles Gultman, Esq.  
REGISTRATION NUMBER: 29,161  
REFERENCE/DOCKET NUMBER: 3907-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-747-0300  
TELEFAX: 516-747-0653  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
US-08-264-042-1

Query Match 28.6%; Score 16; DB 3; Length 741;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32  
|||||  
DB 200 TGAATGCTCATCCGGA 215

RESULT 21  
US-08-264-042-2  
SEQUENCE 2, Application US/08264042  
PATENT NO. 6316004  
GENERAL INFORMATION:  
APPLICANT: Vladimir G. Lunin  
APPLICANT: Olga V. Sergienko  
APPLICANT: Marat-Vladimir L. Khodun  
APPLICANT: Leila B. Bader  
APPLICANT: Vladimir A. Karpov  
APPLICANT: Thomas J. Tikhonenko  
TITLE OF INVENTION: Chimeric Somatostatin Containing Protein  
TITLE OF INVENTION: And Encoding DNA, Plasmids Of Expression, Method For  
TITLE OF INVENTION: Preparing Chimeric Protein, Strain-Products, Immunogenic  
TITLE OF INVENTION: Composition, Method For Increasing The Productivity  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSES: Thomas J. Tikhonenko  
STREET: Karetny ryad, 5/10  
CITY: Moscow  
STATE: Russia  
COUNTRY: Russian Federation  
ZIP: 103006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH, 1.44 MB  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,042  
FILING DATE: 22 - June - 1994  
CLASSIFICATION: 435



PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SU-9303156 and SU-9303157  
FILING DATE: 22 - June - 1993 (both applications)  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles Guttman, Esq.  
REGISTRATION NUMBER: 29,161  
REFERENCE/DOCKET NUMBER: 3907-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-747-0300  
TELEFAX: 516-747-0653  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 741 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
US-08-264-042-2

Query Match 28.6%; Score 16; DB 3; Length 741;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 200 TGAATGCTCATCCGGA 215

RESULT 22  
US-08-264-042-3  
Sequence 3, Application US/08264042  
Patent No. 6316004  
GENERAL INFORMATION:  
APPLICANT: Vladimir G. Lunin  
APPLICANT: Olga V. Sergienko  
APPLICANT: Marat-Vladimir L. Khodun  
APPLICANT: Leila B. Bader  
APPLICANT: Vladimir A. Karpov  
APPLICANT: Thomas J. Tikhonenko  
TITLE OF INVENTION: Chimeric Somatostatin Containing Protein  
TITLE OF INVENTION: And Encoding DNA, Plasmids Of Expression, Method For  
TITLE OF INVENTION: Preparing Chimeric Protein, Strain-Products, Immunogenic  
TITLE OF INVENTION: Composition, Method For Increasing The Productivity  
NUMBER OF INVENTIONS: 3  
CORRESPONDENCE ADDRESS:  
ADDRESS: Thomas J. Tikhonenko  
STREET: Karetny Tyad, 5/10  
CITY: Moscow  
STATE: Russia  
COUNTRY: Russian Federation  
ZIP: 103006  
COMPUTER READABLE FORM:  
MEDIUM TYPE: DISKETTE, 3.50 INCH, 1.44 MB  
COMPUTER: IBM PC COMPATIBLE  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: Wordperfect 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/264,042  
FILING DATE: 22 - June - 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: SU-9303156 and SU-9303157  
FILING DATE: 22 - June - 1993 (both applications)  
ATTORNEY/AGENT INFORMATION:  
NAME: Charles Guttman, Esq.  
REGISTRATION NUMBER: 29,161  
REFERENCE/DOCKET NUMBER: 3907-1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 516-747-0300  
TELEFAX: 516-747-0653  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 768 base pairs

TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: unknown  
US-08-264-042-3

Query Match 28.6%; Score 16; DB 3; Length 768;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 227 TGAATGCTCATCCGGA 242

RESULT 23  
US-09-489-039A-4076  
Sequence 4076, Application US/09489039A  
Patent No. 6610836  
GENERAL INFORMATION:  
APPLICANT: Gary Breton et. al  
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA  
FILE REFERENCE: 2709,2004001  
CURRENT APPLICATION NUMBER: US/09/489,039A  
CURRENT FILING DATE: 2000-01-27  
PRIOR APPLICATION NUMBER: US 60/117,747  
PRIOR FILING DATE: 1999-01-29  
NUMBER OF SEQ ID NOS: 14342  
SEQ ID NO 4076  
LENGTH: 768  
TYPE: DNA  
ORGANISM: Klebsiella pneumoniae  
US-09-489-039A-4076

Query Match 28.6%; Score 16; DB 3; Length 768;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
Db 308 TGAATGCTCATCCGGA 323

RESULT 24  
US-09-363-970-3  
Sequence 3, Application US/09363970  
Patent No. 6294711  
GENERAL INFORMATION:  
APPLICANT: Neulwaeater, Frank  
APPLICANT: Cornelissen, Marcus  
APPLICANT: Van Aartsen, Roel  
APPLICANT: Soelaert, Piet  
TITLE OF INVENTION: Gene Expression in Plants  
FILE REFERENCE: 2121-131-P  
CURRENT APPLICATION NUMBER: US/09/363,970  
CURRENT FILING DATE: 1999-07-29  
NUMBER OF SEQ ID NOS: 41  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 3  
LENGTH: 761  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: coding region = nt 5 through 664  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:chloramphenicol  
OTHER INFORMATION: acetyltransferase gene  
US-09-363-970-3

Query Match 28.6%; Score 16; DB 3; Length 761;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 17 TGAATGCTCATCCGA 32  
|||||  
DB 204 TGAATGCTCATCCGA 219

## RESULT 25

US-10-001-052-41  
; Sequence 41, Application US/10001052  
; Patent No. 6709861  
; GENERAL INFORMATION:  
; APPLICANT: Mead, David A.  
; APPLICANT: Godiska, Ronald  
; TITLE OF INVENTION: CLONING VECTORS AND VECTOR COMPONENTS  
; FILE REFERENCE: MICRO-06635  
; CURRENT APPLICATION NUMBER: US/10/001,052  
; CURRENT FILING DATE: 2001-11-15  
; NUMBER OF SEQ ID NOS: 128  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 41  
; LENGTH: 1750  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic  
US-10-001-052-41

Query Match 28.6%; Score 16; DB 3; Length 1750;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
DB 303 TGAATGCTCATCCGA 318

## RESULT 26

US-09-930-329-1  
; Sequence 1, Application US/09930329  
; Patent No. 6852846  
; GENERAL INFORMATION:  
; APPLICANT: TURPEN, Thomas H.  
; TITLE OF INVENTION: VIRAL AMPLIFICATION OF RECOMBINANT  
; FILE REFERENCE: 008010103DVUS2  
; CURRENT APPLICATION NUMBER: US/09/930,329  
; CURRENT FILING DATE: 2001-08-14  
; PRIOR APPLICATION NUMBER: 09/414,916  
; PRIOR FILING DATE: 1999-10-08  
; PRIOR APPLICATION NUMBER: 08/336,724  
; PRIOR FILING DATE: 1994-11-09  
; NUMBER OF SEQ ID NOS: 3  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1  
; LENGTH: 1824  
; TYPE: RNA  
; ORGANISM: Tobacco Mosaic Virus  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (70) ... (873)  
; OTHER INFORMATION: (epitome)1 peptide encodes for TMV 30kDa movement  
; OTHER INFORMATION: protein (268 residues) and CAR (204 residues).  
; NAME/KEY: CDS  
; LOCATION: (916) ... (1530)  
US-09-930-329-1

Query Match 28.6%; Score 16; DB 3; Length 1824;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
DB 1115 UGAUGCUCUACCCGA 1130

## RESULT 27

US-08-176-414B-1  
; Sequence 1, Application US/08176414B  
; Patent No. 5811653  
; GENERAL INFORMATION:  
; APPLICANT: Turpen, Thomas H.  
; TITLE OF INVENTION: VIRAL AMPLIFICATION OF RECOMBINANT  
; TITLE OF INVENTION: MESSENGER RNA IN TRANSGENIC PLANTS  
; NUMBER OF SEQUENCES: 3  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Howrey & Simon  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington D.C.  
; STATE: District of Columbia  
; COUNTRY: United States of America  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/176,414B  
; FILING DATE: 29-Dec-1993  
; CLASSIFICATION: 800  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Halluin, Albert P.  
; REGISTRATION NUMBER: 25,227  
; REFERENCE/DOCKET NUMBER: 00801.0038.999  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-463-8109  
; TELEFAX: 650-463-8400  
; TELEX:  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1825 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: RNA (genomic)  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 70..1527  
US-08-176-414B-1

Query Match 28.6%; Score 16; DB 2; Length 1825;  
Best Local Similarity 75.0%; Pred. No. 16;  
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
DB 1115 UGAUGCUCUACCCGA 1130

## RESULT 28

US-08-336-724-1  
; Sequence 1, Application US/08336724  
; Patent No. 5965794  
; GENERAL INFORMATION:  
; APPLICANT: Turpen, Thomas H.  
; TITLE OF INVENTION: VIRAL AMPLIFICATION OF  
; TITLE OF INVENTION: RECOMBINANT MESSENGER RNA IN TRANSGENIC PLANTS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESS: Limbach & Limbach  
; STREET: 2001 Ferry Building  
; CITY: San Francisco  
; STATE: CAL  
; ZIP: 94111  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk



```

; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/336,724
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/997,733
; FILING DATE: 30-DEC-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Halluin, Albert P.
; REGISTRATION NUMBER: 25,227
; REFERENCE/DOCKET NUMBER: BIOG-20220 USA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-433-4150
; TELEFAX: 415-433-8716
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1825
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: RNA (episomal), peptide
; DESCRIPTION: Peptide encodes for TMV 30kDa
; DESCRIPTION: movement protein (268 residues) and CAT (204
; HYPOTHETICAL: residues).
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Tobacco Mosaic Virus
; IMMEDIATE SOURCE:
; CLONE:
; FEATURE:
;
US-08-336-724-1
;
Query Match 28.6%; Score 16; DB 2; Length 1825;
Best Local Similarity 75.0%; Pred. No. 16;
Matches 12; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32
Db 1115 UGAUGCUCACUCCGGA 1130

RESULT 29
US-09-358-856C-2
; Sequence 2, Application US/09358856C
; Patent No. 6537777
; GENERAL INFORMATION:
; APPLICANT: GELLERFORS, Par
; APPLICANT: FOCH, Jens
; TITLE OF INVENTION: NEW THERAPEUTIC METHOD FOR TREATING PATIENTS WITH ACUTE
; TITLE OF INVENTION: INTERMITTENT PORPHYRIA (AIP) AND OTHER PORPHYRIC
; TITLE OF INVENTION: DISEASES
; FILE REFERENCE: GELLERFORS-1A
; CURRENT APPLICATION NUMBER: US/09/358,856C
; CURRENT FILING DATE: 1999-07-22
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 3225
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Sequence of the Ecor I - Hind III linear fragment
; Patent No. 6537777
; OTHER INFORMATION: used for transformation in the hemic disruption
; OTHER INFORMATION: strategy
US-09-358-856C-2

Query Match 28.6%; Score 16; DB 3; Length 3225;
Best Local Similarity 100.0%; Pred. No. 16;
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Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32
Db 1376 TGAATGCTCATCCGGA 1391

RESULT 30
US-08-507-455-4
; Sequence 4, Application US/08507455
; Patent No. 5695961
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: BIFUNCTIONAL EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHIVE P.C.
; STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
; CITY: ARLINGTON
; STATE: VIRGINIA
; COUNTRY: USA
; ZIP: 22201-4714
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/507,455
; FILING DATE: 08-SEP-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GB 9303988.1
; FILING DATE: 26-FEB-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: MITCHARD, LEONARD C
; REGISTRATION NUMBER: 29,009
; REFERENCE/DOCKET NUMBER: 1498-72
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3249 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Saccharomyces cerevisiae
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: 290..291
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: 426..427
; NAME/KEY: misc_recomb
; LOCATION: 1213..1214
; FEATURE:
; NAME/KEY: misc_recomb
; LOCATION: 2143..2144
;
US-08-507-455-4

Query Match 28.6%; Score 16; DB 2; Length 3249;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGGA 32
Db 660 TGAATGCTCATCCGGA 675

RESULT 31
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US-09-793-372-1
; Sequence 1, Application US/09793372
; Patent No. 6696278
; GENERAL INFORMATION:
; APPLICANT: Carsten-Peter, Carstens
; TITLE OF INVENTION: A Method of Transfer of DNA Segments
; FILE REFERENCE: 25436/1240
; CURRENT APPLICATION NUMBER: US/09/793,372
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 1
; LENGTH: 3400
; TYPE: DNA
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Nucleotide sequence of plasmid pBC SK+
US-09-793-372-1

Query Match      28.6%; Score 16; DB 3; Length 3400;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 TGAATGCTCATCCGGA 32
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Db      2324 TGAATGCTCATCCGGA 2339

RESULT 32
US-09-742-373-10
; Sequence 10, Application US/09742373
; Patent No. 6562946
; GENERAL INFORMATION:
; APPLICANT: Althaus, Harald
; TITLE OF INVENTION: Human Procalcitonin and the Preparation and Use Thereof
; FILE REFERENCE: 05552.1445-00
; CURRENT APPLICATION NUMBER: US/09/742,373
; CURRENT FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 19962434.8
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 10016278.9
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 10027954.6
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3462
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Vectorsequence ,
US-09-742-373-10

Query Match      28.6%; Score 16; DB 3; Length 3462;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 TGAATGCTCATCCGGA 32
        |||
Db      545 TGAATGCTCATCCGGA 560

RESULT 33
US-10-394-058-10
; Sequence 10, Application US/10394058
; Patent No. 6905687
; GENERAL INFORMATION:
; APPLICANT: Althaus, Harald
; APPLICANT: Hauser, Hans-Peter
; TITLE OF INVENTION: Human Procalcitonin and the Preparation and Use Thereof
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; FILE REFERENCE: 05552.1445-00
; CURRENT APPLICATION NUMBER: US/10/394,058
; CURRENT FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: US/09/742,373
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 19962434.8
; PRIOR FILING DATE: 1999-12-22
; PRIOR APPLICATION NUMBER: 10016278.9
; PRIOR FILING DATE: 2000-04-03
; PRIOR APPLICATION NUMBER: 10027954.6
; PRIOR FILING DATE: 2000-06-08
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 10
; LENGTH: 3462
; TYPE: DNA
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Vectorsequence ,
US-10-394-058-10

Query Match      28.6%; Score 16; DB 3; Length 3462;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 TGAATGCTCATCCGGA 32
        |||
Db      545 TGAATGCTCATCCGGA 560

RESULT 34
US-09-640-882-1
; Sequence 1, Application US/09640882
; Patent No. 6720142
; GENERAL INFORMATION:
; APPLICANT: Hall, Barry G.
; TITLE OF INVENTION: METHOD OF DETERMINING EVOLUTIONARY POTENTIAL OF MUTANT
; TITLE OF INVENTION: RESISTANCE GENES AND USE THEREOF TO SCREEN FOR DRUG
; TITLE OF INVENTION: EFFICACY
; FILE REFERENCE: 176/60851
; CURRENT APPLICATION NUMBER: US/09/640,882
; CURRENT FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 60/149,813
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 3801
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: plasmid pACSE
US-09-640-882-1

Query Match      28.6%; Score 16; DB 3; Length 3801;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      17 TGAATGCTCATCCGGA 32
        |||
Db      3782 TGAATGCTCATCCGGA 3797

RESULT 35
US-07-623-953-1/c
; Sequence 1, Application US/07623953
; Patent No. 5364782
; GENERAL INFORMATION:
; APPLICANT: Quak, Wilhelmus J
; APPLICANT: Laroche, Yves
; APPLICANT: Vollebregt, Adrianus W.H.
; APPLICANT: Stanssens, Patrick
```



APPLICANT: Lauwereys, Marc  
TITLE OF INVENTION: MUTANT MICROBIAL ALPHA-AMYLASES WITH  
TITLE OF INVENTION: INCREASED THERMAL, ACID AND/OR ALKALINE STABILITY  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESS: COOLEY GODWARD CASTRO HUDDLESON & TATUM  
STREET: FIVE PALO ALTO SQUARE, 4TH FLOOR  
CITY: PALO ALTO  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/623,953  
FILING DATE: 19901129  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Rae-Venter, Barbara  
REGISTRATION NUMBER: 32,750  
REFERENCE/DOCKET NUMBER: GBRO-025/00US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-494-7622  
TELEFAX: 415-857-0663  
TELEX: 380816 COOLEY PA  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: circular  
US-07-623-953-1

Query Match 28.6%; Score 16; DB 2; Length 3803;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGA 32  
Db 3321 TGAATGCTCATCCGA 3306

RESULT 36  
US-07-640-476-1/c  
Sequence 1, Application US/07640476  
Patent No. 5376536  
GENERAL INFORMATION:  
APPLICANT: OUK, WILHELMUS  
APPLICANT: LUITEN, RUDOLF G. M.  
APPLICANT: SCHURHUIZEN, PAUL W.  
APPLICANT: KRABET, NADIR  
TITLE OF INVENTION: NOVEL GLUCOSE ISOMERASE ENZYMES AND  
TITLE OF INVENTION: THEIR USE  
NUMBER OF SEQUENCES: 22  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Morrison & Foerster  
STREET: 545 Middlefield Road, Suite 200  
CITY: Menlo Park  
STATE: CA  
COUNTRY: USA  
ZIP: 94025  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/07/640,476  
FILING DATE: 19910110

CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Kate H. Murashige  
REGISTRATION NUMBER: 29,959  
REFERENCE/DOCKET NUMBER: 24615-20009.20  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 327-7250  
TELEFAX: (415) 327-2951  
TELEX: 706141  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3803 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: circular  
HYPOTHETICAL: NO  
PUBLICATION INFORMATION:  
AUTHORS: Stanssens, P  
DATE: July-1987  
US-07-640-476-1

Query Match 28.6%; Score 16; DB 2; Length 3803;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGA 32  
Db 3321 TGAATGCTCATCCGA 3306

RESULT 37  
US-08-675-566-8  
Sequence 8, Application US/08675566  
Patent No. 6090393  
GENERAL INFORMATION:  
APPLICANT: Fischer, Laurent  
TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
TITLE OF INVENTION: RECOMBINANT VIRUSES, METHODS FOR MAKING, AND USES THEREOF  
NUMBER OF SEQUENCES: 120  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Curtis, Morris & Safford, P. C.  
STREET: 530 Fifth Avenue  
CITY: New York  
STATE: New York  
COUNTRY: United States of America  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/675,566  
FILING DATE: 03-JUL-1996  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Frommer Esq., William S.  
REGISTRATION NUMBER: 25,506  
REFERENCE/DOCKET NUMBER: 454310-2890  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (212)840-3333  
TELEFAX: (212)840-0712  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3822 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-675-566-8

Query Match 28.6%; Score 16; DB 3; Length 3822;  
Best Local Similarity 100.0%; Pred. No. 16;



Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
|||||  
Db 408 TGAATGCTCATCCGGA 423

RESULT 38  
US-08-675-566-11  
; Sequence 11, Application US/08675566  
; Patent No. 6090393  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Laurent  
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Curtis, Morris & Safford, P.C.  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,566  
; FILING DATE: 03-JUL-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer Esq., William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2890  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)840-3333  
; TELEFAX: (212)840-0712  
; INFORMATION FOR SEQ ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3861 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-675-566-11

Query Match 28.6%; Score 16; DB 3; Length 3861;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
|||||  
Db 551 TGAATGCTCATCCGGA 566

RESULT 39  
US-09-744-016A-15  
; Sequence 15, Application US/09744016A  
; Patent No. 6875581  
; GENERAL INFORMATION:  
; APPLICANT: Dr. Voelkel, Heige  
; TITLE OF INVENTION: Method for screening of modulators of calcineurin  
; FILE REFERENCES: A34157PCT  
; CURRENT APPLICATION NUMBER: US/09/744,016A  
; CURRENT FILING DATE: 2001-10-03  
; PRIOR APPLICATION NUMBER: EP96113876  
; PRIOR FILING DATE: 1998-07-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 15

LENGTH: 3881  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (115)..(576)  
; OTHER INFORMATION: copper/zinc superoxide dismutase  
; NAME/KEY: misc feature  
; LOCATION: (577)..(582)  
; OTHER INFORMATION: carboxypeptidase-A cleavage site  
; NAME/KEY: misc feature  
; LOCATION: (578)..(603)  
; OTHER INFORMATION: histidine tag  
US-09-744-016A-15

Query Match 28.6%; Score 16; DB 3; Length 3881;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
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Db 960 TGAATGCTCATCCGGA 975

RESULT 40  
US-08-675-566-12  
; Sequence 12, Application US/08675566  
; Patent No. 6090393  
; GENERAL INFORMATION:  
; APPLICANT: Fischer, Laurent  
; TITLE OF INVENTION: PROMOTERS, EXPRESSION CASSETTES,  
; NUMBER OF SEQUENCES: 120  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSER: Curtis, Morris & Safford, P.C.  
; STREET: 530 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: United States of America  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/675,566  
; FILING DATE: 03-JUL-1996  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Frommer Esq., William S.  
; REGISTRATION NUMBER: 25,506  
; REFERENCE/DOCKET NUMBER: 454310-2890  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (212)840-3333  
; TELEFAX: (212)840-0712  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3888 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
US-08-675-566-12

Query Match 28.6%; Score 16; DB 3; Length 3888;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGGA 32  
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Db 551 TGAATGCTCATCCGGA 566



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GenCore version 5.1.7  
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Published Applications\_NA\_Main:\*

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- 2: /cgn2\_6/ptodata/1/pubpna/US08\_PUBCOMB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
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#### SUMMARIES

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C 2	23	41.1	23	10	US-11-018-377-66
C 3	18	32.1	631	7	US-10-424-599-121945
C 4	17	30.4	100	3	US-09-924-035A-660
C 5	17	30.4	201	3	US-09-938-842A-37
C 6	17	30.4	201	3	US-09-938-842A-37
C 7	17	30.4	500	3	US-09-895-040A-34
C 8	17	30.4	622	5	US-10-027-632-185154
C 9	17	30.4	622	5	US-10-027-632-185155
C 10	17	30.4	622	5	US-10-027-632-185156
C 11	17	30.4	622	5	US-10-027-632-185157
C 12	17	30.4	622	5	US-10-027-632-185158
C 13	17	30.4	622	5	US-10-027-632-185159
C 14	17	30.4	622	6	US-10-027-632-185154
C 15	17	30.4	622	6	US-10-027-632-185155
C 16	17	30.4	622	6	US-10-027-632-185156
C 17	17	30.4	622	6	US-10-027-632-185157
C 18	17	30.4	622	6	US-10-027-632-185158
C 19	17	30.4	1142	5	US-10-027-632-118722
C 20	17	30.4	1142	6	US-10-027-632-118722
C 21	17	30.4	1651	5	US-10-027-632-208605
C 22	17	30.4	1930	4	US-09-925-065A-692911
C 23	17	30.4	1930	4	US-09-925-065A-692912

C 24	17	30.4	1930	4	US-09-925-065A-692913	Sequence 692913, A
C 25	17	30.4	1930	4	US-09-925-065A-692914	Sequence 692914, A
C 26	17	30.4	1930	4	US-09-925-065A-692915	Sequence 692915, A
C 27	16	28.6	25	10	US-11-060-756-118490	Sequence 118490, A
C 28	16	28.6	25	10	US-11-060-756-118491	Sequence 118491, A
C 29	16	28.6	30	8	US-10-484-232-2	Sequence 2, Appl1
C 30	16	28.6	213	7	US-10-767-701-16720	Sequence 16720, A
C 31	16	28.6	324	9	US-10-450-763-3300	Sequence 3300, Ap
C 32	16	28.6	364	7	US-10-424-559-112332	Sequence 112332, A
C 33	16	28.6	405	9	US-10-450-763-7475	Sequence 7475, Ap
C 34	16	28.6	496	9	US-10-450-763-13740	Sequence 13740, A
C 35	16	28.6	526	4	US-09-925-065A-334218	Sequence 334218, A
C 36	16	28.6	561	7	US-10-333-184-124	Sequence 124, App
C 37	16	28.6	575	9	US-10-972-079-33594	Sequence 73594, A
C 38	16	28.6	584	4	US-09-925-065A-169496	Sequence 169496, A
C 39	16	28.6	593	4	US-09-925-065A-266664	Sequence 266664, A
C 40	16	28.6	595	4	US-09-925-065A-902120	Sequence 902120, A
C 41	16	28.6	600	10	US-11-060-756-3498	Sequence 3498, Ap
C 42	16	28.6	600	10	US-11-060-756-3499	Sequence 3499, Ap
C 43	16	28.6	600	10	US-11-060-756-7770	Sequence 7770, Ap
C 44	16	28.6	600	10	US-11-060-756-7771	Sequence 7771, Ap
C 45	16	28.6	627	4	US-09-925-065A-315548	Sequence 315548, A
C 46	16	28.6	627	4	US-09-925-065A-315549	Sequence 315549, A
C 47	16	28.6	658	7	US-10-332-733-28	Sequence 28, Appl
C 48	16	28.6	666	9	US-10-450-763-1382	Sequence 1382, Ap
C 49	16	28.6	666	9	US-10-450-763-1383	Sequence 1383, A
C 50	16	28.6	666	9	US-10-450-763-1384	Sequence 1384, Ap
C 51	16	28.6	690	4	US-09-925-065A-7304	Sequence 7304, Ap
C 52	16	28.6	727	4	US-09-925-065A-923129	Sequence 923129, A
C 53	16	28.6	760	8	US-10-748-055-13	Sequence 15402, A
C 54	16	28.6	830	5	US-10-450-763-15402	Sequence 168708, A
C 55	16	28.6	830	5	US-10-027-632-168708	Sequence 168709, A
C 56	16	28.6	830	5	US-10-027-632-168708	Sequence 168709, A
C 57	16	28.6	830	6	US-10-027-632-168709	Sequence 24642, A
C 58	16	28.6	855	9	US-10-450-763-24542	Sequence 3, Appl1
C 59	16	28.6	935	8	US-10-654-898A-3	Sequence 13246, A
C 60	16	28.6	945	9	US-10-927-040-3	Sequence 21664, A
C 61	16	28.6	961	9	US-10-450-763-13246	Sequence 24519, A
C 62	16	28.6	1002	9	US-10-450-763-18098	Sequence 14782, A
C 63	16	28.6	1044	9	US-10-450-763-18098	Sequence 4276, Ap
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C 65	16	28.6	1086	9	US-10-450-763-13426	Sequence 1227, A
C 66	16	28.6	1086	9	US-10-450-763-13426	Sequence 13426, A
C 67	16	28.6	1086	9	US-10-450-763-21664	Sequence 21664, A
C 68	16	28.6	1095	10	US-11-063-223-12	Sequence 12, Appl
C 69	16	28.6	1095	10	US-11-063-223-13	Sequence 13, Appl
C 70	16	28.6	1096	10	US-11-063-223-13	Sequence 5, Appl1
C 71	16	28.6	1099	10	US-11-063-223-35	Sequence 35, Appl
C 72	16	28.6	1099	10	US-11-063-223-36	Sequence 36, Appl
C 73	16	28.6	1101	7	US-10-424-599-4782	Sequence 14782, A
C 74	16	28.6	1125	9	US-10-450-763-4276	Sequence 4276, Ap
C 75	16	28.6	1137	7	US-10-680-286-1	Sequence 1, Appl1
C 76	16	28.6	1172	9	US-10-450-763-13227	Sequence 13227, A
C 77	16	28.6	1191	8	US-10-654-898A-37	Sequence 7, Appl1
C 78	16	28.6	1221	9	US-10-450-763-12343	Sequence 12343, A
C 79	16	28.6	1233	9	US-10-450-763-24092	Sequence 24092, A
C 80	16	28.6	1245	9	US-10-450-763-28586	Sequence 28586, A
C 81	16	28.6	1254	9	US-10-511-327-2	Sequence 2, Appl1
C 82	16	28.6	1270	7	US-10-680-286-11	Sequence 11, Appl1
C 83	16	28.6	1284	9	US-10-450-763-25642	Sequence 25642, A
C 84	16	28.6	1314	9	US-10-450-763-7312	Sequence 7312, Ap
C 85	16	28.6	1317	9	US-10-450-763-10689	Sequence 10689, A
C 86	16	28.6	1330	7	US-10-680-286-6	Sequence 6, Appl1
C 87	16	28.6	1340	7	US-10-275-263-2	Sequence 2, Appl1
C 88	16	28.6	1350	9	US-10-450-763-27406	Sequence 27406, A
C 89	16	28.6	1350	9	US-10-450-763-27406	Sequence 27406, A
C 90	16	28.6	1352	9	US-10-302-997-14	Sequence 3, Appl1
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C 92	16	28.6	1381	7	US-11-060-756-70	Sequence 70, Appl
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C 94	16	28.6	1400	10	US-11-060-756-71	Sequence 71, Appl
C 95	16	28.6	1400	10	US-11-060-756-971	Sequence 971, Ap
C 96	16	28.6	1400	10	US-11-060-756-4342	Sequence 4342, Ap



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C 98	16	28.6	1400	10	US-11-060-756-5243	Sequence 5243, Ap	171	16	2694	9	US-10-450-763-24589	Sequence 24589, A
C 99	16	28.6	1413	9	US-10-450-763-13355	Sequence 13355, A	172	16	2714	6	US-10-068-664A-34	Sequence 34, Appl
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C 113	16	28.6	1529	8	US-10-484-233-4	Sequence 4, Appl1	C 186	16	3226	9	US-10-450-763-13243	Sequence 13433, A
C 114	16	28.6	1529	8	US-10-484-233-4	Sequence 4, Appl1	C 187	16	3267	8	US-10-828-679-5	Sequence 5, Appl1
C 115	16	28.6	1590	6	US-10-450-763-16423	Sequence 16423, A	188	16	3273	9	US-10-450-763-36159	Sequence 26159, A
C 116	16	28.6	1599	6	US-10-341-959-3	Sequence 3, Appl1	C 189	16	3288	9	US-10-450-763-21593	Sequence 21593, A
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C 123	16	28.6	1653	9	US-10-450-763-13224	Sequence 13224, A	196	16	3384	9	US-10-450-763-24535	Sequence 24535, A
C 124	16	28.6	1680	9	US-10-450-763-27515	Sequence 27515, A	197	16	3384	9	US-10-291-128-92	Sequence 92, Appl
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126	16	28.6	1719	9	US-10-450-763-26362	Sequence 26362, A	199	16	3420	7	US-10-385-415-1	Sequence 1, Appl1
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128	16	28.6	1750	8	US-10-740-714-41	Sequence 41, Appl	201	16	3462	6	US-10-394-058-10	Sequence 10, Appl
129	16	28.6	1750	8	US-10-783-534-41	Sequence 41, Appl	202	16	3462	7	US-10-341-889-4	Sequence 4, Appl1
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C 131	16	28.6	1767	9	US-10-450-763-23601	Sequence 23601, A	C 204	16	3501	9	US-10-450-763-25747	Sequence 25747, A
C 132	16	28.6	1767	9	US-10-450-763-24557	Sequence 24557, A	C 205	16	3529	7	US-10-416-708A-4	Sequence 4, Appl1
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135	16	28.6	1824	3	US-09-930-342-1	Sequence 1, Appl1	208	16	3876	7	US-10-385-415-27	Sequence 27, Appl
136	16	28.6	1824	10	US-11-004-043-1	Sequence 1, Appl1	209	16	3876	7	US-10-385-415-28	Sequence 28, Appl
137	16	28.6	1846	6	US-10-023-208-63	Sequence 63, Appl1	210	16	3879	7	US-10-385-415-5	Sequence 5, Appl1
138	16	28.6	1864	3	US-09-950-492-3	Sequence 3, Appl1	211	16	3879	7	US-10-385-415-6	Sequence 6, Appl1
139	16	28.6	1906	6	US-10-068-664A-37	Sequence 37, Appl	212	16	3879	7	US-10-385-415-7	Sequence 7, Appl1
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143	16	28.6	1992	9	US-10-450-763-20946	Sequence 20946, A	216	16	3888	3	US-09-909-238F-20	Sequence 20, Appl
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148	16	28.6	2101	9	US-10-823-432-10	Sequence 10, Appl	221	16	3912	7	US-11-003-103A-5	Sequence 5, Appl1
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151	16	28.6	2106	9	US-10-450-763-25769	Sequence 25769, A	224	16	3927	7	US-10-385-415-22	Sequence 22, Appl
152	16	28.6	2154	9	US-10-450-763-5225	Sequence 5225, Ap	225	16	3932	7	US-10-385-415-14	Sequence 14, Appl
C 153	16	28.6	2167	3	US-09-962-436-283	Sequence 283, App	226	16	3932	7	US-10-385-415-14	Sequence 14, Appl
C 154	16	28.6	2175	10	US-10-843-641A-2742	Sequence 2742, Ap	227	16	3936	7	US-10-385-415-13	Sequence 13, Appl
C 155	16	28.6	2175	10	US-11-010-559-15	Sequence 15, Appl1	228	16	3945	7	US-10-385-415-25	Sequence 25, Appl
C 156	16	28.6	2181	10	US-11-010-559-18	Sequence 18, Appl	229	16	3957	7	US-10-385-415-24	Sequence 24, Appl
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C 158	16	28.6	2210	7	US-10-437-963-91339	Sequence 91339, A	231	16	4010	6	US-09-836-077-40	Sequence 40, Appl
C 159	16	28.6	2230	7	US-10-450-763-13351	Sequence 13351, A	232	16	4019	3	US-10-836-077-39	Sequence 39, Appl
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162	16	28.6	2499	9	US-10-450-763-4017	Sequence 4017, Ap	234	16	4045	3	US-10-658-753-37	Sequence 37, Appl
163	16	28.6	2499	9	US-10-450-763-25756	Sequence 25756, A	235	16	4055	5	US-10-037-270-706	Sequence 706, App
164	16	28.6	2503	9	US-10-450-763-24596	Sequence 24596, A	C 237	16	4055	5	US-10-117-722-706	Sequence 706, App
165	16	28.6	2538	9	US-10-450-763-21843	Sequence 21843, A	238	16	4055	6	US-10-117-722-706	Sequence 706, App
166	16	28.6	2544	9	US-10-450-763-4027	Sequence 4027, Ap	C 239	16	4055	6	US-10-122-851-706	Sequence 706, App
C 167	16	28.6	2589	10	US-11-010-559-20	Sequence 20, Appl	C 240	16	4055	6	US-10-122-851-706	Sequence 706, App
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C 169	16	28.6	2601	9	US-10-450-763-7440	Sequence 7440, Ap	242	16	4140	9	US-10-450-763-5707	Sequence 5707, Ap



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244	16	28.6	4247	8	US-10-640-422-156	Sequence 156, App	C 317	16	28.6	7341	8	US-10-622-088-112	Sequence 112, App
245	16	28.6	4311	7	US-10-221-124A-2	Sequence 2, Appli	C 318	16	28.6	7437	9	US-10-877-952-19	Sequence 19, Appli
246	16	28.6	4368	7	US-10-385-415-10	Sequence 10, Appli	C 319	16	28.6	7440	9	US-10-877-952-116	Sequence 116, App
247	16	28.6	4380	7	US-10-385-415-12	Sequence 12, Appli	C 320	16	28.6	7480	9	US-10-877-952-21	Sequence 21, Appli
248	16	28.6	4416	7	US-10-450-763-21862	Sequence 21862, A	C 321	16	28.6	7487	5	US-10-055-794-4	Sequence 4, Appli
249	16	28.6	4422	9	US-10-450-763-8264	Sequence 8264, Ap	C 322	16	28.6	7519	9	US-10-877-952-231	Sequence 231, App
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C 251	16	28.6	4470	6	US-10-151-690-21	Sequence 21, Appli	C 324	16	28.6	7519	7	US-10-612-410-1	Sequence 1, Appli
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C 260	16	28.6	4773	8	US-10-640-422-158	Sequence 158, App	C 333	16	28.6	8500	7	US-10-266-947-7	Sequence 7, Appli
C 261	16	28.6	4777	8	US-10-640-422-159	Sequence 159, App	C 334	16	28.6	8547	8	US-10-474-536-46	Sequence 46, Appli
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C 267	16	28.6	5064	7	US-10-385-415-11	Sequence 11, Appli	C 340	16	28.6	8609	8	US-10-735-442-64	Sequence 64, Appli
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C 273	16	28.6	5178	9	US-10-688-255-6	Sequence 6, Appli	C 346	16	28.6	8688	9	US-10-913-501-2	Sequence 2, Appli
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C 276	16	28.6	5448	9	US-10-671-995A-2	Sequence 2, Appli	C 349	16	28.6	8849	9	US-10-450-763-25781	Sequence 25781, A
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C 285	16	28.6	5830	9	US-10-450-763-15764	Sequence 15764, A	C 358	16	28.6	9484	5	US-10-032-393-49	Sequence 49, Appli
C 286	16	28.6	5938	9	US-10-450-763-23199	Sequence 23199, A	C 359	16	28.6	9652	5	US-10-007-527A-7	Sequence 7, Appli
C 287	16	28.6	5952	9	US-10-450-763-21645	Sequence 21645, A	C 360	16	28.6	9652	5	US-10-007-452-7	Sequence 7, Appli
C 288	16	28.6	5986	7	US-10-343-859-5	Sequence 5, Appli	C 361	16	28.6	9652	7	US-10-415-562A-7	Sequence 7, Appli
C 289	16	28.6	5996	7	US-10-416-708A-41	Sequence 41, Appli	C 362	16	28.6	9652	10	US-11-069-691-7	Sequence 7, Appli
C 290	16	28.6	6033	9	US-10-450-763-21643	Sequence 21643, A	C 363	16	28.6	9737	6	US-10-331-329-22	Sequence 22, Appli
C 291	16	28.6	6122	5	US-10-006-591-1	Sequence 1, Appli	C 364	16	28.6	9737	6	US-10-331-329-23	Sequence 23, Appli
C 292	16	28.6	6372	9	US-10-997-651-2	Sequence 2, Appli	C 365	16	28.6	9737	6	US-10-331-329-28	Sequence 28, Appli
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C 296	16	28.6	6501	3	US-09-767-515-2	Sequence 2, Appli	C 369	16	28.6	10463	6	US-10-389-120-1	Sequence 1, Appli
C 297	16	28.6	6501	7	US-10-612-713-1	Sequence 1, Appli	C 370	16	28.6	10903	7	US-10-612-224-1	Sequence 1, Appli
C 298	16	28.6	6501	7	US-10-612-713-2	Sequence 2, Appli	C 371	16	28.6	11120	9	US-10-450-763-21861	Sequence 21861, A
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C 300	16	28.6	6520	5	US-10-997-651-38	Sequence 38, Appli	C 373	16	28.6	11241	5	US-10-007-452A-6	Sequence 6, Appli
C 301	16	28.6	6525	5	US-10-055-794-3	Sequence 3, Appli	C 374	16	28.6	11241	5	US-10-007-452-6	Sequence 6, Appli
C 302	16	28.6	6782	7	US-10-420-529-12	Sequence 12, Appli	C 375	16	28.6	11241	9	US-10-415-562A-6	Sequence 6, Appli
C 303	16	28.6	6809	9	US-10-877-952-87	Sequence 87, Appli	C 376	16	28.6	11241	10	US-10-430-129-13	Sequence 13, Appli
C 304	16	28.6	6809	9	US-10-877-952-101	Sequence 101, App	C 377	16	28.6	11241	10	US-11-069-691-6	Sequence 6, Appli
C 305	16	28.6	6809	9	US-10-877-952-236	Sequence 236, App	C 378	16	28.6	11918	7	US-10-612-224-2	Sequence 2, Appli
C 306	16	28.6	6809	9	US-10-877-952-237	Sequence 237, App	C 379	16	28.6	11918	10	US-11-082-454-46	Sequence 46, Appli
C 307	16	28.6	6876	7	US-10-450-763-29836	Sequence 29836, A	C 380	16	28.6	12733	5	US-10-032-393-8	Sequence 8, Appli
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C 311	16	28.6	7271	9	US-10-450-763-4319	Sequence 4319, Ap	C 384	16	28.6	13227	7	US-10-612-224-4	Sequence 4, Appli
C 312	16	28.6	7278	7	US-10-097-034A-37	Sequence 37, Appli	C 385	16	28.6	13274	7	US-10-332-026A-20	Sequence 20, Appli
C 313	16	28.6	7326	7	US-10-450-763-3321	Sequence 3321, Ap	C 386	16	28.6	13278	7	US-10-612-224-3	Sequence 3, Appli
C 314	16	28.6	7336	5	US-10-084-814-3	Sequence 3, Appli	C 387	16	28.6	13478	8	US-10-479-497-1	Sequence 1, Appli
C 315	16	28.6	7336	7	US-10-442-013-4	Sequence 4, Appli	C 388	16	28.6	14000	8	US-10-383-838-8	Sequence 8, Appli



C 389	16	28.6	14468	6	US-10-295-362-19	Sequence 19, Appl	462	15	26.8	599	9	US-10-972-079-56832	Sequence 56832, A
C 390	16	28.6	14561	10	US-11-082-454-49	Sequence 46, Appl	C 463	15	26.8	600	4	US-09-925-065A-527405	Sequence 527405, A
C 391	16	28.6	15882	6	US-10-440-419-56	Sequence 56, Appl	464	15	26.8	600	9	US-10-972-079-37574	Sequence 37574, A
C 392	16	28.6	15900	6	US-10-440-419-55	Sequence 55, Appl	465	15	26.8	600	9	US-10-972-079-90133	Sequence 90133, A
C 393	16	28.6	17815	10	US-11-082-454-54	Sequence 57, Appl	C 466	15	26.8	609	4	US-09-925-065A-785545	Sequence 785545, A
C 394	16	28.6	18031	10	US-11-082-454-57	Sequence 57, Appl	467	15	26.8	616	4	US-09-925-065A-683076	Sequence 683076, A
C 395	16	28.6	18691	5	US-10-055-001A-13	Sequence 13, Appl	468	15	26.8	621	4	US-09-925-065A-556974	Sequence 556974, A
C 396	16	28.6	18691	10	US-11-033-553-13	Sequence 13, Appl	469	15	26.8	627	4	US-09-925-065A-703071	Sequence 703071, A
C 397	16	28.6	18691	10	US-11-034-069-13	Sequence 13, Appl	470	15	26.8	627	4	US-09-925-065A-703072	Sequence 703072, A
C 398	16	28.6	27413	5	US-10-087-192-1477	Sequence 1477, Ap	471	15	26.8	627	4	US-09-925-065A-703073	Sequence 703073, A
C 399	16	28.6	34864	8	US-10-622-088-87	Sequence 87, Appl	472	15	26.8	631	4	US-09-925-065A-777272	Sequence 777272, A
C 400	16	28.6	36686	8	US-10-622-088-83	Sequence 83, Appl	C 473	15	26.8	638	4	US-09-925-065A-518354	Sequence 518354, A
C 401	16	28.6	75815	8	US-10-856-218A-36	Sequence 36, Appl	C 474	15	26.8	648	4	US-09-925-065A-813226	Sequence 813226, A
C 402	16	28.6	75815	10	US-11-047-184-46	Sequence 36, Appl	C 475	15	26.8	651	7	US-10-021-333-7055	Sequence 7055, Ap
C 403	16	28.6	77872	10	US-10-856-218A-44	Sequence 44, Appl	C 476	15	26.8	651	8	US-10-767-795-1801	Sequence 1801, Ap
C 404	16	28.6	77872	10	US-11-047-184-44	Sequence 44, Appl	477	15	26.8	654	5	US-10-027-632-114439	Sequence 114439, A
C 405	16	28.6	96593	7	US-10-052-482-106	Sequence 106, App	478	15	26.8	654	6	US-10-027-632-114439	Sequence 114439, A
C 406	16	28.6	117754	5	US-10-087-192-28	Sequence 28, Appl	479	15	26.8	663	5	US-10-027-632-196943	Sequence 196943, A
C 407	16	28.6	165221	5	US-10-087-192-1015	Sequence 1015, Ap	480	15	26.8	663	5	US-10-027-632-196944	Sequence 196944, A
C 408	16	28.6	218802	9	US-10-897-508-1	Sequence 1, Appli	481	15	26.8	663	5	US-10-027-632-196943	Sequence 196943, A
C 409	15	26.8	19	7	US-10-634-862-1	Sequence 1, Appli	482	15	26.8	663	6	US-10-027-632-196944	Sequence 196944, A
C 410	15	26.8	25	7	US-10-719-956-13680	Sequence 163690, Sequence 452833, Sequence 253206,	483	15	26.8	663	6	US-10-027-632-196945	Sequence 196945, A
C 411	15	26.8	25	10	US-11-036-317-452833	Sequence 253206,	484	15	26.8	663	6	US-10-027-632-196945	Sequence 196945, A
C 412	15	26.8	25	10	US-11-060-756-253206	Sequence 4, Appli	485	15	26.8	669	5	US-09-925-065A-690133	Sequence 690133, A
C 413	15	26.8	25	3	US-09-967-604-4	Sequence 2, Appli	486	15	26.8	669	5	US-10-027-632-129671	Sequence 129671, A
C 414	15	26.8	34	3	US-09-288-971-1	Sequence 2, Appli	487	15	26.8	669	5	US-10-027-632-129671	Sequence 129671, A
C 415	15	26.8	185	8	US-10-425-115-77208	Sequence 77208, A	488	15	26.8	669	6	US-10-027-632-129671	Sequence 129671, A
C 416	15	26.8	201	8	US-10-719-993-1636	Sequence 1636, A	489	15	26.8	699	6	US-10-425-115-933	Sequence 23, Appl
C 417	15	26.8	201	8	US-10-719-993-1660	Sequence 1660, A	490	15	26.8	712	8	US-10-087-192-1262	Sequence 1262, Ap
C 418	15	26.8	201	8	US-10-719-993-1660	Sequence 1660, A	491	15	26.8	879	5	US-10-087-192-1262	Sequence 1262, Ap
C 419	15	26.8	201	8	US-10-719-993-16758	Sequence 16758, A	492	15	26.8	962	7	US-10-767-701-1793	Sequence 1793, Ap
C 420	15	26.8	370	5	US-10-060-036-1913	Sequence 1913, Ap	493	15	26.8	1060	8	US-10-425-115-933	Sequence 25, Appl
C 421	15	26.8	452	4	US-09-925-065A-583100	Sequence 583100, Sequence 259142,	494	15	26.8	1092	4	US-09-925-065A-20400	Sequence 20400, A
C 422	15	26.8	467	4	US-09-925-065A-259142	Sequence 236, App	495	15	26.8	1092	4	US-09-925-065A-20401	Sequence 20401, A
C 423	15	26.8	474	3	US-09-938-842A-236	Sequence 236, App	496	15	26.8	1092	4	US-09-925-065A-20402	Sequence 20402, A
C 424	15	26.8	474	3	US-09-938-842A-236	Sequence 236, App	497	15	26.8	1092	4	US-09-925-065A-20403	Sequence 20403, A
C 425	15	26.8	476	7	US-10-424-599-100895	Sequence 100895, Sequence 739668,	498	15	26.8	1110	9	US-10-450-763-22383	Sequence 22383, A
C 426	15	26.8	477	4	US-09-925-065A-739668	Sequence 224, App	499	15	26.8	1182	9	US-10-484-605-1	Sequence 1, Appl1
C 427	15	26.8	482	3	US-09-764-876-72	Sequence 72, Appl	500	15	26.8	1182	9	US-10-789-144-1	Sequence 1, Appl1
C 428	15	26.8	482	3	US-09-764-876-72	Sequence 389, App	501	15	26.8	1230	7	US-10-437-963-42265	Sequence 42265, A
C 429	15	26.8	482	3	US-09-764-876-72	Sequence 389, App	502	15	26.8	1245	7	US-10-424-599-102518	Sequence 102518, A
C 430	15	26.8	482	3	US-10-242-355-186	Sequence 186, App	503	15	26.8	1287	7	US-10-282-122A-26143	Sequence 26143, A
C 431	15	26.8	494	4	US-09-925-065A-855641	Sequence 855641, Sequence 855642,	504	15	26.8	1290	7	US-10-282-122A-26143	Sequence 26143, A
C 432	15	26.8	494	4	US-09-925-065A-855641	Sequence 855641, Sequence 855642,	505	15	26.8	1377	7	US-10-398-221-1677	Sequence 1677, Ap
C 433	15	26.8	494	4	US-09-925-065A-855641	Sequence 855641, Sequence 855642,	506	15	26.8	1377	7	US-10-398-221-1677	Sequence 1677, Ap
C 434	15	26.8	502	4	US-09-925-065A-855641	Sequence 855641, Sequence 855642,	507	15	26.8	1438	5	US-10-027-632-249310	Sequence 249310, A
C 435	15	26.8	505	4	US-09-925-065A-855641	Sequence 855641, Sequence 855642,	508	15	26.8	1438	5	US-10-027-632-249310	Sequence 249310, A
C 436	15	26.8	524	4	US-09-925-065A-109645	Sequence 109645, Sequence 204153,	509	15	26.8	1438	6	US-10-027-632-249310	Sequence 249310, A
C 437	15	26.8	524	4	US-09-925-065A-109645	Sequence 109645, Sequence 204153,	510	15	26.8	1438	6	US-10-027-632-249310	Sequence 249310, A
C 438	15	26.8	524	4	US-09-925-065A-109645	Sequence 109645, Sequence 204153,	511	15	26.8	1455	6	US-10-369-493-40215	Sequence 40215, A
C 439	15	26.8	530	4	US-09-925-065A-176353	Sequence 176353, Sequence 176354,	512	15	26.8	1647	9	US-10-450-763-22035	Sequence 22035, A
C 440	15	26.8	530	4	US-09-925-065A-176353	Sequence 176353, Sequence 176354,	513	15	26.8	1678	5	US-10-002-634A-8	Sequence 8, Appl1
C 441	15	26.8	533	7	US-10-152-319A-631	Sequence 631, App	514	15	26.8	1693	5	US-10-958-862-8	Sequence 8, Appl1
C 442	15	26.8	538	4	US-09-925-065A-421768	Sequence 421768, Sequence 296404,	515	15	26.8	1693	5	US-10-027-632-286076	Sequence 286076, A
C 443	15	26.8	541	4	US-09-925-065A-296404	Sequence 296404, Sequence 926362,	516	15	26.8	1693	5	US-10-027-632-286076	Sequence 286076, A
C 444	15	26.8	552	4	US-09-925-065A-296362	Sequence 926362, Sequence 204333, A	517	15	26.8	1693	5	US-10-027-632-286076	Sequence 286076, A
C 445	15	26.8	557	4	US-09-925-065A-20333	Sequence 204333, A Sequence 204300, A	518	15	26.8	1693	5	US-10-027-632-286076	Sequence 286076, A
C 446	15	26.8	558	6	US-10-029-386-20480	Sequence 927577, Sequence 927577,	519	15	26.8	1916	7	US-10-437-963-445	Sequence 445, App
C 447	15	26.8	573	4	US-09-925-065A-927577	Sequence 927577, Sequence 950911, A	520	15	26.8	1954	4	US-10-450-763-22036	Sequence 22036, A
C 448	15	26.8	576	4	US-09-925-065A-41906	Sequence 41906, Sequence 950911, A	521	15	26.8	1986	6	US-10-278-536-95	Sequence 95, Appl
C 449	15	26.8	579	4	US-09-925-065A-950911	Sequence 950911, Sequence 270703, A	522	15	26.8	1986	6	US-10-412-639B-247	Sequence 247, Appl
C 450	15	26.8	583	5	US-10-027-632-270703	Sequence 270703, Sequence 270703, A	523	15	26.8	1990	7	US-10-027-632-249311	Sequence 249311, A
C 451	15	26.8	583	5	US-10-027-632-270703	Sequence 270703, Sequence 109646,	524	15	26.8	1990	6	US-10-027-632-249311	Sequence 249311, A
C 452	15	26.8	584	4	US-09-925-065A-109646	Sequence 109646, Sequence 109647,	525	15	26.8	2129	6	US-10-486-706-457	Sequence 457, App
C 453	15	26.8	584	4	US-09-925-065A-109647	Sequence 109647, Sequence 109648,	526	15	26.8	2182	6	US-10-108-260A-2045	Sequence 2045, App
C 454	15	26.8	584	4	US-09-925-065A-109648	Sequence 109648, Sequence 571143, A	527	15	26.8	2289	7	US-09-925-065A-1527	Sequence 1527, Ap
C 455	15	26.8	586	4	US-09-925-065A-571143	Sequence 571143, Sequence 441855, A	528	15	26.8	2290	7	US-10-425-114-21271	Sequence 73, Appl
C 456	15	26.8	589	4	US-09-925-065A-441855	Sequence 441855, Sequence 69078, A	529	15	26.8	2313	5	US-10-044-090-73	Sequence 29208, Ap
C 457	15	26.8	589	7	US-10-437-963-60778	Sequence 69078, A Sequence 62807, A	530	15	26.8	2368	8	US-10-425-114-8244	Sequence 8244, Ap
C 458	15	26.8	594	4	US-09-925-065A-328207	Sequence 328207, Ap Sequence 536772, A	531	15	26.8	2503	7	US-10-425-114-8244	Sequence 8244, Ap
C 459	15	26.8	594	6	US-10-029-386-6766	Sequence 536772, Sequence 142399, A	532	15	26.8	2615	8	US-10-424-599-58106	Sequence 58106, A
C 460	15	26.8	598	4	US-09-925-065A-536772	Sequence 142399, A	533	15	26.8	2770	5	US-10-087-192-896	Sequence 896, App
C 461	15	26.8	599	7	US-10-424-599-142399	Sequence 142399, A	534	15	26.8	2770	5	US-10-087-192-896	Sequence 896, App







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C 682	14	25.0	509	3	US-09-764-847-1663	Sequence 1663, Ap	C 755	14	25.0	565	4	US-09-925-065A-88670	Sequence 88670, A
C 683	14	25.0	509	5	US-10-092-154-1137	Sequence 1137, Ap	C 756	14	25.0	565	4	US-09-925-065A-558932	Sequence 558932,
C 684	14	25.0	509	5	US-10-092-154-1663	Sequence 1663, Ap	C 757	14	25.0	565	4	US-09-925-065A-554933	Sequence 554933,
C 685	14	25.0	510	8	US-10-357-930-10514	Sequence 10514, A	C 758	14	25.0	566	4	US-09-925-065A-359546	Sequence 359546,
C 686	14	25.0	510	3	US-09-783-590-5965	Sequence 5965, Ap	C 759	14	25.0	566	4	US-09-925-065A-525936	Sequence 525936,
C 687	14	25.0	510	3	US-09-764-847-365	Sequence 365, Ap	C 760	14	25.0	568	4	US-09-925-065A-194921	Sequence 194921,
C 688	14	25.0	510	4	US-09-925-065A-562313	Sequence 562313,	C 761	14	25.0	568	4	US-09-925-065A-414178	Sequence 414178,
C 689	14	25.0	510	4	US-09-925-065A-562314	Sequence 562314,	C 762	14	25.0	568	4	US-09-925-065A-414179	Sequence 414179,
C 690	14	25.0	510	4	US-09-925-065A-562315	Sequence 562315,	C 763	14	25.0	568	4	US-09-925-065A-933574	Sequence 933574,
C 691	14	25.0	510	4	US-09-925-065A-562316	Sequence 562316,	C 764	14	25.0	568	4	US-09-925-065A-933575	Sequence 933575,
C 692	14	25.0	510	5	US-10-093-154-365	Sequence 365, Ap	C 765	14	25.0	568	4	US-09-925-065A-952009	Sequence 952009,
C 693	14	25.0	512	4	US-09-925-065A-771097	Sequence 771097,	C 766	14	25.0	569	4	US-09-925-065A-648456	Sequence 648456,
C 694	14	25.0	515	4	US-09-925-065A-824833	Sequence 824833,	C 767	14	25.0	569	4	US-09-925-065A-803579	Sequence 803579,
C 695	14	25.0	519	4	US-09-925-065A-839336	Sequence 839336,	C 768	14	25.0	569	4	US-09-925-065A-803580	Sequence 803580,
C 696	14	25.0	519	6	US-10-029-386-946	Sequence 946, Ap	C 769	14	25.0	572	4	US-09-925-065A-783997	Sequence 783997,
C 697	14	25.0	524	4	US-09-925-065A-182227	Sequence 182227,	C 770	14	25.0	573	4	US-09-925-065A-191873	Sequence 191873,
C 698	14	25.0	526	4	US-09-925-065A-822800	Sequence 822800,	C 771	14	25.0	573	4	US-09-925-065A-191874	Sequence 191874,
C 699	14	25.0	529	4	US-09-925-065A-524175	Sequence 524175,	C 772	14	25.0	573	4	US-09-925-065A-191875	Sequence 191875,
C 700	14	25.0	529	4	US-09-925-065A-524176	Sequence 524176,	C 773	14	25.0	573	4	US-09-925-065A-191878	Sequence 191878,
C 701	14	25.0	530	4	US-09-925-065A-945717	Sequence 945717,	C 774	14	25.0	573	4	US-09-925-065A-377779	Sequence 377779,
C 702	14	25.0	531	4	US-09-925-065A-855557	Sequence 855557,	C 775	14	25.0	573	4	US-09-925-065A-747168	Sequence 747168,
C 703	14	25.0	532	4	US-09-925-065A-946293	Sequence 946293,	C 776	14	25.0	573	4	US-09-925-065A-747169	Sequence 747169,
C 704	14	25.0	534	4	US-09-925-065A-227750	Sequence 227750,	C 777	14	25.0	574	6	US-10-029-366-9253	Sequence 8253, Ap
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977 14 25.0 672 4 US-09-925-065A-93824 Sequence 93824, A
978 14 25.0 677 5 US-10-027-632-134305 Sequence 134305,
979 14 25.0 677 6 US-10-027-632-134305 Sequence 134305,
980 14 25.0 678 5 US-10-027-632-113698 Sequence 113698,
981 14 25.0 678 5 US-10-027-632-113698 Sequence 113698,
982 14 25.0 678 6 US-10-027-632-113698 Sequence 113698,
983 14 25.0 678 6 US-10-027-632-113699 Sequence 113699,
984 14 25.0 680 5 US-10-027-632-98730 Sequence 98730, A
985 14 25.0 680 6 US-10-027-632-98730 Sequence 98730, A
986 14 25.0 683 3 US-09-917-800A-9 Sequence 9, Appli
987 14 25.0 688 4 US-09-925-065A-868519 Sequence 868519,
988 14 25.0 691 8 US-10-767-795-5575 Sequence 5575, Ap
989 14 25.0 694 4 US-09-925-065A-895268 Sequence 895268,
990 14 25.0 696 4 US-09-925-065A-895214 Sequence 895214,
991 14 25.0 696 4 US-09-925-065A-944150 Sequence 944150,
992 14 25.0 701 4 US-09-925-065A-949140 Sequence 949140,
993 14 25.0 712 4 US-09-925-065A-58613 Sequence 58613, A
994 14 25.0 716 3 US-09-764-868-475 Sequence 475, App
995 14 25.0 717 6 US-10-264-237-1390 Sequence 1390, Ap
996 14 25.0 718 3 US-09-816-079-5 Sequence 5, Appli
997 14 25.0 719 4 US-09-925-065A-83170 Sequence 83170, A
998 14 25.0 719 5 US-10-027-632-247785 Sequence 247785,
999 14 25.0 719 5 US-10-027-632-247786 Sequence 247786,
c1000 14 25.0 719 6 US-10-027-632-247785 Sequence 247785,
```

## ALIGNMENTS

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RESULT 1
US-10-376-323-66/c
; Sequence 66, Application US/10376323
; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BACAPB4L
US-10-376-323-66
```

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Query Match 41.1%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 7 CGTGTATGTTGAATGCTCATCC 29
DB 23 CGTGTATGTTGAATGCTCATCC 1
```

```
RESULT 2
US-11-018-377-66/c
; Sequence 66, Application US/11018377
; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
```

```
; APPLICANT: Norwood, David A.
; APPLICANT: Masielost, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 66
; LENGTH: 23
; TYPE: DNA
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: BACAPB4L
US-11-018-377-66
```

```
Query Match 41.1%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.01;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 7 CGTGTATGTTGAATGCTCATCC 29
DB 23 CGTGTATGTTGAATGCTCATCC 1
```

```
RESULT 3
US-10-424-599-121945
; Sequence 121945, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 121945
; LENGTH: 631
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_81122C.1
US-10-424-599-121945
```

```
Query Match 32.1%; Score 18; DB 7; Length 631;
Best Local Similarity 100.0%; Pred. No. 5.5;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 GCATTCGTTGTTGTTG 18
DB 433 GCATTCGTTGTTGTTG 450
```

```
RESULT 4
US-09-924-035A-660/c
; Sequence 660, Application US/09924035A
; Patent No. US20020142319A1
; GENERAL INFORMATION:
; APPLICANT: Gr-lach, Jim
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE REFERENCE: 2011US
; CURRENT APPLICATION NUMBER: US/09/924,035A
; CURRENT FILING DATE: 2000-08-11
```



; PRIOR APPLICATION NUMBER: US 60/148,784  
; PRIOR FILING DATE: 1999-08-13  
; NUMBER OF SEQ ID NOS: 900  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 660  
; LENGTH: 100  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-924-035A-660

Query Match 30.4%; Score 17; DB 3; Length 100;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 12 TTGTTGAATGCTCATC 28  
Db 23 TATGTTGAATGCTCATC 7

RESULT 5  
US-09-938-842A-37  
; Sequence 37, Application US/09938842A  
; Patent No. US20020160378A1  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO: 37  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-37

Query Match 30.4%; Score 17; DB 3; Length 201;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TTCGCTGATGTTGAA 20  
Db 161 TTCGCTGATGTTGAA 177

RESULT 6  
US-09-938-842A-37  
; Sequence 37, Application US/09938842A  
; Publication No. US20040009476A9  
; GENERAL INFORMATION:  
; APPLICANT: Harper, Jeff  
; APPLICANT: Kreps, Joel  
; APPLICANT: Wang, Xun  
; APPLICANT: Zhu, Tong  
; TITLE OF INVENTION: STRESS-REGULATED GENES OF PLANTS, TRANSGENIC PLANTS CONTAINING  
; FILE REFERENCE: SCRIPI300-3  
; CURRENT APPLICATION NUMBER: US/09/938,842A  
; CURRENT FILING DATE: 2001-08-24  
; PRIOR APPLICATION NUMBER: US 60/227,866  
; PRIOR FILING DATE: 2000-08-24  
; PRIOR APPLICATION NUMBER: US 60/264,647  
; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/300,111  
; PRIOR FILING DATE: 2001-06-22  
; NUMBER OF SEQ ID NOS: 5379  
; SEQ ID NO: 37  
; LENGTH: 201  
; TYPE: DNA  
; ORGANISM: Arabidopsis thaliana  
US-09-938-842A-37

Query Match 30.4%; Score 17; DB 3; Length 201;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 TTCGCTGATGTTGAA 20  
Db 161 TTCGCTGATGTTGAA 177

RESULT 7  
US-09-895-040A-34  
; Sequence 34, Application US/09895040A  
; Patent No. US20020123474A1  
; GENERAL INFORMATION:  
; APPLICANT: Shannon, Mark  
; APPLICANT: Ji, Yonggang  
; TITLE OF INVENTION: HUMAN GTP-RHO BINDING PROTEIN 2  
; FILE REFERENCE: AROMICA-11  
; CURRENT APPLICATION NUMBER: US/09/895,040A  
; CURRENT FILING DATE: 2001-06-29  
; PRIOR APPLICATION NUMBER: PCT/US01/00666  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00667  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00664  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00669  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00665  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00668  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00663  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: PCT/US01/00670  
; PRIOR FILING DATE: 2001-01-30  
; PRIOR APPLICATION NUMBER: US 09/864,761  
; PRIOR FILING DATE: 2001-05-23  
; NUMBER OF SEQ ID NOS: 180  
; SOFTWARE: Aeonica Sequence Listing Engine  
; SEQ ID NO: 34  
; LENGTH: 500  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-895-040A-34

Query Match 30.4%; Score 17; DB 3; Length 500;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 9 TGGATGTTGAATGCTC 25  
Db 287 TGGATGTTGAATGCTC 303

RESULT 8  
US-10-027-632-185154  
; Sequence 185154, Application US/10027632  
; Publication No. US20020198371A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
; FILE REFERENCE: 108627.129



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; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185154
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-185154

Query Match
Best Local Similarity 30.4%; Score 17; DB 5; Length 622;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24
DB 548 GTGGTATGTTGAATGCT 564

RESULT 9
US-10-027-632-185155
; Sequence 185155, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185155
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-185155

Query Match
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24
DB 548 GTGGTATGTTGAATGCT 564
```

```

RESULT 10
US-10-027-632-185156
; Sequence 185156, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185156
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-185156

Query Match
Best Local Similarity 30.4%; Score 17; DB 5; Length 622;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24
DB 548 GTGGTATGTTGAATGCT 564

RESULT 11
US-10-027-632-185157
; Sequence 185157, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 185157
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
; US-10-027-632-185157
```



```
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185157

Query Match      30.4%; Score 17; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 12
US-10-027-632-185158
; Sequence 185158, Application US/10027632
; Publication No. US20020198372A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMERASE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185158
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185158

Query Match      30.4%; Score 17; DB 5; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 13
US-10-027-632-185154
; Sequence 185154, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMERASE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218

; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185154
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185155

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 14
US-10-027-632-185155
; Sequence 185155, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMERASE: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
; PRIOR FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185155
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185155

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 15
US-10-027-632-185156
; Sequence 185156, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
```



```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185156
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185156

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 16
US-10-027-632-185157
; Sequence 185157, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185157
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185157

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564
```

```

; TITLE OF INVENTION: Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185158
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185158

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 17
US-10-027-632-185158
; Sequence 185158, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 185158
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-185158

Query Match      30.4%; Score 17; DB 6; Length 622;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      8 GTGGTATGTTGAATGCT 24
Db      548 GTGGTATGTTGAATGCT 564

RESULT 18
US-10-027-632-118722/c
; Sequence 118722, Application US/10027632
; Publication No. US20020198371A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; FILE REFERENCE: 108827.129
; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 118722
; LENGTH: 622
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-118722/c
```



SEQ ID NO 118722  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-118722

Query Match 30.4%: Score 17; DB 5; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24  
|||||  
Db 373 GTGGTATGTTGAATGCT 357

RESULT 19  
US-10-027-632-118722/c  
Sequence 118722, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 118722  
LENGTH: 1142  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-118722

Query Match 30.4%: Score 17; DB 6; Length 1142;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24  
|||||  
Db 373 GTGGTATGTTGAATGCT 357

RESULT 20  
US-10-027-632-208605/c  
Sequence 208605, Application US/10027632  
Publication No. US20020198371A1  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 208605  
LENGTH: 1651  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-208605

Query Match 30.4%: Score 17; DB 5; Length 1651;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24  
|||||  
Db 1406 GTGGTATGTTGAATGCT 1390

RESULT 21  
US-10-027-632-208605/c  
Sequence 208605, Application US/10027632  
Publication No. US20030204075A9  
GENERAL INFORMATION:

APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide  
FILE REFERENCE: 108827.129  
CURRENT APPLICATION NUMBER: US/10/027,632  
CURRENT FILING DATE: 2002-04-30  
PRIOR APPLICATION NUMBER: US 60/218,006  
PRIOR FILING DATE: 2000-07-12  
PRIOR APPLICATION NUMBER: US 60/198,676  
PRIOR FILING DATE: 2000-04-20  
PRIOR APPLICATION NUMBER: US 60/193,483  
PRIOR FILING DATE: 2000-03-29  
PRIOR APPLICATION NUMBER: US 60/185,218  
PRIOR FILING DATE: 2000-02-24  
PRIOR APPLICATION NUMBER: US 60/167,363  
PRIOR FILING DATE: 1999-11-23  
PRIOR APPLICATION NUMBER: US 60/156,358  
PRIOR FILING DATE: 1999-09-28  
PRIOR APPLICATION NUMBER: US 60/146,002  
PRIOR FILING DATE: 1999-08-09  
NUMBER OF SEQ ID NOS: 325720  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 208605  
LENGTH: 1651  
TYPE: DNA  
ORGANISM: Human  
US-10-027-632-208605

Query Match 30.4%: Score 17; DB 6; Length 1651;  
Best Local Similarity 100.0%; Pred. No. 19;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 GTGGTATGTTGAATGCT 24  
|||||  
Db 1406 GTGGTATGTTGAATGCT 1390

RESULT 22  
US-09-925-065A-692911/c  
Sequence 692911, Application US/09925065A  
Publication No. US20050228172A9  
GENERAL INFORMATION:



```
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692911
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692911
```

```
Query Match      30.4%; Score 17; DB 4; Length 1930;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 GTGGTATGTTGAATGCT 24
Db      357 GTGGTATGTTGAATGCT 341
```

```
RESULT 23
US-09-925-065A-692912/C
; Sequence 692912, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692912
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692912
```

```
Query Match      30.4%; Score 17; DB 4; Length 1930;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 GTGGTATGTTGAATGCT 24
Db      357 GTGGTATGTTGAATGCT 341
```

```
RESULT 24
US-09-925-065A-692913/C
```

```
; Sequence 692913, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692913
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692913
```

```
Query Match      30.4%; Score 17; DB 4; Length 1930;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 GTGGTATGTTGAATGCT 24
Db      357 GTGGTATGTTGAATGCT 341
```

```
RESULT 25
US-09-925-065A-692914/C
; Sequence 692914, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692914
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692914
```

```
Query Match      30.4%; Score 17; DB 4; Length 1930;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 GTGGTATGTTGAATGCT 24
Db      357 GTGGTATGTTGAATGCT 341
```



```
RESULT 26
US-09-925-065A-692915/C
; Sequence 692915, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692915
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-692915

Query Match      30.4%; Score 17; DB 4; Length 1930;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 GTGGTATGTTGATGCT 24
Db      357 GTGGTATGTTGATGCT 341

RESULT 27
US-11-060-756-118490/C
; Sequence 118490, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118490
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-118490

Query Match      28.6%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TGCTCATCCGATCCA 36
Db      20 TGCTCATCCGATCCA 5

RESULT 28
US-11-060-756-118491/C
; Sequence 118491, Application US/11060756
; Publication No. US20050221354A1
; GENERAL INFORMATION:
; APPLICANT: Wyeth
; APPLICANT: Mounts, William Martin
; TITLE OF INVENTION: Nucleic Acid Arrays for Monitoring Expression Profiles of Drug
; TITLE OF INVENTION: Target Genes
; FILE REFERENCE: AM101083 (031896-042000)
; CURRENT APPLICATION NUMBER: US/11/060,756
; CURRENT FILING DATE: 2005-02-18
; NUMBER OF SEQ ID NOS: 303284
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 118491
; LENGTH: 25
; TYPE: DNA
; ORGANISM: probe
US-11-060-756-118491

Query Match      28.6%; Score 16; DB 10; Length 25;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      21 TGCTCATCCGATCCA 36
Db      20 TGCTCATCCGATCCA 5

RESULT 29
US-10-484-232-2/C
; Sequence 2, Application US/10484232
; Publication No. US20040259252A1
; GENERAL INFORMATION:
; APPLICANT: Sanders, Mitchell C.
; APPLICANT: Hamilton, Maureen
; TITLE OF INVENTION: A Vector Containing an Enhanced p15A
; TITLE OF INVENTION: Origin of Replication
; FILE REFERENCE: 3265.1000-003
; CURRENT APPLICATION NUMBER: US/10/484,232
; CURRENT FILING DATE: 2004-01-16
; PRIOR APPLICATION NUMBER: PCT/US02/23089
; PRIOR FILING DATE: 2002-07-18
; PRIOR APPLICATION NUMBER: 60/306,344
; PRIOR FILING DATE: 2001-07-18
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 30
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: PCR Primer
US-10-484-232-2

Query Match      28.6%; Score 16; DB 8; Length 30;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
Db      25 TGAATGCTCATCCGGA 10

RESULT 30
US-10-767-701-16720
; Sequence 16720, Application US/10767701
; Publication No. US20040172684A1
; GENERAL INFORMATION:
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated with
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53535)B
; CURRENT APPLICATION NUMBER: US/10/767,701
; CURRENT FILING DATE: 2004-01-29
; NUMBER OF SEQ ID NOS: 63128
```



```
; SEQ ID NO 16720
; LENGTH: 213
; TYPE: DNA
; ORGANISM: Sorghum bicolor
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3481-023-P1-K1-D10
US-10-767-701-16720

Query Match      28.6%; Score 16; DB 7; Length 213;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      22 GCTCATCCGATCCGAG 37
      |||
Db      44 GCTCATCCGATCCGAG 59

RESULT 31
US-10-450-763-3300
; Sequence 3300, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 3300
; LENGTH: 324
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (52)..(258)
; OTHER INFORMATION: 73% homologous to Homo sapiens CAT-SP-C hybrid
US-10-450-763-3300

Query Match      28.6%; Score 16; DB 9; Length 324;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
      |||
Db      191 TGAATGCTCATCCGGA 206

RESULT 32
US-10-424-599-112332
; Sequence 112332, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa Thomas J
; APPLICANT: Kovalic David K
; APPLICANT: Zhou Yihua
; APPLICANT: Cao Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated with
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; PRIOR FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 285684
; SEQ ID NO 112332
; LENGTH: 364
; TYPE: DNA
```

```
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_7244C.1
US-10-424-599-112332

Query Match      28.6%; Score 16; DB 7; Length 364;
Best Local Similarity 100.0%; Pred. No. 77;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      34 CCAGAGCAATGAGAA 49
      |||
Db      181 CCAGAGCAATGAGAA 196

RESULT 33
US-10-450-763-7475/C
; Sequence 7475, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 7475
; LENGTH: 405
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (6)..(146)
; OTHER INFORMATION: 97% homologous to Cloning vector pZC320 SopA, accession number
US-10-450-763-7475

Query Match      28.6%; Score 16; DB 9; Length 405;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
      |||
Db      185 TGAATGCTCATCCGGA 170

RESULT 34
US-10-450-763-13740/C
; Sequence 13740, Application US/10450763
; Publication No. US20050196754A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: NOVEL NUCLEIC ACIDS AND POLYPEPTIDES
; FILE REFERENCE: 790CIP3/US
; CURRENT APPLICATION NUMBER: US/10/450,763
; PRIOR FILING DATE: 2003-06-11
; PRIOR APPLICATION NUMBER: PCT/US01/08631
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/540,217
; PRIOR FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: 09/649,167
; PRIOR FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 60736
; SOFTWARE: Custom
; SEQ ID NO 13740
; LENGTH: 496
; TYPE: DNA
```



```

; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SIMILAR
; LOCATION: (1) .. (1158)
; OTHER INFORMATION: 91% homologous to Homo sapiens putative p150.accession number
; OTHER INFORMATION: US3572, Smith-Waterman Score=1849.
US-10-450-763-13740
```

```
Query Match          28.6%; Score 16; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      17 TGAATGCTCATCCGGA 32
Db      39 TGAATGCTCATCCGGA 24
```

```

RESULT 35
US-09-925-065A-334218
; Sequence 334218, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 334218
; LENGTH: 526
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-334218
```

```
Query Match          28.6%; Score 16; DB 4; Length 526;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      40 GCATGCAATTACAC 55
Db      239 GCATGCAATTACAC 254
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```

RESULT 36
US-10-333-184-124
; Sequence 124, Application US/10333184
; Publication No. US20040088762A1
; GENERAL INFORMATION:
; APPLICANT: Reddy, Avutu
; APPLICANT: Larrinua, Ignacio
; APPLICANT: Skokut, Thomas
; APPLICANT: Smith, Doug
; APPLICANT: Hu, Zihua
; APPLICANT: Ruegger, Max
; APPLICANT: Shukla, Vipula
; APPLICANT: Bauer, Teresa
; APPLICANT: Weglartz, Ted
; APPLICANT: Blakslee, Beth
; APPLICANT: Oriado, Jeremiah
; APPLICANT: Savickas, Philip
; APPLICANT: McCreary, David
```

```

; APPLICANT: Miller, Barbara
; APPLICANT: della-Cioppa, Gregory
; TITLE OF INVENTION: Nucleic Acid Compositions Conferring Dwarfism Phenotype
; FILE REFERENCE: DOW-04681
; CURRENT APPLICATION NUMBER: US/10/333,184
; CURRENT FILING DATE: 2003-10-10
; PRIOR APPLICATION NUMBER: 60/219,809
; PRIOR FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 124
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Nicotiana benthamiana
US-10-333-184-124
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Query Match          28.6%; Score 16; DB 7; Length 561;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      36 AGAGCAATGCAATT 51
Db      492 AGAGCAATGCAATT 507
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RESULT 37
US-10-972-079-73594/C
; Sequence 73594, Application US/10972079
; Publication No. US20050153317A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: ROSENFELD, David
; APPLICANT: KERR, Richard
; APPLICANT: BATES, Stephen
; APPLICANT: HOLM, Tom
; TITLE OF INVENTION: METHODS & SYSTEMS FOR INFERRING TRAITS TO BREED & MANAGE NON-B
; FILE REFERENCE: MM1110-2
; CURRENT APPLICATION NUMBER: US/10/972,079
; CURRENT FILING DATE: 2004-10-22
; PRIOR APPLICATION NUMBER: US 60/514,333
; PRIOR FILING DATE: 2003-10-24
; NUMBER OF SEQ ID NOS: 96631
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 73594
; LENGTH: 575
; TYPE: DNA
; ORGANISM: Chicken
US-10-972-079-73594
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Query Match          28.6%; Score 16; DB 9; Length 575;
Best Local Similarity 100.0%; Pred. No. 75;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      35 CAGAGCAATGCAAT 50
Db      157 CAGAGCAATGCAAT 142
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```

RESULT 38
US-09-925-065A-169496/C
; Sequence 169496, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
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; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 169496
; LENGTH: 584
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-169496

Query Match      28.6%; Score 16; DB 4; Length 584;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGCA 32
      |||||||
Db      468 TGAATGCTCATCCGCA 453

RESULT 39
US-09-925-065A-266664
; Sequence 266664, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 266664
; LENGTH: 593
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-266664

Query Match      28.6%; Score 16; DB 4; Length 593;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      39 AGCAATGAGATTACA 54
      |||||||
Db      65 AGCAATGAGATTACA 80

RESULT 40
US-09-925-065A-902120/c
; Sequence 902120, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
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; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 902120
; LENGTH: 595
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-902120

Query Match      28.6%; Score 16; DB 4; Length 595;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GTATGTTGAATGCTCA 26
      |||||||
Db      518 GTATGTTGAATGCTCA 503

Search completed: April 12, 2006, 06:03:37
Job time : 170.689 secs
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OM nucleic - nucleic search, using sw model

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Title: US-10-712-654-26

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Searched: 9281099 seqs, 2013915447 residues

Word size: 1

Total number of hits satisfying chosen parameters: 18561424

Minimum DB seq length: 0

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Published Applications NA\_New:\*  
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10: /SIDS5/ptcodata/2/pubpna/US10\_NEW\_PUB.seq3:\*  
11: /SIDS5/ptcodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
12: /SIDS5/ptcodata/2/pubpna/US11\_NEW\_PUB.seq3:\*  
13: /SIDS5/ptcodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
14: /SIDS5/ptcodata/2/pubpna/US11\_NEW\_PUB.seq4:\*  
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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Score	Query	Length	ID	Description
No.					
C 1	30.4	1930	6	US-09-925-065A-692911	Sequence 692911,
C 2	30.4	1930	6	US-09-925-065A-692912	Sequence 692912,
C 3	30.4	1930	6	US-09-925-065A-692913	Sequence 692913,
C 4	30.4	1930	6	US-09-925-065A-692914	Sequence 692914,
C 5	30.4	1930	6	US-09-925-065A-692915	Sequence 692915,
C 6	28.6	526	6	US-09-925-065A-334218	Sequence 334218,
C 7	28.6	536	10	US-10-301-480-407764	Sequence 407764,
C 8	28.6	536	10	US-10-301-480-1021173	Sequence 1021173,
C 9	28.6	567	10	US-10-301-480-261442	Sequence 261442,
C 10	28.6	567	10	US-10-301-480-874851	Sequence 874851,
C 11	28.6	584	6	US-09-925-065A-169496	Sequence 169496,
C 12	28.6	591	11	US-11-116-881A-840	Sequence 840, App
C 13	28.6	593	6	US-09-925-065A-266664	Sequence 266664,
C 14	28.6	595	6	US-09-925-065A-902120	Sequence 902120,
C 15	28.6	627	6	US-09-925-065A-315548	Sequence 315548,
C 16	28.6	627	6	US-09-925-065A-315549	Sequence 315549,
C 17	28.6	628	10	US-10-301-480-390555	Sequence 390555,
C 18	28.6	628	10	US-10-301-480-390556	Sequence 390556,

19	28.6	628	10	US-10-301-480-1003964	Sequence 1003964,
C 20	28.6	628	10	US-10-301-480-1003965	Sequence 1003965,
C 21	28.6	727	6	US-09-925-065A-923129	Sequence 923129,
C 22	28.6	728	10	US-10-301-480-562417	Sequence 562417,
C 23	28.6	728	10	US-10-301-480-1175826	Sequence 1175826,
C 24	28.6	861	14	US-11-194-246-499	Sequence 499, App
C 25	28.6	935	11	US-11-218-787B-3	Sequence 3, App1
C 26	28.6	1080	11	US-11-218-787B-6	Sequence 6, App1
C 27	28.6	1188	11	US-11-235-254-18	Sequence 18, App1
C 28	28.6	3011	8	US-10-750-185-40818	Sequence 40818, A
C 29	28.6	3011	8	US-10-750-623-40818	Sequence 40818, A
C 30	28.6	3914	14	US-11-134-795-8	Sequence 8, App1
C 31	28.6	3999	9	US-10-933-746-40	Sequence 40, App1
C 32	28.6	4019	9	US-10-933-746-39	Sequence 39, App1
C 33	28.6	4428	11	US-11-251-821-41	Sequence 41, App1
C 34	28.6	4470	11	US-11-251-821-40	Sequence 40, App1
C 35	28.6	4627	11	US-11-251-821-42	Sequence 42, App1
C 36	28.6	4627	11	US-11-251-821-43	Sequence 43, App1
C 37	28.6	4907	14	US-11-134-795-1	Sequence 1, App1
C 38	28.6	4922	14	US-11-183-036-5	Sequence 5, App1
C 39	28.6	4938	14	US-11-181-148-1	Sequence 1, App1
C 40	28.6	5027	14	US-11-183-036-4	Sequence 4, App1
C 41	28.6	5190	10	US-10-505-844-1	Sequence 1, App1
C 42	28.6	5558	13	US-11-077-550-137	Sequence 137, App1
C 43	28.6	5584	11	US-11-251-821-39	Sequence 39, App1
C 44	28.6	5676	14	US-11-134-795-5	Sequence 5, App1
C 45	28.6	6171	14	US-11-134-795-3	Sequence 3, App1
C 46	28.6	6191	11	US-11-083-327-25	Sequence 25, App1
C 47	28.6	6435	14	US-11-134-795-7	Sequence 7, App1
C 48	28.6	6464	11	US-11-251-821-38	Sequence 38, App1
C 49	28.6	6525	14	US-11-181-148-3	Sequence 3, App1
C 50	28.6	7487	14	US-11-211-339-30	Sequence 30, App1
C 51	28.6	8408	11	US-11-181-148-4	Sequence 4, App1
C 52	28.6	9430	14	US-11-137-315A-34	Sequence 34, App1
C 53	28.6	9808	8	US-10-966-483-33	Sequence 33, App1
C 54	28.6	9808	14	US-11-021-441-33	Sequence 43, App1
C 55	28.6	12604	14	US-11-137-315A-44	Sequence 44, App1
C 56	28.6	12604	14	US-11-180-074-39	Sequence 39, App1
C 57	28.6	14561	14	US-11-137-315A-47	Sequence 47, App1
C 58	28.6	14561	14	US-11-180-074-42	Sequence 42, App1
C 59	28.6	48000	14	US-11-159-597-20	Sequence 20, App1
C 60	28.6	48000	14	US-11-117-187-186	Sequence 186, App
C 61	28.6	67088	14	US-11-117-187-189	Sequence 189, App
C 62	28.6	83391	14	US-11-117-187-194	Sequence 194, App
C 63	28.6	92584	14	US-11-117-187-194	Sequence 194, App
C 64	28.6	95223	14	US-11-117-187-188	Sequence 188, App
C 65	28.6	121001	14	US-11-117-187-190	Sequence 190, App
C 66	28.6	452	6	US-09-925-065A-583100	Sequence 583100,
C 67	28.6	454	14	US-11-128-061-2070	Sequence 2070, App
C 68	28.6	454	14	US-11-128-061-5712	Sequence 5712, App
C 69	28.6	454	14	US-11-128-049-2070	Sequence 2070, App
C 70	28.6	454	14	US-11-128-049-5712	Sequence 5712, App
C 71	28.6	467	6	US-09-925-065A-259142	Sequence 259142,
C 72	28.6	468	10	US-10-301-480-337706	Sequence 337706,
C 73	28.6	468	10	US-10-301-480-951115	Sequence 951115,
C 74	28.6	477	6	US-09-925-065A-739668	Sequence 739668,
C 75	28.6	4944	6	US-09-925-065A-855641	Sequence 855641,
C 76	28.6	4944	6	US-09-925-065A-855642	Sequence 855642,
C 77	28.6	4944	6	US-09-925-065A-855643	Sequence 855643,
C 78	28.6	502	6	US-09-925-065A-784577	Sequence 784577,
C 79	28.6	505	6	US-09-925-065A-846042	Sequence 846042,
C 80	28.6	513	9	US-10-301-480-209270	Sequence 209270,
C 81	28.6	513	10	US-10-301-480-822679	Sequence 822679,
C 82	28.6	520	10	US-10-301-480-292313	Sequence 292313,
C 83	28.6	520	10	US-10-301-480-905722	Sequence 905722,
C 84	28.6	524	6	US-09-925-065A-109645	Sequence 109645,
C 85	28.6	524	6	US-09-925-065A-204153	Sequence 204153,
C 86	28.6	524	6	US-09-925-065A-836063	Sequence 836063,
C 87	28.6	527	10	US-10-301-480-373239	Sequence 373239,
C 88	28.6	527	10	US-10-301-480-986648	Sequence 986648,
C 89	28.6	530	6	US-09-925-065A-176353	Sequence 176353,
C 90	28.6	530	6	US-09-925-065A-176354	Sequence 176354,
C 91	28.6	538	6	US-09-925-065A-421768	Sequence 421768,



C 92	15	26.8	541	6	US-09-925-065A-296404	Sequence 296404,	155	15	26.8	1215	11	US-11-096-668A-22151	Sequence 22151,
C 93	15	26.8	552	6	US-09-925-065A-296362	Sequence 296362,	C 166	15	26.8	1400	14	US-11-128-061-4715	Sequence 4715, A
C 94	15	26.8	554	10	US-10-301-480-486501	Sequence 486501,	C 167	15	26.8	1400	14	US-11-128-049-4715	Sequence 4715, A
C 95	15	26.8	554	10	US-10-301-480-1099910	Sequence 1099910,	C 168	15	26.8	1438	9	US-10-301-480-84068	Sequence 84068, A
C 96	15	26.8	556	10	US-10-301-480-575961	Sequence 575961,	C 169	15	26.8	1438	9	US-10-301-480-84069	Sequence 84069, A
C 97	15	26.8	556	10	US-10-301-480-1189390	Sequence 1189390,	C 170	15	26.8	1438	9	US-10-301-480-84070	Sequence 84070, A
C 98	15	26.8	557	6	US-09-925-065A-20333	Sequence 20333, A	C 171	15	26.8	1438	10	US-10-301-480-697477	Sequence 697477, A
C 99	15	26.8	557	6	US-10-301-480-121570	Sequence 121570,	C 172	15	26.8	1438	10	US-10-301-480-697478	Sequence 697478, A
C 100	15	26.8	557	10	US-10-301-480-734979	Sequence 734979,	C 173	15	26.8	1438	10	US-10-301-480-697479	Sequence 697479, A
C 101	15	26.8	564	9	US-10-301-480-23478	Sequence 23478, A	C 174	15	26.8	1600	8	US-10-750-165-26887	Sequence 26887, A
C 102	15	26.8	564	9	US-10-301-480-23479	Sequence 23479, A	C 175	15	26.8	1600	8	US-10-750-165-26887	Sequence 26887, A
C 103	15	26.8	564	9	US-10-301-480-23480	Sequence 23480, A	C 176	15	26.8	1649	8	US-10-750-165-62130	Sequence 62130, A
C 104	15	26.8	564	10	US-10-301-480-636887	Sequence 636887, A	C 177	15	26.8	1649	8	US-10-750-165-62130	Sequence 62130, A
C 105	15	26.8	564	10	US-10-301-480-636888	Sequence 636888,	C 178	15	26.8	1693	9	US-10-301-480-90871	Sequence 90871, A
C 106	15	26.8	564	10	US-10-301-480-636889	Sequence 636889,	C 179	15	26.8	1693	9	US-10-301-480-90872	Sequence 90872, A
C 107	15	26.8	567	9	US-10-301-480-209271	Sequence 209271,	C 180	15	26.8	1693	10	US-10-301-480-704280	Sequence 704280, A
C 108	15	26.8	567	9	US-10-301-480-209272	Sequence 209272,	C 181	15	26.8	1693	10	US-10-301-480-704281	Sequence 704281, A
C 109	15	26.8	567	9	US-10-301-480-209273	Sequence 209273,	C 182	15	26.8	2289	6	US-09-925-065A-1527	Sequence 1527, App
C 110	15	26.8	567	10	US-10-301-480-822680	Sequence 822680,	C 183	15	26.8	2289	9	US-10-301-480-102764	Sequence 102764, A
C 111	15	26.8	567	10	US-10-301-480-822681	Sequence 822681,	C 184	15	26.8	2289	10	US-10-301-480-116173	Sequence 116173, A
C 112	15	26.8	567	10	US-10-301-480-822682	Sequence 822682,	C 185	15	26.8	2488	8	US-10-750-165-44429	Sequence 44429, A
C 113	15	26.8	573	6	US-09-925-065A-927577	Sequence 927577,	C 186	15	26.8	2488	8	US-10-750-165-44429	Sequence 44429, A
C 114	15	26.8	576	6	US-09-925-065A-419096	Sequence 419096,	C 187	15	26.8	2695	8	US-10-750-165-47378	Sequence 47378, A
C 115	15	26.8	579	6	US-09-925-065A-960911	Sequence 960911,	C 188	15	26.8	2695	8	US-10-750-165-47378	Sequence 47378, A
C 116	15	26.8	584	6	US-09-925-065A-109641	Sequence 109641,	C 189	15	26.8	2826	14	US-11-121-419-18	Sequence 18, App
C 117	15	26.8	584	6	US-09-925-065A-109647	Sequence 109647,	C 190	15	26.8	2962	14	US-11-128-061-1073	Sequence 1073, A
C 118	15	26.8	584	6	US-09-925-065A-109648	Sequence 109648,	C 191	15	26.8	2962	14	US-11-128-049-1073	Sequence 1073, A
C 119	15	26.8	585	10	US-10-301-480-484253	Sequence 484253,	C 192	15	26.8	3123	14	US-11-136-527-2842	Sequence 2842, A
C 120	15	26.8	585	10	US-10-301-480-1097662	Sequence 1097662,	C 193	15	26.8	4156	11	US-11-072-512-321	Sequence 321, App
C 121	15	26.8	586	6	US-09-925-065A-571143	Sequence 571143,	C 194	15	26.8	1805704	14	US-11-121-086-70	Sequence 70, App
C 122	15	26.8	586	10	US-10-301-480-507523	Sequence 507523,	C 195	15	26.8	3481071	9	US-10-330-773-122	Sequence 122, App
C 123	15	26.8	586	10	US-10-301-480-1120932	Sequence 1120932,	C 196	15	26.8	19	12	US-11-101-244-105863	Sequence 105863, A
C 124	15	26.8	589	6	US-09-925-065A-441855	Sequence 441855,	C 197	14	25.0	19	13	US-11-083-784-105863	Sequence 105863, A
C 125	15	26.8	594	6	US-09-925-065A-338207	Sequence 338207,	C 198	14	25.0	24	8	US-10-310-914A-27404	Sequence 27404, A
C 126	15	26.8	598	6	US-09-925-065A-536772	Sequence 536772,	C 199	14	25.0	25	9	US-10-932-182A-22772	Sequence 22772, A
C 127	15	26.8	600	6	US-09-925-065A-327405	Sequence 327405,	C 200	14	25.0	25	9	US-10-932-182A-22772	Sequence 22772, A
C 128	15	26.8	609	6	US-09-925-065A-786545	Sequence 786545,	C 201	14	25.0	25	14	US-11-121-849-216137	Sequence 216137, A
C 129	15	26.8	614	10	US-10-301-480-502550	Sequence 502550,	C 202	14	25.0	25	14	US-11-121-849-263074	Sequence 263074, A
C 130	15	26.8	614	10	US-10-301-480-1115999	Sequence 1115999,	C 203	14	25.0	25	14	US-11-121-849-599387	Sequence 599387, A
C 131	15	26.8	616	6	US-09-925-065A-683076	Sequence 683076,	C 204	14	25.0	27	14	US-11-101-851-17	Sequence 17, App
C 132	15	26.8	621	6	US-09-925-065A-556974	Sequence 556974,	C 205	14	25.0	28	7	US-10-503-590A-6	Sequence 6, App11
C 133	15	26.8	627	6	US-09-925-065A-703071	Sequence 703071,	C 206	14	25.0	119	8	US-10-310-914A-6803	Sequence 6803, App
C 134	15	26.8	627	6	US-09-925-065A-703072	Sequence 703072,	C 207	14	25.0	201	8	US-10-995-561-56396	Sequence 56396, A
C 135	15	26.8	627	6	US-09-925-065A-703073	Sequence 703073,	C 208	14	25.0	201	14	US-11-124-368A-5198	Sequence 5198, A
C 136	15	26.8	631	6	US-09-925-065A-777272	Sequence 777272,	C 209	14	25.0	210	9	US-10-932-182A-1527	Sequence 1527, App
C 137	15	26.8	638	6	US-09-925-065A-538354	Sequence 538354,	C 210	14	25.0	210	9	US-10-932-182A-1527	Sequence 1527, App
C 138	15	26.8	645	9	US-10-301-480-51839	Sequence 51839, A	C 211	14	25.0	224	6	US-09-925-065A-577521	Sequence 577521, A
C 139	15	26.8	645	9	US-10-301-480-51840	Sequence 51840, A	C 212	14	25.0	353	6	US-09-925-065A-486352	Sequence 486352, A
C 140	15	26.8	645	9	US-10-301-480-51841	Sequence 51841, A	C 213	14	25.0	353	6	US-09-925-065A-486354	Sequence 486354, A
C 141	15	26.8	645	10	US-10-301-480-665248	Sequence 665248,	C 214	14	25.0	391	6	US-09-925-065A-145802	Sequence 145802, A
C 142	15	26.8	645	10	US-10-301-480-665249	Sequence 665249,	C 215	14	25.0	391	6	US-09-925-065A-145803	Sequence 145803, A
C 143	15	26.8	645	10	US-10-301-480-665250	Sequence 665250,	C 216	14	25.0	391	6	US-09-925-065A-145804	Sequence 145804, A
C 144	15	26.8	648	6	US-09-925-065A-813326	Sequence 813326,	C 217	14	25.0	408	6	US-09-925-065A-260291	Sequence 260291, A
C 145	15	26.8	669	6	US-09-925-065A-690133	Sequence 690133,	C 218	14	25.0	408	6	US-09-925-065A-260292	Sequence 260292, A
C 146	15	26.8	663	11	US-11-172-740-935	Sequence 935, App	C 219	14	25.0	412	6	US-09-925-065A-753	Sequence 753, App
C 147	15	26.8	1092	6	US-09-925-065A-20399	Sequence 20399, A	C 220	14	25.0	412	6	US-10-301-480-108772	Sequence 108772, A
C 148	15	26.8	1092	6	US-09-925-065A-20400	Sequence 20400, A	C 221	14	25.0	412	10	US-10-301-480-122181	Sequence 122181, A
C 149	15	26.8	1092	6	US-09-925-065A-20401	Sequence 20401, A	C 222	14	25.0	435	6	US-09-925-065A-572511	Sequence 572511, A
C 150	15	26.8	1092	6	US-09-925-065A-20402	Sequence 20402, A	C 223	14	25.0	435	10	US-10-301-480-103930	Sequence 103930, A
C 151	15	26.8	1092	6	US-09-925-065A-20403	Sequence 20403, A	C 224	14	25.0	435	10	US-10-301-480-103930	Sequence 103930, A
C 152	15	26.8	1092	9	US-10-301-480-121636	Sequence 121636,	C 225	14	25.0	440	6	US-09-925-065A-369522	Sequence 369522, A
C 153	15	26.8	1092	9	US-10-301-480-121637	Sequence 121637,	C 226	14	25.0	448	6	US-09-925-065A-183219	Sequence 183219, A
C 154	15	26.8	1092	9	US-10-301-480-121638	Sequence 121638,	C 227	14	25.0	458	6	US-09-925-065A-183219	Sequence 183219, A
C 155	15	26.8	1092	9	US-10-301-480-121639	Sequence 121639,	C 228	14	25.0	458	6	US-09-925-065A-232322	Sequence 232322, A
C 156	15	26.8	1092	9	US-10-301-480-121640	Sequence 121640,	C 229	14	25.0	472	6	US-09-925-065A-335573	Sequence 335573, A
C 157	15	26.8	1092	10	US-10-301-480-735045	Sequence 735045,	C 230	14	25.0	472	10	US-10-301-480-397714	Sequence 397714, A
C 158	15	26.8	1092	10	US-10-301-480-735046	Sequence 735046,	C 231	14	25.0	472	10	US-10-301-480-1011123	Sequence 1011123, A
C 159	15	26.8	1092	10	US-10-301-480-735047	Sequence 735047,	C 232	14	25.0	482	10	US-10-301-480-108963	Sequence 108963, A
C 160	15	26.8	1092	10	US-10-301-480-735048	Sequence 735048,	C 233	14	25.0	482	10	US-10-301-480-1022372	Sequence 1022372, A
C 161	15	26.8	1092	10	US-10-301-480-735049	Sequence 735049,	C 234	14	25.0	482	6	US-09-925-065A-512590	Sequence 512590, A
C 162	15	26.8	1165	9	US-10-301-480-36230	Sequence 36230, A	C 235	14	25.0	485	6	US-09-925-065A-200753	Sequence 200753, A
C 163	15	26.8	1165	10	US-10-301-480-6649639	Sequence 6649639,	C 236	14	25.0	487	10	US-10-301-480-289341	Sequence 289341, A
C 164	15	26.8	1182	8	US-10-330-083-1	Sequence 1, App11	C 237	14	25.0	487	10	US-10-301-480-902750	Sequence 902750, A



238	14	25.0	504	6	US-09-925-065A-783652	Sequence 783652,	c 311	14	25.0	551	10	US-10-301-480-311911	Sequence 311911,
239	14	25.0	504	6	US-09-925-065A-783653	Sequence 783653,	c 312	14	25.0	551	10	US-10-301-480-925320	Sequence 925320,
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241	14	25.0	510	6	US-09-925-065A-562314	Sequence 562314,	c 314	14	25.0	556	6	US-09-925-065A-938802	Sequence 938802,
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243	14	25.0	510	6	US-09-925-065A-562316	Sequence 562316,	c 316	14	25.0	556	10	US-10-301-480-1075737	Sequence 1075737,
c 244	14	25.0	512	9	US-09-925-065A-771097	Sequence 771097,	c 317	14	25.0	558	6	US-09-925-065A-802193	Sequence 802195,
245	14	25.0	512	9	US-10-301-480-19312	Sequence 19312, A	c 318	14	25.0	558	6	US-09-925-065A-318113	Sequence 818113,
246	14	25.0	512	10	US-10-301-480-632721	Sequence 632721,	c 319	14	25.0	559	6	US-09-925-065A-414987	Sequence 414987,
c 247	14	25.0	519	6	US-09-925-065A-824633	Sequence 824633,	c 320	14	25.0	560	6	US-09-925-065A-237178	Sequence 237178, A
248	14	25.0	519	6	US-09-925-065A-839436	Sequence 839436,	c 321	14	25.0	560	6	US-09-925-065A-191876	Sequence 191876,
249	14	25.0	521	10	US-10-301-480-427236	Sequence 427236,	c 322	14	25.0	560	6	US-09-925-065A-191877	Sequence 191877,
250	14	25.0	521	10	US-10-301-480-1040645	Sequence 1040645,	c 323	14	25.0	560	6	US-09-925-065A-767241	Sequence 767241,
c 251	14	25.0	524	6	US-09-925-065A-882827	Sequence 882827,	c 324	14	25.0	560	9	US-10-301-480-124955	Sequence 124955,
c 252	14	25.0	526	6	US-09-925-065A-822800	Sequence 822800,	c 325	14	25.0	560	10	US-10-301-480-281462	Sequence 281462,
c 253	14	25.0	529	6	US-09-925-065A-524175	Sequence 524175,	c 326	14	25.0	560	10	US-10-301-480-281463	Sequence 281463,
c 254	14	25.0	529	6	US-09-925-065A-524176	Sequence 524176,	c 327	14	25.0	560	10	US-10-301-480-738864	Sequence 738864,
c 255	14	25.0	530	6	US-09-925-065A-945717	Sequence 945717,	c 328	14	25.0	560	10	US-10-301-480-894871	Sequence 894871,
c 256	14	25.0	531	6	US-09-925-065A-855557	Sequence 855557,	c 329	14	25.0	560	10	US-10-301-480-894872	Sequence 894872,
c 257	14	25.0	532	6	US-09-925-065A-946293	Sequence 946293,	c 330	14	25.0	561	6	US-09-925-065A-137848	Sequence 137848,
c 258	14	25.0	534	6	US-09-925-065A-227750	Sequence 227750,	c 331	14	25.0	561	10	US-10-301-480-466804	Sequence 466804,
c 259	14	25.0	534	6	US-09-925-065A-317462	Sequence 317462,	c 332	14	25.0	561	10	US-10-301-480-1080313	Sequence 1080313,
c 260	14	25.0	534	10	US-10-301-480-372814	Sequence 372814,	c 333	14	25.0	562	6	US-09-925-065A-651557	Sequence 651557,
c 261	14	25.0	535	6	US-09-925-065A-114539	Sequence 114539,	c 334	14	25.0	563	6	US-09-925-065A-153879	Sequence 153879,
c 262	14	25.0	536	6	US-09-925-065A-362408	Sequence 362408,	c 335	14	25.0	563	6	US-09-925-065A-153880	Sequence 153880,
c 263	14	25.0	537	9	US-10-301-480-886223	Sequence 886223,	c 336	14	25.0	563	6	US-09-925-065A-412058	Sequence 412058,
c 264	14	25.0	539	9	US-10-301-480-213581	Sequence 213581,	c 337	14	25.0	563	10	US-10-301-480-480067	Sequence 480067,
c 265	14	25.0	539	10	US-10-301-480-826590	Sequence 826590,	c 338	14	25.0	563	10	US-10-301-480-480066	Sequence 480066,
c 266	14	25.0	540	6	US-09-925-065A-115067	Sequence 115067,	c 339	14	25.0	563	10	US-10-301-480-1093475	Sequence 1093475,
c 267	14	25.0	540	10	US-10-301-480-369039	Sequence 369039,	c 340	14	25.0	563	10	US-10-301-480-1093476	Sequence 1093476,
c 268	14	25.0	540	10	US-10-301-480-982448	Sequence 982448,	c 341	14	25.0	565	6	US-09-925-065A-88870	Sequence 88870, A
c 269	14	25.0	541	6	US-09-925-065A-292159	Sequence 292159,	c 342	14	25.0	565	6	US-09-925-065A-554932	Sequence 554932,
c 270	14	25.0	541	6	US-09-925-065A-292160	Sequence 292160,	c 343	14	25.0	565	6	US-09-925-065A-554933	Sequence 554933,
c 271	14	25.0	541	6	US-09-925-065A-292161	Sequence 292161,	c 344	14	25.0	565	9	US-10-301-480-190111	Sequence 190111,
c 272	14	25.0	541	6	US-09-925-065A-410786	Sequence 410786,	c 345	14	25.0	565	10	US-10-301-480-803520	Sequence 803520,
c 273	14	25.0	541	10	US-10-301-480-247470	Sequence 247470,	c 346	14	25.0	566	6	US-09-925-065A-399546	Sequence 399546,
c 274	14	25.0	541	10	US-10-301-480-247471	Sequence 247471,	c 347	14	25.0	566	6	US-09-925-065A-525936	Sequence 525936,
c 275	14	25.0	541	10	US-10-301-480-860879	Sequence 860879,	c 348	14	25.0	566	10	US-10-301-480-443636	Sequence 443636,
c 276	14	25.0	542	10	US-10-301-480-860880	Sequence 860880,	c 349	14	25.0	566	10	US-10-301-480-1057045	Sequence 1057045,
c 277	14	25.0	542	10	US-10-301-480-392283	Sequence 392283,	c 350	14	25.0	566	6	US-09-925-065A-194921	Sequence 194921,
c 278	14	25.0	542	10	US-10-301-480-1005792	Sequence 1005792,	c 351	14	25.0	568	6	US-09-925-065A-414178	Sequence 414178,
c 279	14	25.0	543	6	US-09-925-065A-165800	Sequence 165800,	c 352	14	25.0	568	6	US-09-925-065A-414179	Sequence 414179,
c 280	14	25.0	543	6	US-09-925-065A-165801	Sequence 165801,	c 353	14	25.0	568	6	US-09-925-065A-933574	Sequence 933574,
c 281	14	25.0	543	6	US-09-925-065A-278180	Sequence 278180,	c 354	14	25.0	568	6	US-09-925-065A-933575	Sequence 933575,
c 282	14	25.0	543	6	US-09-925-065A-355754	Sequence 355754,	c 355	14	25.0	568	6	US-09-925-065A-932099	Sequence 932099,
c 283	14	25.0	543	10	US-10-301-480-433278	Sequence 433278,	c 356	14	25.0	569	6	US-09-925-065A-649456	Sequence 649456,
c 284	14	25.0	544	6	US-09-925-065A-83749	Sequence 83749, A	c 357	14	25.0	569	6	US-09-925-065A-803579	Sequence 803579,
c 285	14	25.0	544	6	US-09-925-065A-466230	Sequence 466230,	c 358	14	25.0	569	6	US-09-925-065A-803580	Sequence 803580,
c 286	14	25.0	544	6	US-09-925-065A-466231	Sequence 466231,	c 359	14	25.0	570	10	US-10-301-480-69129	Sequence 69129, A
c 287	14	25.0	544	6	US-09-925-065A-466232	Sequence 466232,	c 360	14	25.0	570	10	US-10-301-480-265516	Sequence 265516,
c 288	14	25.0	544	9	US-10-301-480-184989	Sequence 184989,	c 361	14	25.0	570	10	US-10-301-480-682538	Sequence 682538,
c 289	14	25.0	544	9	US-10-301-480-798398	Sequence 798398,	c 362	14	25.0	570	10	US-10-301-480-878925	Sequence 878925,
c 290	14	25.0	545	10	US-10-301-480-258072	Sequence 258072,	c 363	14	25.0	571	10	US-10-301-480-478189	Sequence 478189,
c 291	14	25.0	545	10	US-10-301-480-258073	Sequence 258073,	c 364	14	25.0	571	10	US-10-301-480-191598	Sequence 191598,
c 292	14	25.0	545	10	US-10-301-480-871481	Sequence 871481,	c 365	14	25.0	572	6	US-09-925-065A-782997	Sequence 782997,
c 293	14	25.0	545	10	US-10-301-480-871482	Sequence 871482,	c 366	14	25.0	573	6	US-09-925-065A-191873	Sequence 191873,
c 294	14	25.0	545	10	US-10-301-480-871482	Sequence 871482,	c 367	14	25.0	573	6	US-09-925-065A-191874	Sequence 191874,
c 295	14	25.0	546	6	US-09-925-065A-461528	Sequence 461528,	c 368	14	25.0	573	6	US-09-925-065A-191875	Sequence 191875,
c 296	14	25.0	546	6	US-10-301-480-378456	Sequence 378456,	c 369	14	25.0	573	6	US-09-925-065A-191878	Sequence 191878,
c 297	14	25.0	546	10	US-10-301-480-931865	Sequence 931865,	c 370	14	25.0	573	6	US-09-925-065A-377779	Sequence 377779,
c 298	14	25.0	546	6	US-09-925-065A-632805	Sequence 632805,	c 371	14	25.0	573	6	US-09-925-065A-747168	Sequence 747168,
c 299	14	25.0	548	6	US-09-925-065A-632806	Sequence 632806,	c 372	14	25.0	573	6	US-09-925-065A-747169	Sequence 747169,
c 300	14	25.0	548	6	US-09-925-065A-632807	Sequence 632807,	c 373	14	25.0	574	10	US-10-301-480-480710	Sequence 480710,
c 301	14	25.0	548	6	US-09-925-065A-634611	Sequence 634611,	c 374	14	25.0	574	10	US-10-301-480-1094119	Sequence 1094119,
c 302	14	25.0	548	9	US-10-301-480-214065	Sequence 214065,	c 375	14	25.0	576	6	US-09-925-065A-804474	Sequence 804475,
c 303	14	25.0	548	10	US-10-301-480-518418	Sequence 518418,	c 376	14	25.0	576	6	US-09-925-065A-804475	Sequence 804475,
c 304	14	25.0	548	10	US-10-301-480-827474	Sequence 827474,	c 377	14	25.0	576	6	US-09-925-065A-804476	Sequence 804476,
c 305	14	25.0	548	10	US-10-301-480-113827	Sequence 113827,	c 378	14	25.0	576	9	US-10-301-480-79223	Sequence 79223, A
c 306	14	25.0	549	6	US-09-925-065A-636797	Sequence 636797,	c 379	14	25.0	576	10	US-10-301-480-692632	Sequence 692632,
c 307	14	25.0	550	6	US-10-301-480-355203	Sequence 355203,	c 380	14	25.0	577	6	US-09-925-065A-131056	Sequence 131056,
c 308	14	25.0	550	10	US-10-301-480-477069	Sequence 477069,	c 381	14	25.0	577	10	US-10-301-480-404971	Sequence 404971,
c 309	14	25.0	550	10	US-10-301-480-968612	Sequence 968612,	c 382	14	25.0	577	10	US-10-301-480-404972	Sequence 404972,
c 310	14	25.0	550	10	US-10-301-480-1090478	Sequence 1090478,	c 383	14	25.0	577	10	US-10-301-480-404973	Sequence 404973,



C 384	14	25.0	577	10	US-10-301-480-404974	Sequence 404974,	457	14	25.0	591	10	US-10-301-480-236245	Sequence 236245,
C 385	14	25.0	577	10	US-10-301-480-1018380	Sequence 1018380,	458	14	25.0	591	10	US-10-301-480-849653	Sequence 849653,
C 386	14	25.0	577	10	US-10-301-480-1018381	Sequence 1018381,	459	14	25.0	591	10	US-10-301-480-849654	Sequence 849654,
C 387	14	25.0	577	10	US-10-301-480-1018382	Sequence 1018382,	460	14	25.0	593	6	US-09-925-065A-165594	Sequence 165594,
C 388	14	25.0	577	10	US-10-301-480-1018383	Sequence 1018383,	461	14	25.0	593	6	US-09-925-065A-197536	Sequence 197536,
C 389	14	25.0	578	6	US-09-925-065A-106175	Sequence 106174,	462	14	25.0	593	6	US-09-925-065A-331165	Sequence 331165,
C 390	14	25.0	578	6	US-09-925-065A-406175	Sequence 406175,	463	14	25.0	593	6	US-09-925-065A-331166	Sequence 331166,
C 391	14	25.0	578	6	US-09-925-065A-406176	Sequence 406176,	464	14	25.0	593	6	US-09-925-065A-331167	Sequence 331167,
C 392	14	25.0	578	10	US-10-301-480-258807	Sequence 258807,	465	14	25.0	593	6	US-09-925-065A-331168	Sequence 331168,
C 393	14	25.0	578	10	US-10-301-480-281459	Sequence 281459,	466	14	25.0	595	6	US-09-925-065A-174000	Sequence 174000,
C 394	14	25.0	578	10	US-10-301-480-872216	Sequence 872216,	467	14	25.0	595	6	US-09-925-065A-184652	Sequence 184652,
C 395	14	25.0	578	10	US-10-301-480-872216	Sequence 894868,	468	14	25.0	595	6	US-09-925-065A-184653	Sequence 184653,
C 396	14	25.0	579	6	US-09-925-065A-41866	Sequence 41866, A	469	14	25.0	597	6	US-09-925-065A-482785	Sequence 482785,
C 397	14	25.0	579	6	US-09-925-065A-605035	Sequence 605035,	470	14	25.0	597	6	US-09-925-065A-738087	Sequence 738087,
C 398	14	25.0	579	9	US-10-301-480-143104	Sequence 143104,	471	14	25.0	597	6	US-09-925-065A-738088	Sequence 738088,
C 399	14	25.0	579	10	US-10-301-480-472874	Sequence 472874,	472	14	25.0	597	9	US-10-301-480-143934	Sequence 143934,
C 400	14	25.0	579	10	US-10-301-480-472875	Sequence 472875,	473	14	25.0	597	10	US-10-301-480-828343	Sequence 828343,
C 401	14	25.0	579	10	US-10-301-480-472876	Sequence 472876,	474	14	25.0	598	6	US-09-925-065A-182784	Sequence 182784,
C 402	14	25.0	579	10	US-10-301-480-756513	Sequence 756513,	475	14	25.0	598	6	US-09-925-065A-482785	Sequence 482785,
C 403	14	25.0	579	10	US-10-301-480-1086283	Sequence 1086283,	476	14	25.0	598	8	US-10-750-185-70405	Sequence 70405, A
C 404	14	25.0	579	10	US-10-301-480-1086284	Sequence 1086284,	477	14	25.0	598	8	US-10-750-623-70405	Sequence 70405, A
C 405	14	25.0	579	10	US-10-301-480-1086285	Sequence 1086285,	478	14	25.0	599	10	US-10-301-480-487188	Sequence 487188,
C 406	14	25.0	580	6	US-09-925-065A-373763	Sequence 373763,	479	14	25.0	599	10	US-10-301-480-487189	Sequence 487189,
C 407	14	25.0	580	10	US-10-301-480-447169	Sequence 447169,	480	14	25.0	599	10	US-10-301-480-1100597	Sequence 1100597,
C 408	14	25.0	580	10	US-10-301-480-1060578	Sequence 1060578,	481	14	25.0	599	10	US-10-301-480-1100598	Sequence 1100598,
C 409	14	25.0	581	6	US-09-925-065A-595101	Sequence 595101,	482	14	25.0	600	6	US-09-925-065A-933973	Sequence 933973,
C 410	14	25.0	581	10	US-10-301-480-881460	Sequence 881460,	483	14	25.0	600	6	US-09-925-065A-933974	Sequence 933974,
C 411	14	25.0	583	10	US-10-301-480-301332	Sequence 301332,	484	14	25.0	600	10	US-10-301-480-286480	Sequence 286480,
C 412	14	25.0	583	10	US-10-301-480-428093	Sequence 428093,	485	14	25.0	600	10	US-10-301-480-899889	Sequence 899889,
C 413	14	25.0	583	10	US-10-301-480-428093	Sequence 428094,	486	14	25.0	600	14	US-11-128-061-6990	Sequence 6990, Ap
C 414	14	25.0	583	10	US-10-301-480-914721	Sequence 914721,	487	14	25.0	601	6	US-11-128-049-6990	Sequence 6990, Ap
C 415	14	25.0	583	10	US-10-301-480-1041502	Sequence 1041502,	488	14	25.0	601	6	US-09-925-065A-746794	Sequence 746794,
C 416	14	25.0	583	10	US-10-301-480-1041503	Sequence 1041503,	489	14	25.0	603	6	US-09-925-065A-645863	Sequence 645863,
C 417	14	25.0	584	6	US-09-925-065A-356755	Sequence 356755,	490	14	25.0	605	6	US-09-925-065A-192253	Sequence 192253,
C 418	14	25.0	584	6	US-09-925-065A-356756	Sequence 356756,	491	14	25.0	606	6	US-09-925-065A-651311	Sequence 651311,
C 419	14	25.0	584	10	US-10-301-480-227475	Sequence 227475,	492	14	25.0	606	6	US-09-925-065A-907883	Sequence 907883,
C 420	14	25.0	584	10	US-10-301-480-881461	Sequence 881461,	493	14	25.0	607	6	US-09-925-065A-362402	Sequence 362402,
C 421	14	25.0	584	10	US-10-301-480-881464	Sequence 881464,	494	14	25.0	607	6	US-09-925-065A-362403	Sequence 362403,
C 422	14	25.0	584	10	US-10-301-480-840884	Sequence 840884,	495	14	25.0	607	6	US-09-925-065A-362404	Sequence 362404,
C 423	14	25.0	584	10	US-10-301-480-894869	Sequence 894869,	496	14	25.0	607	6	US-09-925-065A-362405	Sequence 362405,
C 424	14	25.0	584	10	US-10-301-480-894870	Sequence 894870,	497	14	25.0	608	6	US-09-925-065A-910174	Sequence 910174,
C 425	14	25.0	584	10	US-10-301-480-894873	Sequence 894873,	498	14	25.0	608	10	US-10-301-480-881808	Sequence 881808,
C 426	14	25.0	586	9	US-10-301-480-61739	Sequence 61739, A	499	14	25.0	608	10	US-10-301-480-895217	Sequence 895217,
C 427	14	25.0	586	9	US-10-301-480-61740	Sequence 61740, A	500	14	25.0	609	6	US-09-925-065A-253372	Sequence 253372,
C 428	14	25.0	586	10	US-10-301-480-675148	Sequence 675148,	501	14	25.0	609	6	US-09-925-065A-253373	Sequence 253373,
C 429	14	25.0	586	10	US-10-301-480-675149	Sequence 675149,	502	14	25.0	610	9	US-10-301-480-59111	Sequence 59112, A
C 430	14	25.0	587	6	US-09-925-065A-116043	Sequence 116043,	503	14	25.0	610	9	US-10-301-480-59112	Sequence 672520,
C 431	14	25.0	588	6	US-09-925-065A-440582	Sequence 440582,	504	14	25.0	610	10	US-10-301-480-672520	Sequence 672521,
C 432	14	25.0	588	6	US-09-925-065A-440583	Sequence 440583,	505	14	25.0	610	10	US-10-301-480-672521	Sequence 743644,
C 433	14	25.0	588	6	US-09-925-065A-440584	Sequence 440584,	506	14	25.0	611	6	US-09-925-065A-803254	Sequence 803254,
C 434	14	25.0	588	6	US-09-925-065A-441856	Sequence 441856,	507	14	25.0	611	6	US-09-925-065A-803254	Sequence 803254,
C 435	14	25.0	589	6	US-09-925-065A-764856	Sequence 764856,	508	14	25.0	611	6	US-09-925-065A-818504	Sequence 818504,
C 436	14	25.0	589	6	US-09-925-065A-764697	Sequence 764697,	509	14	25.0	611	6	US-09-925-065A-818504	Sequence 818504,
C 437	14	25.0	589	6	US-09-925-065A-883836	Sequence 883836,	510	14	25.0	612	6	US-09-925-065A-17104	Sequence 17104, A
C 438	14	25.0	589	6	US-09-925-065A-883837	Sequence 883837,	511	14	25.0	612	6	US-09-925-065A-17104	Sequence 769690,
C 439	14	25.0	589	6	US-09-925-065A-883838	Sequence 883838,	512	14	25.0	612	9	US-10-301-480-118341	Sequence 118341,
C 440	14	25.0	589	9	US-09-925-065A-910201	Sequence 910201,	513	14	25.0	612	10	US-10-301-480-731750	Sequence 731750,
C 441	14	25.0	589	9	US-10-301-480-66441	Sequence 66441, A	514	14	25.0	614	6	US-09-925-065A-912333	Sequence 912333,
C 442	14	25.0	589	10	US-10-301-480-501513	Sequence 501513,	515	14	25.0	614	6	US-09-925-065A-916981	Sequence 916981,
C 443	14	25.0	589	10	US-10-301-480-501514	Sequence 501514,	516	14	25.0	614	6	US-10-301-480-502591	Sequence 502591,
C 444	14	25.0	589	10	US-10-301-480-501515	Sequence 501515,	517	14	25.0	614	10	US-10-301-480-1116000	Sequence 1116000,
C 445	14	25.0	589	10	US-10-301-480-679850	Sequence 679850,	518	14	25.0	615	6	US-09-925-065A-587527	Sequence 587527,
C 446	14	25.0	589	10	US-10-301-480-1114922	Sequence 1114922,	519	14	25.0	615	6	US-09-925-065A-587527	Sequence 5967, Ap
C 447	14	25.0	589	10	US-10-301-480-1114923	Sequence 1114923,	520	14	25.0	615	9	US-10-933-182A-5964	Sequence 5964, Ap
C 448	14	25.0	589	10	US-10-301-480-1114924	Sequence 1114924,	521	14	25.0	615	10	US-10-301-480-433272	Sequence 433272,
C 449	14	25.0	590	6	US-09-925-065A-141327	Sequence 141327,	522	14	25.0	615	10	US-10-301-480-433273	Sequence 433273,
C 450	14	25.0	590	6	US-09-925-065A-141328	Sequence 141328,	523	14	25.0	615	10	US-10-301-480-433274	Sequence 433275,
C 451	14	25.0	590	6	US-09-925-065A-214539	Sequence 214539,	524	14	25.0	615	10	US-10-301-480-433275	Sequence 433275,
C 452	14	25.0	590	10	US-10-301-480-274956	Sequence 274956,	525	14	25.0	615	10	US-10-301-480-1046681	Sequence 1046681,
C 453	14	25.0	590	10	US-10-301-480-274957	Sequence 274957,	526	14	25.0	615	10	US-10-301-480-1046682	Sequence 1046682,
C 454	14	25.0	590	10	US-10-301-480-888365	Sequence 888365,	527	14	25.0	615	10	US-10-301-480-1046683	Sequence 1046683,
C 455	14	25.0	590	10	US-10-301-480-888366	Sequence 888366,	528	14	25.0	615	10	US-10-301-480-1046684	Sequence 1046684,
C 456	14	25.0	591	10	US-10-301-480-236244	Sequence 236244,	529	14	25.0	616	6	US-09-925-065A-873103	Sequence 873103,



C 530	14	25.0	616	6	US-09-925-065A-873104	Sequence 873104,	C 603	14	25.0	652	10	US-10-301-480-639188	Sequence 639188,
531	14	25.0	616	6	US-09-925-065A-874267	Sequence 874267,	C 604	14	25.0	652	10	US-10-301-480-700276	Sequence 700276,
532	14	25.0	616	6	US-09-925-065A-876823	Sequence 876823,	C 605	14	25.0	656	6	US-09-925-065A-860170	Sequence 860170,
C 533	14	25.0	619	6	US-09-925-065A-558130	Sequence 558130,	C 606	14	25.0	657	6	US-09-925-065A-421830	Sequence 421830,
C 534	14	25.0	619	6	US-09-925-065A-558131	Sequence 558131,	C 607	14	25.0	660	6	US-09-925-065A-885513	Sequence 885513,
C 535	14	25.0	620	6	US-09-925-065A-905569	Sequence 905569,	C 608	14	25.0	660	6	US-09-925-065A-885514	Sequence 885514,
C 536	14	25.0	620	6	US-09-925-065A-926350	Sequence 926350	C 609	14	25.0	664	10	US-10-301-480-486540	Sequence 486540,
C 537	14	25.0	620	6	US-09-925-065A-936862	Sequence 936862,	C 610	14	25.0	664	10	US-10-301-480-1099949	Sequence 1099949,
C 538	14	25.0	620	6	US-09-925-065A-953641	Sequence 953641,	C 611	14	25.0	669	6	US-09-925-065A-889373	Sequence 889373,
C 539	14	25.0	620	6	US-09-925-065A-953642	Sequence 953642,	C 612	14	25.0	669	6	US-09-925-065A-889383	Sequence 889383,
C 540	14	25.0	620	6	US-09-925-065A-953643	Sequence 953643,	C 613	14	25.0	670	6	US-09-925-065A-937214	Sequence 937214,
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542	14	25.0	621	6	US-09-925-065A-560842	Sequence 560842,	C 615	14	25.0	672	6	US-09-925-065A-93823	Sequence 93823, A
543	14	25.0	622	6	US-09-925-065A-648449	Sequence 648449,	C 616	14	25.0	672	9	US-10-301-480-195065	Sequence 195065,
C 544	14	25.0	622	10	US-10-301-480-582848	Sequence 582848,	C 617	14	25.0	672	9	US-10-301-480-195066	Sequence 195066,
C 545	14	25.0	622	10	US-10-301-480-1196257	Sequence 1196257,	C 618	14	25.0	672	10	US-10-301-480-808474	Sequence 808474,
C 546	14	25.0	623	6	US-09-925-065A-927920	Sequence 927920,	C 619	14	25.0	672	10	US-10-301-480-808475	Sequence 808475,
547	14	25.0	624	10	US-10-301-480-439632	Sequence 439632,	C 620	14	25.0	686	9	US-10-301-480-82956	Sequence 82956,
548	14	25.0	624	10	US-10-301-480-439632	Sequence 439632,	C 621	14	25.0	686	9	US-10-301-480-82957	Sequence 82957,
C 549	14	25.0	624	10	US-09-925-065A-648888	Sequence 648888,	C 622	14	25.0	686	10	US-10-301-480-696365	Sequence 696365,
C 550	14	25.0	625	6	US-09-925-065A-886035	Sequence 886035,	C 623	14	25.0	686	10	US-10-301-480-696366	Sequence 696366,
C 551	14	25.0	625	6	US-09-925-065A-911217	Sequence 911217,	C 624	14	25.0	688	6	US-09-925-065A-868519	Sequence 868519,
C 552	14	25.0	626	6	US-09-925-065A-780926	Sequence 780926,	C 625	14	25.0	694	6	US-09-925-065A-895268	Sequence 895268,
553	14	25.0	626	6	US-09-925-065A-842066	Sequence 842066,	C 626	14	25.0	696	6	US-09-925-065A-944150	Sequence 944150,
554	14	25.0	627	6	US-09-925-065A-709405	Sequence 709405,	C 627	14	25.0	696	6	US-09-925-065A-944150	Sequence 944150,
555	14	25.0	629	6	US-09-925-065A-567343	Sequence 567343,	C 628	14	25.0	701	6	US-09-925-065A-944140	Sequence 944140,
556	14	25.0	630	14	US-11-128-061-3348	Sequence 3348, Ap	C 629	14	25.0	712	6	US-09-925-065A-58613	Sequence 58613, A
557	14	25.0	630	14	US-11-128-049-3348	Sequence 3348, Ap	C 630	14	25.0	712	9	US-10-301-480-159851	Sequence 159851,
558	14	25.0	631	6	US-09-925-065A-867523	Sequence 867523,	C 631	14	25.0	712	10	US-10-301-480-773260	Sequence 773260,
C 559	14	25.0	631	6	US-09-925-065A-900020	Sequence 900020,	C 632	14	25.0	718	8	US-10-750-185-19395	Sequence 49395, A
C 560	14	25.0	631	6	US-09-925-065A-923187	Sequence 923187,	C 633	14	25.0	718	8	US-10-750-185-19395	Sequence 49395, A
C 561	14	25.0	631	6	US-09-925-065A-923188	Sequence 923188,	C 634	14	25.0	718	10	US-10-301-480-585958	Sequence 585958,
C 562	14	25.0	632	6	US-09-925-065A-889799	Sequence 889799,	C 635	14	25.0	718	10	US-10-301-480-1199367	Sequence 1199367,
C 563	14	25.0	632	6	US-09-925-065A-889980	Sequence 889980,	C 636	14	25.0	719	9	US-09-925-065A-83170	Sequence 83170, A
C 564	14	25.0	632	6	US-09-925-065A-913438	Sequence 913438,	C 637	14	25.0	719	9	US-10-301-480-184410	Sequence 184410,
565	14	25.0	633	6	US-09-925-065A-768696	Sequence 768696,	C 638	14	25.0	732	6	US-09-925-065A-643619	Sequence 643619,
566	14	25.0	633	6	US-09-925-065A-863911	Sequence 863911,	C 639	14	25.0	732	6	US-09-925-065A-797819	Sequence 797819,
567	14	25.0	633	6	US-09-925-065A-863912	Sequence 863912,	C 640	14	25.0	732	6	US-09-925-065A-41291	Sequence 41291, A
568	14	25.0	633	6	US-09-925-065A-900810	Sequence 900810,	C 641	14	25.0	732	9	US-09-925-065A-41292	Sequence 41292, A
C 569	14	25.0	633	10	US-10-301-480-280851	Sequence 280851,	C 642	14	25.0	732	9	US-10-301-480-107673	Sequence 107673,
C 570	14	25.0	633	10	US-10-301-480-894260	Sequence 894260,	C 643	14	25.0	732	9	US-10-301-480-142529	Sequence 142529,
C 571	14	25.0	634	6	US-09-925-065A-191217	Sequence 191217,	C 644	14	25.0	732	9	US-10-301-480-142530	Sequence 142530,
C 572	14	25.0	634	6	US-09-925-065A-905894	Sequence 905894,	C 645	14	25.0	732	10	US-10-301-480-721082	Sequence 721082,
C 573	14	25.0	635	6	US-09-925-065A-783422	Sequence 783422,	C 646	14	25.0	732	10	US-10-301-480-755938	Sequence 755938,
C 574	14	25.0	635	6	US-09-925-065A-783423	Sequence 783423,	C 647	14	25.0	732	10	US-10-301-480-755939	Sequence 755939,
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C 577	14	25.0	637	6	US-09-925-065A-875074	Sequence 875074,	C 650	14	25.0	735	9	US-10-301-480-173367	Sequence 173367,
578	14	25.0	637	6	US-09-925-065A-922298	Sequence 922298,	C 651	14	25.0	735	9	US-10-301-480-173368	Sequence 173368,
579	14	25.0	640	6	US-09-925-065A-888232	Sequence 888232,	C 652	14	25.0	735	10	US-10-301-480-786776	Sequence 786776,
C 580	14	25.0	641	6	US-09-925-065A-736231	Sequence 736231,	C 653	14	25.0	735	10	US-10-301-480-786777	Sequence 786777,
C 581	14	25.0	641	6	US-09-925-065A-736232	Sequence 736232,	C 654	14	25.0	742	6	US-09-925-065A-925544	Sequence 925544,
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584	14	25.0	641	10	US-10-301-480-938767	Sequence 938767,	C 657	14	25.0	766	8	US-10-750-185-63124	Sequence 63124, A
585	14	25.0	641	10	US-10-301-480-938768	Sequence 938768,	C 658	14	25.0	766	8	US-10-750-185-63124	Sequence 63124, A
C 586	14	25.0	643	6	US-09-925-065A-800473	Sequence 800473,	C 659	14	25.0	789	10	US-10-301-480-570955	Sequence 570955,
C 587	14	25.0	643	6	US-09-925-065A-800474	Sequence 800474,	C 660	14	25.0	789	10	US-10-301-480-1184364	Sequence 1184364,
C 588	14	25.0	644	6	US-09-925-065A-922021	Sequence 922021,	C 661	14	25.0	814	8	US-10-750-185-50022	Sequence 50022, A
C 589	14	25.0	645	6	US-09-925-065A-870653	Sequence 870653,	C 662	14	25.0	814	8	US-10-750-185-50022	Sequence 50022, A
C 590	14	25.0	645	6	US-09-925-065A-870654	Sequence 870654,	C 663	14	25.0	820	6	US-09-925-065A-949148	Sequence 949148,
C 591	14	25.0	645	6	US-09-925-065A-901870	Sequence 901870,	C 664	14	25.0	838	10	US-10-301-480-563999	Sequence 562999,
C 592	14	25.0	645	6	US-09-925-065A-904221	Sequence 904221,	C 665	14	25.0	838	10	US-10-301-480-563999	Sequence 563999,
593	14	25.0	646	6	US-09-925-065A-868520	Sequence 868520,	C 666	14	25.0	845	10	US-10-301-480-1176408	Sequence 1176408,
C 594	14	25.0	646	6	US-09-925-065A-868520	Sequence 868520,	C 667	14	25.0	845	10	US-10-301-480-594930	Sequence 594930,
595	14	25.0	647	6	US-09-925-065A-886810	Sequence 886810,	C 668	14	25.0	846	6	US-09-925-065A-1208339	Sequence 1208339,
C 596	14	25.0	647	6	US-09-925-065A-369523	Sequence 369523,	C 669	14	25.0	854	8	US-09-925-065A-949857	Sequence 949857,
C 597	14	25.0	647	6	US-09-925-065A-892033	Sequence 892033,	C 670	14	25.0	854	8	US-10-750-185-43539	Sequence 43539, A
C 598	14	25.0	647	6	US-09-925-065A-892034	Sequence 892034,	C 671	14	25.0	854	10	US-10-301-480-543744	Sequence 543744,
C 599	14	25.0	647	6	US-09-925-065A-896044	Sequence 896044,	C 672	14	25.0	893	10	US-10-301-480-1157153	Sequence 1157153,
C 600	14	25.0	652	9	US-10-301-480-25778	Sequence 25778, A	C 673	14	25.0	893	10	US-10-301-480-1157153	Sequence 1157153,
C 601	14	25.0	652	9	US-10-301-480-25779	Sequence 25779, A	C 674	14	25.0	965	6	US-09-925-065A-58327	Sequence 58327, A
C 602	14	25.0	652	9	US-10-301-480-86867	Sequence 86867, A	C 675	14	25.0	965	6	US-09-925-065A-58328	Sequence 58328, A
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C 678	14	25.0	965	9	US-10-301-480-159566	Sequence 159566,	751	14	25.0	2220	6	US-09-925-065A-30201	Sequence 30201, A
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C 692	14	25.0	989	10	US-10-301-480-608167	Sequence 608167,	765	14	25.0	2223	8	US-10-750-185-16254	Sequence 36254, A
C 693	14	25.0	989	10	US-10-301-480-1146725	Sequence 1146725,	766	14	25.0	2273	8	US-10-750-623-36254	Sequence 36254, A
C 694	14	25.0	994	10	US-10-301-480-1221576	Sequence 1221576,	767	14	25.0	2279	8	US-10-750-185-28253	Sequence 28253, A
C 695	14	25.0	994	10	US-10-301-480-531794	Sequence 531794,	768	14	25.0	2279	8	US-10-750-623-28253	Sequence 28253, A
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C 697	14	25.0	994	10	US-10-301-480-1190522	Sequence 1190522,	770	14	25.0	2819	8	US-10-750-185-41065	Sequence 41065, A
C 698	14	25.0	995	10	US-10-301-480-552788	Sequence 552788,	771	14	25.0	2819	8	US-10-750-623-41065	Sequence 41065, A
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C 701	14	25.0	995	10	US-10-301-480-1167029	Sequence 1167029,	774	14	25.0	3251	8	US-10-750-185-31054	Sequence 31054, A
C 702	14	25.0	997	10	US-10-301-480-575342	Sequence 575342,	775	14	25.0	3427	8	US-10-750-623-32977	Sequence 32977, A
C 703	14	25.0	997	10	US-10-301-480-584226	Sequence 584226,	776	14	25.0	3427	8	US-10-750-185-32977	Sequence 32977, A
C 704	14	25.0	997	10	US-10-301-480-1188751	Sequence 1188751,	777	14	25.0	4237	14	US-11-169-941-74	Sequence 74, Appl
C 705	14	25.0	997	10	US-10-301-480-1197635	Sequence 1197635,	778	14	25.0	4237	14	US-11-169-941-74	Sequence 2051, Ap
C 706	14	25.0	1063	11	US-11-096-568A-1197635	Sequence 1197635,	779	14	25.0	4685	14	US-11-121-197-2051	Sequence 8, Appl1
C 707	14	25.0	1103	9	US-10-301-480-26312	Sequence 26312, A	780	14	25.0	5024	14	US-11-121-197-2051	Sequence 8, Appl1
C 708	14	25.0	1103	9	US-10-301-480-26312	Sequence 26312, A	781	14	25.0	12165	9	US-10-893-483-8	Sequence 8, Appl1
C 709	14	25.0	1103	9	US-10-301-480-26312	Sequence 26312, A	782	14	25.0	14002	14	US-11-193-187-190	Sequence 190, Appl
C 710	14	25.0	1103	10	US-10-301-480-539721	Sequence 539721,	783	14	25.0	21852	8	US-10-928-466A-181	Sequence 181, Appl
C 711	14	25.0	1103	10	US-10-301-480-539722	Sequence 539722,	784	14	25.0	27553	9	US-10-928-466A-183	Sequence 183, Appl
C 712	14	25.0	1103	10	US-10-301-480-539723	Sequence 539723,	785	14	25.0	27553	9	US-10-928-466A-185	Sequence 185, Appl
C 713	14	25.0	1125	11	US-11-096-568A-19011	Sequence 19011, A	786	14	25.0	88607	14	US-11-011-332A-149	Sequence 249, Appl
C 714	14	25.0	1188	6	US-09-925-065A-112855	Sequence 112855,	787	14	25.0	90336	14	US-10-330-773-625	Sequence 773, Appl
C 715	14	25.0	1296	6	US-09-925-065A-545997	Sequence 545997,	788	14	25.0	100000	14	US-11-117-187-195	Sequence 187, Appl
C 716	14	25.0	1296	10	US-10-301-480-523937	Sequence 523937,	789	14	25.0	121001	9	US-11-124-677A-5024	Sequence 5024, Ap
C 717	14	25.0	1296	10	US-10-301-480-1137346	Sequence 1137346,	790	14	25.0	121001	9	US-11-117-187-190	Sequence 190, Appl
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C 719	14	25.0	1305	6	US-10-301-480-141735	Sequence 141735,	792	14	25.0	124285	9	US-10-893-483-105	Sequence 105, Appl
C 720	14	25.0	1305	6	US-10-301-480-141735	Sequence 141735,	793	14	25.0	124285	9	US-10-893-483-105	Sequence 105, Appl
C 721	14	25.0	1305	6	US-10-301-480-141735	Sequence 141735,	794	14	25.0	124285	9	US-10-893-483-105	Sequence 105, Appl
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C 727	14	25.0	1305	6	US-10-301-480-141735	Sequence 141735,	800	14	25.0	124285	9	US-10-893-483-105	Sequence 105, Appl
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C 827	13	23.2	19	12	US-11-101-244-785107	Sequence 785107,	C 900	13	23.2	201	14	US-11-124-3684-13938	Sequence 13938, A
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C 837	13	23.2	19	13	US-11-083-784-361382	Sequence 361382,	C 910	13	23.2	232	6	US-09-925-065A-534954	Sequence 534954,
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C 840	13	23.2	19	13	US-11-083-784-560249	Sequence 560249,	C 913	13	23.2	246	14	US-11-186-282-37	Sequence 37, Ap1
C 841	13	23.2	19	13	US-11-083-784-560353	Sequence 560353,	C 914	13	23.2	302	6	US-09-925-065A-222546	Sequence 222546,
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C 848	13	23.2	25	9	US-10-932-182A-177136	Sequence 177136,	C 921	13	23.2	340	10	US-10-301-480-926735	Sequence 926735,
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C 850	13	23.2	25	9	US-10-932-182A-177136	Sequence 177136,	C 923	13	23.2	363	6	US-09-925-065A-176538	Sequence 176538,
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C 857	13	23.2	25	14	US-11-121-849-323512	Sequence 323512,	C 930	13	23.2	380	10	US-10-301-480-961061	Sequence 961061,
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C 863	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 936	13	23.2	402	10	US-10-301-480-628023	Sequence 628023,
C 864	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 937	13	23.2	402	10	US-10-301-480-628024	Sequence 628024,
C 865	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 938	13	23.2	407	9	US-10-301-480-21819	Sequence 21819, A
C 866	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 939	13	23.2	407	10	US-10-301-480-635228	Sequence 635228,
C 867	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 940	13	23.2	408	6	US-09-925-065A-115212	Sequence 115212,
C 868	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 941	13	23.2	408	6	US-10-301-480-214198	Sequence 214198,
C 869	13	23.2	25	14	US-11-121-849-546890	Sequence 546890,	C 942	13	23.2	408	10	US-10-301-480-827607	Sequence 827607,
C 870	13	23.2	31	8	US-10-857-780-3295	Sequence 3295, Ap	C 943	13	23.2	411	6	US-09-925-065A-481873	Sequence 481873,
C 871	13	23.2	47	11	US-11-304-311-536	Sequence 536, Ap	C 944	13	23.2	418	9	US-10-301-480-14616	Sequence 14616, A
C 872	13	23.2	47	11	US-11-304-311-537	Sequence 537, Ap	C 945	13	23.2	418	9	US-10-301-480-14616	Sequence 14616, A
C 873	13	23.2	50	14	US-11-175-859-37306	Sequence 37306, A	C 946	13	23.2	418	10	US-11-128-061-1852	Sequence 1852, Ap
C 874	13	23.2	50	14	US-11-175-859-44486	Sequence 44486, A	C 947	13	23.2	418	14	US-11-128-061-1852	Sequence 1852, Ap
C 875	13	23.2	50	14	US-11-175-859-44486	Sequence 44486, A	C 948	13	23.2	418	14	US-11-128-061-1852	Sequence 1852, Ap
C 876	13	23.2	51	9	US-10-981-356A-15	Sequence 15, Ap1	C 949	13	23.2	418	14	US-11-128-061-1852	Sequence 1852, Ap
C 877	13	23.2	78	14	US-11-096-046-15	Sequence 15, Ap1	C 950	13	23.2	423	8	US-10-750-185-2179	Sequence 2179, Ap
C 878	13	23.2	78	14	US-11-096-046-15	Sequence 15, Ap1	C 951	13	23.2	423	8	US-10-750-185-2179	Sequence 2179, Ap
C 879	13	23.2	179	14	US-11-128-061-647	Sequence 647, Ap	C 952	13	23.2	427	6	US-09-925-065A-229620	Sequence 229620,
C 880	13	23.2	179	14	US-11-128-061-647	Sequence 647, Ap	C 953	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 881	13	23.2	179	14	US-11-128-061-647	Sequence 647, Ap	C 954	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 882	13	23.2	179	14	US-11-128-061-647	Sequence 647, Ap	C 955	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 883	13	23.2	184	8	US-10-995-561-8236	Sequence 8236, Ap	C 956	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 884	13	23.2	200	14	US-11-098-686-1818	Sequence 1818, Ap	C 957	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 885	13	23.2	200	14	US-11-098-686-1818	Sequence 1818, Ap	C 958	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 886	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 959	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 887	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 960	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 888	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 961	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 889	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 962	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 890	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 963	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 891	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 964	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 892	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 965	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 893	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 966	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,
C 894	13	23.2	201	8	US-10-995-561-8266	Sequence 8266, Ap	C 967	13	23.2	428	6	US-09-925-065A-229620	Sequence 229620,



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C 968 13 23.2 447 6 US-09-925-065A-377388 Sequence 377388,
C 969 13 23.2 447 6 US-09-925-065A-377389 Sequence 377389,
C 970 13 23.2 447 10 US-10-301-480-434456 Sequence 434456,
C 971 13 23.2 447 10 US-10-301-480-434457 Sequence 434457,
C 972 13 23.2 447 10 US-10-301-480-1047865 Sequence 1047865,
C 973 13 23.2 447 10 US-10-301-480-1047866 Sequence 1047866,
C 974 13 23.2 448 10 US-10-301-480-446828 Sequence 446828,
C 975 13 23.2 448 10 US-10-301-480-446829 Sequence 446829,
C 976 13 23.2 448 10 US-10-301-480-1060237 Sequence 1060237,
C 977 13 23.2 448 10 US-10-301-480-1060238 Sequence 1060238,
C 978 13 23.2 450 6 US-09-925-065A-305747 Sequence 305747,
C 979 13 23.2 451 10 US-10-301-480-381734 Sequence 381734,
C 980 13 23.2 451 10 US-10-301-480-995143 Sequence 995143,
C 981 13 23.2 459 6 US-09-925-065A-253866 Sequence 253866,
C 982 13 23.2 459 6 US-09-925-065A-289495 Sequence 289495,
C 983 13 23.2 459 6 US-09-925-065A-289496 Sequence 289496,
C 984 13 23.2 460 9 US-10-301-480-77090 Sequence 77090, A
C 985 13 23.2 460 10 US-10-301-480-690499 Sequence 690499,
C 986 13 23.2 463 6 US-09-925-065A-372530 Sequence 372530,
C 987 13 23.2 464 6 US-09-925-065A-178681 Sequence 178681,
C 988 13 23.2 464 10 US-10-301-480-269656 Sequence 269656,
C 989 13 23.2 464 10 US-10-301-480-883065 Sequence 883065,
C 990 13 23.2 467 6 US-09-925-065A-581130 Sequence 581130,
C 991 13 23.2 467 6 US-09-925-065A-332953 Sequence 332953,
C 992 13 23.2 467 10 US-10-301-480-946362 Sequence 946362,
C 993 13 23.2 467 10 US-09-925-065A-338798 Sequence 338798,
C 994 13 23.2 469 6 US-10-301-480-442468 Sequence 442468,
C 995 13 23.2 469 10 US-10-301-480-1055877 Sequence 1055877,
C 996 13 23.2 470 6 US-09-925-065A-627345 Sequence 627345,
C 997 13 23.2 474 6 US-09-925-065A-741483 Sequence 741483,
C 998 13 23.2 480 6 US-09-925-065A-231381 Sequence 231381,
C 999 13 23.2 480 6 US-09-925-065A-231382 Sequence 231382,
1000 13 23.2 480 6 US-09-925-065A-231382 Sequence 231382,
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## ALIGNMENTS

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RESULT 1
US-09-925-065A-692911/c
; Sequence 692911, Application US/09925065A
; Publication No. US20040181048A1
;
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692911
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692911
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Query Match 30.4%; Score 17; DB 6; Length 1930;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 357 GTGGATGTTGATGCT 341
RESULT 2
US-09-925-065A-692912/c
; Sequence 692912, Application US/09925065A
; Publication No. US20040181048A1
;
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692912
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692912
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Query Match 30.4%; Score 17; DB 6; Length 1930;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Oy 8 GTGGATGTTGATGCT 24
Db 357 GTGGATGTTGATGCT 341
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```
RESULT 3
US-09-925-065A-692913/c
; Sequence 692913, Application US/09925065A
; Publication No. US20040181048A1
;
GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; NUCLEOTIDE POLYMORPHISMS IN THE HUMAN GENOME
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 692913
; LENGTH: 1930
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-925-065A-692913
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Query Match 30.4%; Score 17; DB 6; Length 1930;
Best Local Similarity 100.0%; Pred. No. 6.2;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy 8 GTGGTATGTTGAATGCT 24  
|||  
Db 357 GTGGTATGTTGAATGCT 341

RESULT 4  
US-09-925-065A-692914/c  
; Sequence 692914, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925.065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692914  
; LENGTH: 1930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-692914

Query Match 30.4%; Score 17; DB 6; Length 1930;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 GTGGTATGTTGAATGCT 24  
|||  
Db 357 GTGGTATGTTGAATGCT 341

RESULT 5  
US-09-925-065A-692915/c  
; Sequence 692915, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925.065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 692915  
; LENGTH: 1930  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-692915

Query Match 30.4%; Score 17; DB 6; Length 1930;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 GTGGTATGTTGAATGCT 24  
|||  
Db 357 GTGGTATGTTGAATGCT 341

RESULT 6  
US-09-925-065A-334218  
; Sequence 334218, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925.065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 334218  
; LENGTH: 526  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-334218

Query Match 28.6%; Score 16; DB 6; Length 526;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 40 GCAATGAGAAATTACAC 55  
|||  
Db 239 GCAATGAGAAATTACAC 254

RESULT 7  
US-10-301-480-407764  
; Sequence 407764, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301.480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 407764  
; LENGTH: 536  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-407764

Query Match 28.6%; Score 16; DB 10; Length 536;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 40 GCAATGAGATTACAC 55  
|||||  
Db 249 GCAATGAGATTACAC 264

RESULT 8  
US-10-301-480-1021173  
; Sequence 1021173, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1021173  
; LENGTH: 536  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1021173

Query Match 28.6%; Score 16; DB 10; Length 536;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 40 GCAATGAGATTACAC 55  
|||||  
Db 249 GCAATGAGATTACAC 264

RESULT 9  
US-10-301-480-261442/C  
; Sequence 261442, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 261442  
; LENGTH: 567  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-261442

Query Match 28.6%; Score 16; DB 10; Length 567;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
Db 468 TGAATGCTCATCCGA 453

RESULT 10  
US-10-301-480-874851/C  
; Sequence 874851, Application US/10301480

; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; CURRENT FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 874851  
; LENGTH: 567  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-874851

Query Match 28.6%; Score 16; DB 10; Length 567;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
Db 468 TGAATGCTCATCCGA 453

RESULT 11  
US-09-925-065A-169496/C  
; Sequence 169496, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; CURRENT FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 169496  
; LENGTH: 584  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-169496

Query Match 28.6%; Score 16; DB 6; Length 584;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
Db 468 TGAATGCTCATCCGA 453

RESULT 12  
US-11-116-881A-840  
; Sequence 840, Application US/11116881A  
; Publication No. US20060041949A1  
; GENERAL INFORMATION:  
; APPLICANT: Xu, Dongmei



APPLICANT: Nielsen, Mark T.  
TITLE OF INVENTION: Nicotiana Nucleic Acid Molecules and Uses Thereof  
FILE REFERENCE: 07678/141014  
CURRENT APPLICATION NUMBER: US/11/116,881A  
PRIOR FILING DATE: 2005-04-27  
PRIOR APPLICATION NUMBER: 60/665,451  
PRIOR FILING DATE: 2005-03-24  
PRIOR APPLICATION NUMBER: 60/665,097  
PRIOR FILING DATE: 2005-03-24  
PRIOR APPLICATION NUMBER: 60/646,764  
PRIOR FILING DATE: 2005-01-25  
PRIOR APPLICATION NUMBER: 60/607,357  
PRIOR FILING DATE: 2004-09-03  
PRIOR APPLICATION NUMBER: 60/566,235  
PRIOR FILING DATE: 2004-04-29  
PRIOR APPLICATION NUMBER: 10/934,944  
PRIOR FILING DATE: 2004-09-03  
PRIOR APPLICATION NUMBER: 10/943,507  
PRIOR FILING DATE: 2004-09-17  
PRIOR APPLICATION NUMBER: 60/503,989  
PRIOR FILING DATE: 2003-09-18  
PRIOR APPLICATION NUMBER: 60/485,368  
PRIOR FILING DATE: 2003-07-08  
PRIOR APPLICATION NUMBER: 60/418,933  
PRIOR FILING DATE: 2002-10-16  
Remaining Prior Application data removed - See File Wrapper or PALM.  
NUMBER OF SEQ ID NOS: 2300  
SOFTWARE: PatentIn version 3.3  
SEQ ID NO 840  
LENGTH: 591  
TYPE: DNA  
ORGANISM: Nicotiana tabacum  
US-11-116-881A-840

Query Match 28.6%; Score 16; DB 11; Length 591;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 CGGTGATGTTGAATG 22  
Db 546 CGGTGATGTTGAATG 561

RESULT 13  
US-09-925-065A-266664  
Sequence 266664, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 266664  
LENGTH: 593  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-266664

Query Match 28.6%; Score 16; DB 6; Length 593;

Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 39 AGCAATGAGATTACA 54  
Db 65 AGCAATGAGATTACA 80

RESULT 14  
US-09-925-065A-902120/c  
Sequence 902120, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 902120  
LENGTH: 595  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-925-065A-902120

Query Match 28.6%; Score 16; DB 6; Length 595;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 11 GTATGTAATGCTCA 26  
Db 518 GTATGTAATGCTCA 503

RESULT 15  
US-09-925-065A-315548  
Sequence 315548, Application US/09925065A  
Publication No. US20040181048A1  
GENERAL INFORMATION:  
APPLICANT: Wang, David G.  
TITLE OF INVENTION: Identification and Mapping of Single  
FILE REFERENCE: 108827.135  
CURRENT APPLICATION NUMBER: US/09/925,065A  
PRIOR FILING DATE: 2001-08-08  
PRIOR APPLICATION NUMBER: US 60/243,096  
PRIOR FILING DATE: 2000-10-24  
PRIOR APPLICATION NUMBER: US 60/252,147  
PRIOR FILING DATE: 2000-11-20  
PRIOR APPLICATION NUMBER: US 60/250,092  
PRIOR FILING DATE: 2000-11-30  
PRIOR APPLICATION NUMBER: US 60/261,766  
PRIOR FILING DATE: 2001-01-16  
PRIOR APPLICATION NUMBER: US 60/289,846  
PRIOR FILING DATE: 2001-05-09  
NUMBER OF SEQ ID NOS: 957086  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 315548  
LENGTH: 627  
TYPE: DNA  
ORGANISM: Homo sapiens



US-09-925-065A-315548

Query Match 28.6%; Score 16; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAAAT 50  
DB 128 CAGAGCAATGAGAAAT 143

## RESULT 16

US-09-925-065A-315549  
; Sequence 315549, Application US/09925065A  
; Publication No. US20040181048A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome  
; FILE REFERENCE: 108827.135  
; CURRENT APPLICATION NUMBER: US/09/925,065A  
; PRIOR FILING DATE: 2001-08-08  
; PRIOR APPLICATION NUMBER: US 60/243,096  
; PRIOR FILING DATE: 2000-10-24  
; PRIOR APPLICATION NUMBER: US 60/252,147  
; PRIOR FILING DATE: 2000-11-20  
; PRIOR APPLICATION NUMBER: US 60/250,092  
; PRIOR FILING DATE: 2000-11-30  
; PRIOR APPLICATION NUMBER: US 60/261,766  
; PRIOR FILING DATE: 2001-01-16  
; PRIOR APPLICATION NUMBER: US 60/289,846  
; PRIOR FILING DATE: 2001-05-09  
; NUMBER OF SEQ ID NOS: 957086  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 315549  
; LENGTH: 627  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-09-925-065A-315549

Query Match 28.6%; Score 16; DB 6; Length 627;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAAAT 50  
DB 128 CAGAGCAATGAGAAAT 143

RESULT 17  
US-10-301-480-390555  
; Sequence 390555, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 390555  
; LENGTH: 628  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-390555

Query Match 28.6%; Score 16; DB 10; Length 628;

Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAAAT 50  
DB 129 CAGAGCAATGAGAAAT 144

## RESULT 18

US-10-301-480-390556  
; Sequence 390556, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:  
; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 390556  
; LENGTH: 628  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-390556

Query Match 28.6%; Score 16; DB 10; Length 628;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAAAT 50  
DB 129 CAGAGCAATGAGAAAT 144

RESULT 19  
US-10-301-480-1003964  
; Sequence 1003964, Application US/10301480  
; Publication No. US20060057564A1  
; GENERAL INFORMATION:

; APPLICANT: Wang, David G.  
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms  
; FILE REFERENCE: 108827.137  
; CURRENT APPLICATION NUMBER: US/10/301,480  
; PRIOR FILING DATE: 2002-11-21  
; PRIOR APPLICATION NUMBER: US 10/215,598  
; PRIOR FILING DATE: 2002-08-09  
; PRIOR APPLICATION NUMBER: US 60/311,695  
; PRIOR FILING DATE: 2001-08-10  
; NUMBER OF SEQ ID NOS: 1226818  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 1003964  
; LENGTH: 628  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-10-301-480-1003964

Query Match 28.6%; Score 16; DB 10; Length 628;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAAAT 50  
DB 129 CAGAGCAATGAGAAAT 144

## RESULT 20



```
US-10-301-480-1003965
; Sequence 1003965, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1003965
; LENGTH: 628
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1003965

Query Match          28.6%; Score 16; DB 10; Length 628;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 CAGAGCAATGAGAT 50
Db      129 CAGAGCAATGAGAT 144

RESULT 21
US-09-925-065A-923129/c
; Sequence 923129, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; PRIOR FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 923129
; LENGTH: 727
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-923129

Query Match          28.6%; Score 16; DB 6; Length 727;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 GTATGTGAATGCTCA 26
Db      633 GTATGTGAATGCTCA 618

RESULT 22
US-10-301-480-562417/c
; Sequence 562417, Application US/10301480
; Publication No. US20060057564A1

US-10-301-480-1175826/c
; Sequence 1175826, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1175826
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1175826

Query Match          28.6%; Score 16; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 TATGTGAATGCTCAT 27
Db      63 TATGTGAATGCTCAT 48

RESULT 23
US-10-301-480-1175826/c
; Sequence 1175826, Application US/10301480
; Publication No. US20060057564A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms
; FILE REFERENCE: 108827.137
; CURRENT APPLICATION NUMBER: US/10/301,480
; PRIOR FILING DATE: 2002-11-21
; PRIOR APPLICATION NUMBER: US 10/215,598
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: US 60/311,695
; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 1226818
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1175826
; LENGTH: 728
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-301-480-1175826

Query Match          28.6%; Score 16; DB 10; Length 728;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      12 TATGTGAATGCTCAT 27
Db      63 TATGTGAATGCTCAT 48

RESULT 24
US-11-194-246-499
; Sequence 499, Application US/11194246
; Publication No. US20050272089A1
; GENERAL INFORMATION:
; APPLICANT: Mott, John
; APPLICANT: Trepod, Catherine
; APPLICANT: Arvidson, Scalfan
; TITLE OF INVENTION: CRITICAL GENES AND POLYPEPTIDES OF HAEMOPHILUS INFLUENZAE AND
; FILE REFERENCE: 00592.US1 (M&R 268.05920101)
; CURRENT APPLICATION NUMBER: US/11/194,246
; CURRENT FILING DATE: 2005-08-01
```



```

? PRIOR APPLICATION NUMBER: US/10/274,586
? PRIOR FILING DATE: 2002-10-21
? PRIOR APPLICATION NUMBER: US 60/345,438
? PRIOR FILING DATE: 2001-10-19
? NUMBER OF SEQ ID NOS: 621
? SOFTWARE: PatentIn version 3.0
? SEQ ID NO 499
? LENGTH: 861
? TYPE: DNA
? ORGANISM: ARTIFICIAL
? FEATURE:
? OTHER INFORMATION: Sequence of the CM coding sequence and flanking regions
US-11-194-246-499

```

Query Match	28.6%	Score 16;	DB 14;	Length 861;
Best Local Similarity	100.0%	Pred. No. 24;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	17	TGAATGCTCATCCGA	32
Db	354	TGAATGCTCATCCGA	369

```

RESULT 25
US-11-218-787B-3
; Sequence 3, Application US/11218787B
; Publication No. US20060057685A1
; GENERAL INFORMATION:
; APPLICANT: Ajinomoto Co., Inc.
; TITLE OF INVENTION: METHOD FOR PRODUCING ABNORMAL AMINO ACID USING BACTERIUM OF
; TITLE OF INVENTION: ENTEROBACTERIACEAE FAMILY HAVING ALL ACETOHYDROXY ACID SYNTHASES
; FILE REFERENCE: US-180
; CURRENT APPLICATION NUMBER: US/11/218,787B
; CURRENT FILING DATE: 2005-09-06
; PRIOR APPLICATION NUMBER: RU2004127011
; PRIOR FILING DATE: 2004-09-10
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 935
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: cat gene flanked with 11ybn regions
US-11-218-787B-3

```

Query Match	28.6%	Score 16;	DB 11;	Length 935;
Best Local Similarity	100.0%	Pred. No. 24;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

```

QY      17  TGAATGCTCATCCGA  32
          |||||
Db      437  TGAATGCTCATCCGA  452

```

```

RESULT 26
US-11-218-787B-6
; Sequence 6, Application US/11218787B
; Publication No. US20060057655A1
GENERAL INFORMATION:
APPLICANT: Ajinomoto Co., Inc.
TITLE OF INVENTION: METHOD FOR PRODUCING ABNORMAL AMINO ACID USING BACTERIUM OF
TITLE OF INVENTION: ENTEROBACTERIACEAE FAMILY HAVING ALL ACETOHYDROXY ACID SYNTHASE
FILE REFERENCE: US-180
CURRENT APPLICATION NUMBER: US/11/218,787B
CURRENT FILING DATE: 2005-09-06
PRIOR APPLICATION NUMBER: RU2004127011
PRIOR FILING DATE: 2004-09-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 1080
TYPE: DNA

```

```

; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: l|vbn::cat
US-11-218-787B-6

```

Query Match	28.6%	Score 16;	DB 11;	Length 1080;
Best Local Similarity	100.0%	Pred. No. 24;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Oy	17	TGAATGCTCATCCGA	32
Dd	513	TGAATGCTCATCCGA	528

```

RESULT 27
US-11-235-254-18/c
Sequence 18, Application US/11235254
Publication No. US20060035348A1
GENERAL INFORMATION:
APPLICANT: Ajinomoto Co., Inc.
TITLE OF INVENTION: METHOD FOR PRODUCING L-AMINO ACID USING BACTERIUM
TITLE OF INVENTION: HAVING ENHANCED EXPRESSION OF pckA GENE.
FILE REFERENCE: C1280PC4030
CURRENT APPLICATION NUMBER: US/11/235,254
CURRENT FILING DATE: 2005-09-27
PRIOR APPLICATION NUMBER: RU 2003109477
PRIOR FILING DATE: 2003-04-07
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 1188
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Cm-resistance
OTHER INFORMATION: gene, Ppspa promoter and SD sequence of gene 10
OTHER INFORMATION: from phase T7
US-11-235-254-18

```

Query Match	28.64;	Score 16;	DB 11;	Length 1188;
Best Local Similarity	100.04;	Pred. No. 24;		
Matches 16;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	17	TGAATGCTCATCCGA	32
Db	461	TGAATGCTCATCCGA	446

```

RESULT 28
US-10-750-185-40818
; Sequence 40818, Application US/10750185
; Publication No. US20050260630A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11100-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40818
; LENGTH: 3011
; TYPE: DNA
; ORGANISM: Bovine
US-10-750-185-40818 19866880546633

```



Query Match 28.6%; Score 16; DB 8; Length 3011;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAT 50  
|||||  
Db 2798 CAGAGCAATGAGAT 2813

RESULT 29  
US-10-750-623-40818  
; Sequence 40818, Application US/10750623  
; Publication No. US20050287531A1  
; GENERAL INFORMATION:  
; APPLICANT: MMT GENOMICS, INC.  
; APPLICANT: DENIS, Sue K.  
; APPLICANT: KERR, Richard  
; APPLICANT: ROSENFELD, David  
; APPLICANT: HOLM, Tom  
; APPLICANT: BATES, Stephen  
; APPLICANT: FANTIN, Dennis  
; TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS  
; FILE REFERENCE: MM1100-1  
; CURRENT APPLICATION NUMBER: US/10/750,623  
; CURRENT FILING DATE: 2003-12-31  
; PRIOR APPLICATION NUMBER: US 60/437,482  
; PRIOR FILING DATE: 2002-12-31  
; NUMBER OF SEQ ID NOS: 64922  
; SOFTWARE: Patentin version 3.1  
; SEQ ID NO 40818  
; LENGTH: 3011  
; TYPE: DNA  
; ORGANISM: Bovine 19866880546653  
US-10-750-623-40818

Query Match 28.6%; Score 16; DB 8; Length 3011;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 CAGAGCAATGAGAT 50  
|||||  
Db 2798 CAGAGCAATGAGAT 2813

RESULT 30  
US-11-134-795-8/c  
; Sequence 8, Application US/11134795  
; Publication No. US20050273869A1  
; GENERAL INFORMATION:  
; APPLICANT: Court, Donald L  
; APPLICANT: Delta, Simanci  
; APPLICANT: Constantino, Nina  
; TITLE OF INVENTION: PLASMIDS AND PHAGE FOR HOMOLOGOUS RECOMBINATION AND METHODS OF  
; FILE REFERENCE: 4239-68523-04  
; CURRENT APPLICATION NUMBER: US/11/134,795  
; CURRENT FILING DATE: 2005-05-20  
; PRIOR APPLICATION NUMBER: US 60/573,504  
; PRIOR FILING DATE: 2004-05-21  
; PRIOR APPLICATION NUMBER: US60/653,259  
; PRIOR FILING DATE: 2005-02-14  
; PRIOR APPLICATION NUMBER: US 60/655,729  
; PRIOR FILING DATE: 2005-02-22  
; NUMBER OF SEQ ID NOS: 35  
; SOFTWARE: Patentin version 3.3  
; SEQ ID NO 8  
; LENGTH: 3914  
; TYPE: DNA  
; ORGANISM: artificial sequence  
; FEATURE:  
; OTHER INFORMATION: phage genes  
US-11-134-795-8

Query Match 28.6%; Score 16; DB 14; Length 3914;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
Db 2778 TGAATGCTCATCCGA 2763

RESULT 31  
US-10-933-746-40  
; Sequence 40, Application US/10933746  
; Publication No. US20060029998A1  
; GENERAL INFORMATION:  
; APPLICANT: FLECKENSTEIN, Bernhard  
; ENSER, Armin  
; TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEML) AND  
; CORRESPONDING SEMAPHORINS IN OTHER SPECIES  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Frommer Lawrence & Haug LLP  
; STREET: 745 Fifth Avenue  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10151  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/10/933,746  
; FILING DATE: 03-Sep-2004  
; CLASSIFICATION: <Unknown>  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Lawrence, William F.  
; REGISTRATION NUMBER: 28,029  
; REFERENCE/DOCKET NUMBER: 514429-3647  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-588-0800  
; TELEFAX: 212-588-0500  
; INFORMATION FOR SEQ ID NO: 40:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3999 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: DNA (genomic)  
; SEQUENCE DESCRIPTION: SEQ ID NO: 40:  
US-10-933-746-40

Query Match 28.6%; Score 16; DB 9; Length 3999;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGAATGCTCATCCGA 32  
|||||  
Db 1082 TGAATGCTCATCCGA 1097

RESULT 32  
US-10-933-746-39  
; Sequence 39, Application US/10933746  
; Publication No. US20060029998A1  
; GENERAL INFORMATION:  
; APPLICANT: FLECKENSTEIN, Bernhard  
; ENSER, Armin  
; TITLE OF INVENTION: HUMAN SEMAPHORIN L (H-SEML) AND  
; CORRESPONDING SEMAPHORINS IN OTHER SPECIES  
; NUMBER OF SEQUENCES: 44  
; CORRESPONDENCE ADDRESS:  
US-10-933-746-39



```

; ADDRESS: Frommer Lawrence & Haug LLP
; STREET: 745 Fifth Avenue
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10151
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/933,746
; FILING DATE: 03-Sep-2004
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Lawrence, William F.
; REGISTRATION NUMBER: 28,029
; REFERENCE/DOCKET NUMBER: 514429-3647
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-588-0800
; TELEFAX: 212-588-0500
;
; INFORMATION FOR SEQ ID NO: 39:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4019 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; SEQUENCE DESCRIPTION: SEQ ID NO: 39:
US-10-933-746-39

Query Match      28.6%; Score 16; DB 9; Length 4019;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      1102 TGAATGCTCATCCGGA 1117

RESULT 33
US-11-251-821-41/c
; Sequence 41, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MO
; FILE REFERENCE: 0942.5120002
; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23

```

```

; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 41
; LENGTH: 4428
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212
; FEATURE:
; NAME/KEY: gene
; LOCATION: (866)...(1097)
; OTHER INFORMATION: attP1
; FEATURE:
; NAME/KEY: gene
; LOCATION: (1493)...(1798)
; OTHER INFORMATION: ccdb
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2140)...(2799)
; OTHER INFORMATION: cmt
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3047)...(3279)
; OTHER INFORMATION: attP2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3398)...(4128)
; OTHER INFORMATION: Km
; FEATURE:
; NAME/KEY: gene
; LOCATION: (4209)...(4229)
; OTHER INFORMATION: TetOp
US-11-251-821-41

Query Match      28.6%; Score 16; DB 11; Length 4428;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      2600 TGAATGCTCATCCGGA 2585

RESULT 34
US-11-251-821-40/c
; Sequence 40, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID M
; FILE REFERENCE: 0942.5120002
; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09

```



```
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 40
; LENGTH: 4470
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: plasmid pDONR201
; NAME/KEY: gene
; LOCATION: (29)..(260)
; OTHER INFORMATION: atcpl
; FEATURES:
; NAME/KEY: gene
; LOCATION: (656)..(961)
; OTHER INFORMATION: ccdb
; FEATURES:
; NAME/KEY: gene
; LOCATION: (1099)..(1184)
; OTHER INFORMATION: ccda
; FEATURES:
; NAME/KEY: gene
; LOCATION: (1303)..(1962)
; OTHER INFORMATION: cmr
; FEATURES:
; NAME/KEY: gene
; LOCATION: (2210)..(2442)
; OTHER INFORMATION: atcp2
; FEATURES:
; NAME/KEY: gene
; LOCATION: (2565)..(3374)
; OTHER INFORMATION: kmr
; FEATURES:
; NAME/KEY: gene
; LOCATION: (3495)..(4134)
; OTHER INFORMATION: ori
; US-11-251-821-40

Query Match      28.6%; Score 16; DB 11; Length 4470;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      1763 TGAATGCTCATCCGGA 1748

RESULT 35
US-11-251-821-42/c
; Sequence 42, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID MOI
; FILE REFERENCE: 0942.512002
; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
```

```
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 42
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: plasmid pDONR212(F)
; NAME/KEY: gene
; LOCATION: (117)..(248)
; OTHER INFORMATION: atcpl
; FEATURES:
; NAME/KEY: gene
; LOCATION: (644)..(949)
; OTHER INFORMATION: ccdb
; FEATURES:
; NAME/KEY: gene
; LOCATION: (1291)..(1950)
; OTHER INFORMATION: cmr
; FEATURES:
; NAME/KEY: gene
; LOCATION: (2198)..(2430)
; OTHER INFORMATION: atcp2
; FEATURES:
; NAME/KEY: gene
; LOCATION: (2549)..(3279)
; OTHER INFORMATION: kmr
; FEATURES:
; NAME/KEY: gene
; LOCATION: (3360)..(3380)
; OTHER INFORMATION: tetop
; FEATURES:
; NAME/KEY: gene
; LOCATION: (3445)..(4084)
; OTHER INFORMATION: pUC ori
; US-11-251-821-42

Query Match      28.6%; Score 16; DB 11; Length 4627;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      1751 TGAATGCTCATCCGGA 1736

RESULT 36
US-11-251-821-43/c
; Sequence 43, Application US/11251821
; Publication No. US20060035272A1
; GENERAL INFORMATION:
; APPLICANT: BRASCH, MICHAEL A.
; APPLICANT: CHEO, DAVID
; APPLICANT: LI, XIAO
; APPLICANT: ESPOSITO, DOMINIC
; APPLICANT: BYRD, DEVON R.N.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR USE IN ISOLATION OF NUCLEIC ACID I
; FILE REFERENCE: 0942.512002
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; CURRENT APPLICATION NUMBER: US/11/251,821
; CURRENT FILING DATE: 2005-10-18
; PRIOR APPLICATION NUMBER: US 10/640,422
; PRIOR FILING DATE: 2003-08-14
; PRIOR APPLICATION NUMBER: US 60/402,920
; PRIOR FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: US 10/151,690
; PRIOR FILING DATE: 2002-05-21
; PRIOR APPLICATION NUMBER: US 09/907,719
; PRIOR FILING DATE: 2001-07-19
; PRIOR APPLICATION NUMBER: US 60/291,973
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: US 09/732,914
; PRIOR FILING DATE: 2000-12-11
; PRIOR APPLICATION NUMBER: US 60/188,020
; PRIOR FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: US 60/169,983
; PRIOR FILING DATE: 1999-12-10
; PRIOR APPLICATION NUMBER: US 09/177,387
; PRIOR FILING DATE: 1998-10-23
; PRIOR APPLICATION NUMBER: US 60/065,930
; PRIOR FILING DATE: 1997-10-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 4627
; TYPE: DNA
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid pDONR212(R)
; NAME/KEY: gene
; LOCATION: (17)...(248)
; FEATURE:
; OTHER INFORMATION: atcpl1
; NAME/KEY: gene
; LOCATION: (644)...(949)
; FEATURE:
; OTHER INFORMATION: ccdb
; NAME/KEY: gene
; LOCATION: (1291)...(1950)
; OTHER INFORMATION: cmr
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2198)...(2430)
; OTHER INFORMATION: atcp2
; FEATURE:
; NAME/KEY: gene
; LOCATION: (2549)...(3279)
; OTHER INFORMATION: km
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3360)...(3380)
; OTHER INFORMATION: Tecp
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3683)...(4322)
; OTHER INFORMATION: puc ori
; US-11-251-821-43

Query Match      28.6%; Score 16; DB 11; Length 4627;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      1751 TGAATGCTCATCCGGA 1736

RESULT 37
US-11-134-795-1/c
; Sequence 1, Application US/11134795
; Publication No. US20050273869A1

; GENERAL INFORMATION:
; APPLICANT: Court, Donald L
; APPLICANT: Data, Simanti
; APPLICANT: Constantino, Nina
; TITLE OF INVENTION: PLASIDS AND PHAGE FOR HOMOLOGOUS RECOMBINATION AND METHODS OF
; TITLE OF INVENTION: USE
; FILE REFERENCE: 4239-68523-04
; CURRENT APPLICATION NUMBER: US/11/134,795
; CURRENT FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: US 60/573,504
; PRIOR FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: US60/653,259
; PRIOR FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: US 60/655,729
; PRIOR FILING DATE: 2005-02-22
; NUMBER OF SEQ ID NOS: 35
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1
; LENGTH: 4907
; TYPE: DNA
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: plasmid
; US-11-134-795-1

Query Match      28.6%; Score 16; DB 14; Length 4907;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      2800 TGAATGCTCATCCGGA 2785

RESULT 38
US-11-183-036-5/c
; Sequence 5, Application US/11183036
; Publication No. US20060014197A1
; GENERAL INFORMATION:
; APPLICANT: LANDICK, Robert C.
; TITLE OF INVENTION: IN VIVO SCREENING METHODS FOR IDENTIFYING INHIBITORS OF RNA
; TITLE OF INVENTION: POLYMERASES
; FILE REFERENCE: 054030-0106
; CURRENT APPLICATION NUMBER: US/11/183,036
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/588,241
; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 4922
; TYPE: DNA
; ORGANISM: Aequorea victoria
; US-11-183-036-5

Query Match      28.6%; Score 16; DB 14; Length 4922;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      17 TGAATGCTCATCCGGA 32
DB      3519 TGAATGCTCATCCGGA 3504

RESULT 39
US-11-181-148-1/c
; Sequence 1, Application US/11181148
; Publication No. US20060019292A1
; GENERAL INFORMATION:
; APPLICANT: Farmer, Alan Andrew
; TITLE OF INVENTION: SEQUENCE SPECIFIC RECOMBINASE-BASED
; TITLE OF INVENTION: METHODS FOR PRODUCING INTRON CONTAINING VECTORS AND
; TITLE OF INVENTION: COMPOSITIONS FOR USE IN PRACTICING THE SAME
```



```

; FILE REFERENCE: CLON-069CON
; CURRENT APPLICATION NUMBER: US/11/181,148
; CURRENT FILING DATE: 2005-07-13
; PRIOR APPLICATION NUMBER: 60/263,358
; PRIOR FILING DATE: 2001-01-18
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4938
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Vector
US-11-181-148-1

```

```

Query Match      28.6%; Score 16; DB 14; Length 4938;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      17 TGAATGCTCATCCGGA 32
Db      787 TGAATGCTCATCCGGA 772

```

```

RESULT 40
US-11-183-036-4/C
; Sequence 4, Application US/11183036
; Publication No. US20060014197A1
; GENERAL INFORMATION:
; APPLICANT: LANDICK, Robert C.
; TITLE OF INVENTION: IN VIVO SCREENING METHODS FOR IDENTIFYING INHIBITORS OF RNA
; FILE REFERENCE: 054030-0106
; CURRENT APPLICATION NUMBER: US/11/183,036
; CURRENT FILING DATE: 2005-07-15
; PRIOR APPLICATION NUMBER: US 60/588,241
; PRIOR FILING DATE: 2004-07-15
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 5027
; TYPE: DNA
; ORGANISM: Aequorea victoria
US-11-183-036-4

```

```

Query Match      28.6%; Score 16; DB 14; Length 5027;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

QY      17 TGAATGCTCATCCGGA 32
Db      3613 TGAATGCTCATCCGGA 3598

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Job time : 241.711 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 16:27:36 ; Search time 771.045 Seconds  
(without alignments)  
3398.084 Million cell updates/sec

Title: US-10-712-654-26

Perfect score: 56

Sequence: 1 gcattccgctgtatgtgaa.....ggagcaatggaattacacg 56

Scoring table:

OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 41078325 seqs, 23393541228 residues

Word size : 1

Total number of hits satisfying chosen parameters: 82156240

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_est3: \*  
4: gb\_est4: \*  
5: gb\_est5: \*  
6: gb\_est6: \*  
7: gb\_est7: \*  
8: gb\_est8: \*  
9: gb\_est9: \*  
10: gb\_est10: \*  
11: gb\_est11: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33.9	354	2	BB695762	BB695762 QVO-CT022
2	33.9	576	6	AQ724199	AQ724199 HS_2102_A
3	33.9	688	6	CA266323	CA266323 SCGLB204
4	33.9	1135	9	CC239784	CC239784 CH261-81N
5	32.1	259	6	CB333333	CB333333 py3e06.y
6	32.1	401	10	CM470659	CM470659 fdbb001f2
7	32.1	463	10	CM111224	CM111224 104_484_1
8	32.1	462	6	CB811731	CB811731 BN10_001K
9	32.1	511	6	CB822333	CB822333 BN25_044N
10	32.1	516	6	CB817719	CB817719 BN20_042O
11	32.1	539	3	BI471522	BI471522 gag21e02.
12	32.1	545	10	CM493595	CM493595 fdbb001f2
13	32.1	545	10	CB818845	CB818845 BN20_047A
14	32.1	572	3	BI701634	BI701634 gag11b012.
15	32.1	615	6	CB816121	CB816121 BN15_028J
16	32.1	629	6	CB817335	CB817335 BN20_041I
17	32.1	631	6	CB820120	CB820120 BN20_051E
18	32.1	639	6	CB818923	CB818923 BN20_047E
19	32.1	646	6	CA240976	CA240976 SCCTFL307
20	32.1	646	6	CB818270	CB818270 BN20_044O
21	32.1	648	6	CB812327	CB812327 BN10_020M
22	32.1	653	6	CB888947	CB888947 G118.110J

C 23	18	32.1	660	6	CB819000	CB819000 BN20_047I
C 24	18	32.1	685	6	CB817887	CB817887 BN20_043I
C 25	18	32.1	691	10	CM473221	CM473221 fdbb001f2
C 26	18	32.1	696	6	CB861812	CB861812 AZ01_003O
C 27	18	32.1	707	10	CM175990	CM175990 104_588_1
C 28	18	32.1	715	10	CM029106	CM029106 104_256_1
C 29	18	32.1	724	6	CB823726	CB823726 BN25_049M
C 30	18	32.1	724	10	CM029105	CM029105 104_256_1
C 31	18	32.1	729	6	CB824516	CB824516 BN25_053N
C 32	18	32.1	747	10	CM831094	CM831094 OP_Ba008
C 33	18	32.1	755	7	CV203057	CV203057 EST862767
C 34	18	32.1	762	10	CM493596	CM493596 fdbb001f2
C 35	18	32.1	831	6	CA493148	CA493148 AGENCOURT
C 36	18	32.1	842	11	CNS04PNO	AL301833 Tetradon
C 37	18	32.1	918	11	CNS04H8B	AL290612 Tetradon
C 38	18	32.1	931	7	CV210691	CV210691 EST870401
C 39	18	32.1	941	7	CV203058	CV203058 EST862768
C 40	18	32.1	958	7	CV210692	CV210692 EST870402
C 41	18	32.1	974	10	CNS02GTC	AL196761 Tetradon
C 42	18	32.1	986	7	CV203056	CV203056 EST862766
C 43	18	32.1	991	11	CNS03KPG	AL248461 Tetradon
C 44	17	30.4	239	1	AV309300	AV309300 AV309300
C 45	17	30.4	367	1	AL789148	AL789148 AL789148
C 46	17	30.4	424	3	BP583232	BP583232 BP583232
C 47	17	30.4	453	10	CM048668	CM048668 104_287_1
C 48	17	30.4	479	10	CM194029	CM194029 104_617_1
C 49	17	30.4	480	1	AU240260	AU240260 AU240260
C 50	17	30.4	497	3	BQ170631	BQ170631 WHR1792_D
C 51	17	30.4	506	10	CL165419	CL165419 104_360_1
C 52	17	30.4	516	1	AV930801	AV930801 AV930801
C 53	17	30.4	522	5	CA005557	CA005557 HU10A17H
C 54	17	30.4	527	1	AI998238	AI998238 701544854
C 55	17	30.4	551	1	AV929666	AV929666 AV929666
C 56	17	30.4	558	1	AV925657	AV925657 AV925657
C 57	17	30.4	561	9	AQ797879	AQ797879 HS_5488_A
C 58	17	30.4	569	7	CF888220	CF888220 amagtc-25
C 59	17	30.4	571	6	CB896020	CB896020 G174_101J
C 60	17	30.4	573	5	CA008148	CA008148 HU10A17H
C 61	17	30.4	588	1	AV924569	AV924569 AV924569
C 62	17	30.4	595	6	CB387347	CB387347 OSTF078H7
C 63	17	30.4	607	10	CM896439	CM896439 RPT142_12
C 64	17	30.4	609	10	CM206282	CM206282 104_635_1
C 65	17	30.4	634	10	CM412453	CM412453 fdbb001f1
C 66	17	30.4	655	10	CM191823	CM191823 104_614_1
C 67	17	30.4	663	10	CM206283	CM206283 104_635_1
C 68	17	30.4	680	9	B2348067	B2348067 ho55d08.g
C 69	17	30.4	684	10	CM362055	CM362055 fdbb001f0
C 70	17	30.4	695	9	B2079974	B2079974 11b40d11.
C 71	17	30.4	702	10	CNS02HCL	AL197454 Tetradon
C 72	17	30.4	739	1	AJ613864	AJ613864 AJ613864
C 73	17	30.4	808	10	CM560720	CM560720 OA_ABA008
C 74	17	30.4	862	11	CR828291	CR828291 GROAA6CC
C 75	17	30.4	933	10	CG883689	CG883689 ZMMBB049
C 76	17	30.4	939	2	BP219506	BP219506 601883008
C 77	17	30.4	979	10	CL136715	CL136715 ISB1_108G
C 78	17	30.4	990	11	CNS06XAG	AL148466 TS_end_of
C 79	17	30.4	1005	10	CL120868	CL120868 ISB1_79J1
C 80	17	30.4	1020	10	CL113659	CL113659 ISB1_58N1
C 81	17	30.4	1022	9	AZ157715	AZ157715 SP_0058_A
C 82	17	30.4	1150	10	CL110721	CL110721 ISB1_54C6
C 83	16	28.6	102	5	B0759291	B0759291 EB0101_SO
C 84	16	28.6	117	9	BH550223	BH550223 BOHRH6ETP
C 85	16	28.6	146	8	DN837163	DN837163 EST_0300
C 86	16	28.6	197	2	BE095038	BE095038 CM3-BT079
C 87	16	28.6	205	6	CB349243	CB349243 CAB2SGC00
C 88	16	28.6	215	7	CK125555	CK125555 BBS182410
C 89	16	28.6	218	1	AI267699	AI267699 ac93e04.x
C 90	16	28.6	226	2	BE713786	BE713786 MR3-HT071
C 91	16	28.6	239	2	BE713273	BE713273 MR3-HT071
C 92	16	28.6	251	2	BE713753	BE713753 MR3-HT071
C 93	16	28.6	253	2	BE713587	BE713587 MR3-HT071
C 94	16	28.6	280	2	BE713662	BE713662 MR3-HT071
C 95	16	28.6	281	2	BB551134	BB551134 BB551134



96	16	28.6	287	1	AM336138	AM336138	23649	MAR	C 169	16	28.6	518	7	CN624530	CN624530	lae10c10.
97	16	28.6	301	1	AM12875	AM12875	5230	MAR	C 170	16	28.6	518	9	BH236829	BH236829	ATZUC14TF
98	16	28.6	309	1	BH242113	BH242113			C 171	16	28.6	520	1	AL928427	AL928427	AT928427
99	16	28.6	319	8	F11634	F11634	HSCC2ZE111	n	C 172	16	28.6	523	3	B1110394	B1110394	B1110394
100	16	28.6	328	1	AM321287	AM321287	uo29F04.y		C 173	16	28.6	523	9	B2294859	B2294859	CG1145.r1
101	16	28.6	333	7	CN630271	CN630271	laE37e04.		C 174	16	28.6	524	9	BH307585	BH307585	CH230-98F
102	16	28.6	338	1	AM966721	AM966721	701688074		C 175	16	28.6	528	1	AM027381	AM027381	me73h12.x
103	16	28.6	340	8	F06774	F06774	HSC1KD101	n	C 176	16	28.6	528	2	BF665901	BF665901	602119057
104	16	28.6	350	5	DN589602	DN589602	50818.1	L	C 177	16	28.6	528	2	BG545159	BG545159	602572352
105	16	28.6	375	5	BY543096	BY543096			C 178	16	28.6	531	10	CZ680741	CZ680741	OM_BA023
106	16	28.6	377	3	BP961127	BP961127			C 179	16	28.6	532	9	BH242643	BH242643	AUTIT37TF
107	16	28.6	379	1	AM695281	AM695281	NF093B05S		C 180	16	28.6	533	6	CF604194	CF604194	BACCA01_0
108	16	28.6	379	1	AM900432	AM900432	CMO-NN100		C 181	16	28.6	535	7	BF771177	BF771177	lae74h02.
109	16	28.6	379	9	BH241444	BH241444	AUTLB08TF		C 182	16	28.6	542	1	BH238802	BH238802	ATYCC85TF
110	16	28.6	386	2	B1056214	B1056214	PMO-ANN034		C 183	16	28.6	546	1	AA724847	AA724847	ah97b10..8
111	16	28.6	389	6	CB344432	CB344432	CA48EN000		C 184	16	28.6	547	7	CK119939	CK119939	210b16.p1
112	16	28.6	391	6	CB345275	CB345275	CA48EN000		C 185	16	28.6	547	7	CK119939	CK119939	210b16.p1
113	16	28.6	395	10	CW508503	CW508503	OP_BA000		C 186	16	28.6	553	2	B1056283	B1056283	PMO-GN034
114	16	28.6	402	3	BI481234	BI481234	H2RPE-137		C 187	16	28.6	557	5	CK515911	CK515911	rwajb0_00
115	16	28.6	404	1	AM385339	AM385339	RC5-LT000		C 188	16	28.6	557	7	BM948327	BM948327	BM948327
116	16	28.6	412	2	BF667212	BF667212	602121011		C 189	16	28.6	557	9	CK121931	CK121931	212b19.p1
117	16	28.6	417	2	B1070496	B1070496	CM2-NN020		C 190	16	28.6	561	9	BH239208	BH239208	ATYCF42TF
118	16	28.6	420	2	BF946239	BF946239	CM2-NN020		C 191	16	28.6	562	9	BZ293365	BZ293365	CG1443.r1
119	16	28.6	428	7	CO277040	CO277040	EK122730.		C 192	16	28.6	563	9	A2148754	A2148754	SP_0048.A
120	16	28.6	430	1	AI009242	AI009242	EST203693		C 193	16	28.6	564	7	CK119894	CK119894	210E13.p1
121	16	28.6	430	5	BY548245	BY548245	BY548245		C 194	16	28.6	564	9	BZ298182	BZ298182	CG4054..r1
122	16	28.6	432	8	RI8438	RI8438	Y902h07.r1		C 195	16	28.6	566	2	BG505741	BG505741	601860215
123	16	28.6	433	2	B1033136	B1033136	FM3-NN022		C 196	16	28.6	566	6	CA539819	CA539819	C0283F01-
124	16	28.6	434	2	BZ300544	BZ300544	KD0781.r1		C 197	16	28.6	568	10	CM102396	CM102396	104_470_1
125	16	28.6	435	2	BE020188	BE020188	sm39G04.y		C 198	16	28.6	569	7	CK121239	CK121239	203D20.p1
126	16	28.6	435	7	CK757116	CK757116	eca01-9c8		C 199	16	28.6	572	7	CK054180	CK054180	56446r8c
127	16	28.6	442	2	BG363668	BG363668	sacl6h10.		C 200	16	28.6	572	7	CK518822	CK518822	rwaeao_00
128	16	28.6	442	7	CK099968	CK099968	A092P24.5		C 201	16	28.6	573	2	BF978930	BF978930	602147605
129	16	28.6	442	9	AZ438992	AZ438992	IM0229921		C 202	16	28.6	575	6	CD478295	CD478295	eca01-67m
130	16	28.6	449	6	CA538462	CA538462	C0266H10-		C 203	16	28.6	579	7	CN624316	CN624316	tae10c10.
131	16	28.6	456	2	BF031126	BF031126	601558809		C 204	16	28.6	581	2	BF977333	BF977333	602146316
132	16	28.6	456	5	BM909142	BM909142	wm79C06.x		C 205	16	28.6	581	2	BP194864	BP194864	BP194864
133	16	28.6	458	1	AI935981	AI935981	wm79C06.x		C 206	16	28.6	582	3	BP308580	BP308580	BP308580
134	16	28.6	458	9	BH243283	BH243283	AUIH10TF		C 207	16	28.6	582	3	CB295631	CB295631	12832040
135	16	28.6	463	4	CNS0GAFH	CNS0GAFH	Tetradodon		C 208	16	28.6	583	6	CF9883300	CF9883300	mak18b06-
136	16	28.6	466	2	BF947984	BF947984	FM3-NN117		C 209	16	28.6	589	7	CK117847	CK117847	209P12.p1
137	16	28.6	469	7	CO275877	CO275877	EK119028.		C 210	16	28.6	590	7	CK117847	CK117847	209P12.p1
138	16	28.6	471	6	CF653066	CF653066	93-L02057		C 211	16	28.6	591	1	BP961126	BP961126	BP961126
139	16	28.6	473	7	CK902436	CK902436	1m46b11.x		C 212	16	28.6	591	10	CM471261	CM471261	F6bD001f2
140	16	28.6	473	9	BH238642	BH238642	ATYCC59TR		C 213	16	28.6	596	7	CF419222	CF419222	USDA-FP.1
141	16	28.6	474	7	CO314759	CO314759	EK237729.		C 214	16	28.6	596	7	CK121401	CK121401	203611.p1
142	16	28.6	475	1	AU296320	AU296320			C 215	16	28.6	596	9	BH703224	BH703224	BOMOP93TR
143	16	28.6	475	6	CB345182	CB345182	CA48EN000		C 216	16	28.6	598	7	CK119557	CK119557	B13dSG42A
144	16	28.6	475	7	CN774865	CN774865	lae74h02.		C 217	16	28.6	602	7	CK119557	CK119557	210G21.p1
145	16	28.6	482	9	AZ478649	AZ478649	IM0298E21		C 218	16	28.6	603	1	AM935088	AM935088	RC2-DT000
146	16	28.6	482	10	C8515131	C8515131	t1gr-g88-		C 219	16	28.6	603	5	BO399398	BO399398	NISC-mp03
147	16	28.6	483	5	BK529083	BK529083			C 220	16	28.6	604	9	BH239463	BH239463	ATYCH10TF
148	16	28.6	483	6	CD417457	CD417457	Gm_CK818		C 221	16	28.6	605	6	CA230604	CA230604	SCJFFL3C0
149	16	28.6	484	9	AQ227980	AQ227980	HS_2022.B		C 222	16	28.6	606	7	CV000003	CV000003	aaam01-10m
150	16	28.6	487	1	AI936002	AI936002	wm79E06.x		C 223	16	28.6	608	9	AQ962140	AQ962140	LERPD56TF
151	16	28.6	488	1	AM632356	AM632356	EST321201		C 224	16	28.6	614	5	BUS49169	BUS49169	GMB80018A
152	16	28.6	489	7	CO283564	CO283564	EK163655.		C 225	16	28.6	614	9	BH242792	BH242792	AUTIRA43TF
153	16	28.6	492	9	AZ315386	AZ315386			C 226	16	28.6	617	9	BH242792	BH242792	odh73g11.
154	16	28.6	493	9	BZ298780	BZ298780	CG4577.r1		C 227	16	28.6	619	2	BF670239	BF670239	602119875
155	16	28.6	497	3	BZ302090	BZ302090	KD1645.q1		C 228	16	28.6	619	6	CB346050	CB346050	CAB28G000
156	16	28.6	498	3	BF577161	BF577161	602135455		C 229	16	28.6	620	6	CB345309	CB345309	CA48EN000
157	16	28.6	499	5	BM852531	BM852531			C 230	16	28.6	621	2	BF978448	BF978448	B8566619
158	16	28.6	503	5	BM852531	BM852531			C 231	16	28.6	622	2	BUD72672	BUD72672	602148852
159	16	28.6	504	3	BI511478	BI511478	BH160006A		C 232	16	28.6	622	5	BH272672	BH272672	1m46b11.y
160	16	28.6	510	6	AQ735955	AQ735955	HS_2261.A		C 233	16	28.6	622	9	BH239359	BH239359	ATYCH19TF
161	16	28.6	511	6	CB345066	CB345066	CA48EN000		C 234	16	28.6	624	3	BP307317	BP307317	BP307317
162	16	28.6	512	3	BI510036	BI510036	BH170022B		C 235	16	28.6	626	7	CK005182	CK005182	AGENCOURT
163	16	28.6	513	1	AI333554	AI333554	CP96412.x		C 236	16	28.6	626	9	BZ012547	BZ012547	oe165F04.
164	16	28.6	514	3	BP925486	BP925486			C 237	16	28.6	628	8	CD701713	CD701713	EST18237
165	16	28.6	514	7	CK119513	CK119513	211n21.p1		C 238	16	28.6	629	8	DR744936	DR744936	RTCU1_26
166	16	28.6	516	7	CK119240	CK119240	213h02.p1		C 239	16	28.6	629	9	BZ083005	BZ083005	11d79H06-
167	16	28.6	517	5	BM846912	BM846912			C 240	16	28.6	631	9	BH244863	BH244863	AUIUA41TF
168	16	28.6	518	6	CB344744	CB344744	CA48EN000		C 241	16	28.6	632	1	AI859465	AI859465	wm12b06.x



242	16	28.6	632	7	CKI18029	CKI1029	218k16.p1	c 315	16	28.6	671	9	BH966552	BH966552	od332f03.
c 243	16	28.6	633	9	BZ065064	BZ065064	1kx73a03.	c 316	16	28.6	671	9	BZ050849	BZ050849	jnr64f01.
c 244	16	28.6	633	9	BZ083000	BZ083000	11q79b10.	c 317	16	28.6	671	9	BZ057753	BZ057753	11f21d06.
c 245	16	28.6	635	9	BH242429	BH242429	ATrFB55TF	c 318	16	28.6	671	9	BZ080321	BZ080321	11f75a10.
c 246	16	28.6	637	6	CB295832	CB295832	12B22030.	c 319	16	28.6	672	9	BH920890	BH920890	odh94b10.
c 247	16	28.6	637	7	CO237646	CO237646	WS0073.B2	c 320	16	28.6	672	9	BH940238	BH940238	odf76b10.
c 248	16	28.6	637	10	CM349421	CM349421	fadb001f0	c 321	16	28.6	672	9	BH952024	BH952024	odt50e06.
c 249	16	28.6	639	7	CN769089	CN769089	1afE24a10.	c 322	16	28.6	672	9	BZ044091	BZ044091	1k159d01.
c 250	16	28.6	639	9	BH936471	BH936471	odq60h06.	c 323	16	28.6	672	9	BZ075486	BZ075486	1kx08b01.
c 251	16	28.6	641	2	BB632126	BB632126	BB632126	c 324	16	28.6	672	9	BZ080524	BZ080524	11p94b09.
c 252	16	28.6	641	9	BH980420	BH980420	od681d02.	c 325	16	28.6	672	9	BZ080578	BZ080578	11b94g03.
c 253	16	28.6	641	10	CL866469	CL866469	450216.VM	c 326	16	28.6	673	10	AG074968	AG074968	Pan Troc31
c 254	16	28.6	644	9	BH936488	BH936488	odq60b12.	c 327	16	28.6	673	2	BG618129	BG618129	602645043
c 255	16	28.6	646	6	CA110363	CA110363	SCVPHR109	c 328	16	28.6	673	5	BY729455	BY729455	
c 256	16	28.6	647	9	BH986295	BH986295	oe985c07.	c 329	16	28.6	673	9	BH961770	BH961770	odj13b06.
c 257	16	28.6	648	9	BH981516	BH981516	odf93f04.	c 330	16	28.6	673	9	BH961909	BH961909	odh84c03.
c 258	16	28.6	650	2	BF947992	BF947992	PM3-NN117	c 331	16	28.6	673	9	BH965308	BH965308	odh47b07.
c 259	16	28.6	650	6	CD612882	CD612882	56086221J	c 332	16	28.6	673	9	BZ050841	BZ050841	jnr64e02.
c 260	16	28.6	650	9	BH930021	BH930021	odh69b03.	c 333	16	28.6	673	9	BZ052814	BZ052814	jnr13a01.
c 261	16	28.6	650	9	BZ069158	BZ069158	1kx07f05.	c 334	16	28.6	673	9	BZ075205	BZ075205	1kx39d09.
c 262	16	28.6	651	6	CD612881	CD612881	56086221H	c 335	16	28.6	674	9	BH955733	BH955733	od4148c07.
c 263	16	28.6	652	9	BZ044105	BZ044105	1k159h04.	c 336	16	28.6	674	9	BH980295	BH980295	odf74a05.
c 264	16	28.6	652	9	BZ080169	BZ080169	1k158e02.	c 337	16	28.6	674	9	BH981289	BH981289	odf66g04.
c 265	16	28.6	655	5	BH339622	BH339622	603514960	c 338	16	28.6	674	9	BZ043442	BZ043442	1kx57b01.
c 266	16	28.6	655	9	BH960713	BH960713	odq88e01.	c 339	16	28.6	675	2	BG534577	BG534577	602553428
c 267	16	28.6	656	9	BH945497	BH945497	odv14a06.	c 340	16	28.6	675	9	BH922299	BH922299	odh01e09.
c 268	16	28.6	656	9	BH957909	BH957909	odh63g07.	c 341	16	28.6	675	9	BH927611	BH927611	odh22f01.
c 269	16	28.6	657	9	BH969559	BH969559	odh60g03.	c 342	16	28.6	675	9	BH934884	BH934884	odg48b11.
c 270	16	28.6	657	9	BZ046643	BZ046643	1kx60g06.	c 343	16	28.6	675	9	BH954003	BH954003	odt04d07.
c 271	16	28.6	658	7	CK210323	CK210323	FGAS02212	c 344	16	28.6	675	9	BH966107	BH966107	odh50g02.
c 272	16	28.6	658	2	CN650431	CN650431	Eg_PSRGRS	c 345	16	28.6	675	9	BZ065237	BZ065237	11c07h04.
c 273	16	28.6	659	2	BG428488	BG428488	602501004	c 346	16	28.6	675	9	BZ080417	BZ080417	11f75a10.
c 274	16	28.6	659	5	BW196251	BW196251	BM196251	c 347	16	28.6	675	9	BZ086716	BZ086716	11g30d12.
c 275	16	28.6	660	2	BB620936	BB620936	BB620936	c 348	16	28.6	676	2	BF217649	BF217649	601883963
c 276	16	28.6	660	9	BZ043010	BZ043010	1k156c02.	c 349	16	28.6	676	3	BJ664117	BJ664117	Bj664117
c 277	16	28.6	660	9	BZ055154	BZ055154	jnr30h03.	c 350	16	28.6	676	9	BH239768	BH239768	ATYCU76TF
c 278	16	28.6	660	9	BZ076606	BZ076606	1kx87h06.	c 351	16	28.6	676	9	BH927615	BH927615	odh22g02.
c 279	16	28.6	660	9	BZ077287	BZ077287	11c88h06.	c 352	16	28.6	676	9	BH953965	BH953965	odt04f06.
c 280	16	28.6	661	9	BH962669	BH962669	odh09g01.	c 353	16	28.6	676	9	BH954491	BH954491	odg91c04.
c 281	16	28.6	662	9	BH952487	BH952487	odh02e06.	c 354	16	28.6	676	9	BH980523	BH980523	odg81c09.
c 282	16	28.6	662	9	BZ040061	BZ040061	1kx21c10.	c 355	16	28.6	676	9	BZ044079	BZ044079	1k159h12.
c 283	16	28.6	663	3	B0138540	B0138540	NF004D10P	c 356	16	28.6	676	9	BZ044945	BZ044945	1jC37a10.
c 284	16	28.6	663	9	BZ038567	BZ038567	1jux8e06.	c 357	16	28.6	677	9	BZ088553	BZ088553	1kx82d08.
c 285	16	28.6	663	9	BZ065152	BZ065152	11c07a03.	c 358	16	28.6	677	9	BH927363	BH927363	odh93f11.
c 286	16	28.6	664	9	BH957702	BH957702	odf78e08.	c 359	16	28.6	677	9	BH934675	BH934675	od618f12.
c 287	16	28.6	664	9	BH966918	BH966918	odh13c02.	c 360	16	28.6	677	9	BH965995	BH965995	odg90g05.
c 288	16	28.6	664	9	BH933846	BH933846	odf54g04.	c 361	16	28.6	677	9	BH966267	BH966267	odg96d05.
c 289	16	28.6	665	9	BZ007136	BZ007136	oeH21g03.	c 362	16	28.6	677	9	BH972419	BH972419	odt04g12.
c 290	16	28.6	665	9	BZ038573	BZ038573	1jux8g11.	c 363	16	28.6	677	9	BH976468	BH976468	odg02b08.
c 291	16	28.6	665	9	BZ082348	BZ082348	11e25g05.	c 364	16	28.6	677	9	BZ043353	BZ043353	1kE73c02.
c 292	16	28.6	665	9	BZ087709	BZ087709	1kx670f09.	c 365	16	28.6	677	9	BZ044338	BZ044338	1k177d01.
c 293	16	28.6	666	9	BH923713	BH923713	odt80b07.	c 366	16	28.6	677	9	BZ055115	BZ055115	jnr30c10.
c 294	16	28.6	666	9	BZ080580	BZ080580	11p94g05.	c 367	16	28.6	677	9	BZ050712	BZ050712	1kE52a01.
c 295	16	28.6	666	9	BZ082456	BZ082456	11e41f04.	c 368	16	28.6	677	9	BZ060449	BZ060449	1kx16a03.
c 296	16	28.6	666	10	CL540816	CL540816	OB_Ba006	c 369	16	28.6	677	9	BZ067917	BZ067917	1kx17f07.
c 297	16	28.6	667	9	BZ043648	BZ043648	1kK28d08.	c 370	16	28.6	677	9	BZ067917	BZ067917	1kx17f07.
c 298	16	28.6	668	8	DR828988	DR828988	ZM_BFP007	c 371	16	28.6	677	9	BZ068452	BZ068452	1jC09g04.
c 299	16	28.6	668	9	BH929602	BH929602	odt70e06.	c 372	16	28.6	677	9	BZ073513	BZ073513	1kE68f06.
c 300	16	28.6	668	9	BH940511	BH940511	odq88d07.	c 373	16	28.6	677	9	BZ080505	BZ080505	11p94g02.
c 301	16	28.6	668	9	BH962912	BH962912	odj21f04.	c 374	16	28.6	677	10	CL587305	CL587305	OB_Ba008
c 302	16	28.6	668	9	BZ022283	BZ022283	oe994c08.	c 375	16	28.6	678	9	BH929856	BH929856	odt93a09.
c 303	16	28.6	668	9	BZ075484	BZ075484	1kH08a08.	c 376	16	28.6	678	9	BH962380	BH962380	odj48e09.
c 304	16	28.6	669	9	BH946062	BH946062	obu92d12.	c 377	16	28.6	678	9	BH964970	BH964970	odt25e06.
c 305	16	28.6	669	9	BH977633	BH977633	odq60g05.	c 378	16	28.6	678	9	BH965276	BH965276	odh47f09.
c 306	16	28.6	669	9	BZ067452	BZ067452	1jux12a01.	c 379	16	28.6	678	9	BH963442	BH963442	1kx39d09.
c 307	16	28.6	670	9	BH919892	BH919892	maJ96a12.	c 380	16	28.6	678	9	BZ038497	BZ038497	1jux2g10.
c 308	16	28.6	670	9	BH927238	BH927238	odt62d02.	c 381	16	28.6	678	9	BZ055102	BZ055102	jnr30b05.
c 309	16	28.6	670	9	BZ055534	BZ055534	jnr27e08.	c 382	16	28.6	678	9	BZ067299	BZ067299	1kx20c04.
c 310	16	28.6	670	9	BZ080209	BZ080209	11f58h06.	c 383	16	28.6	678	9	BZ082713	BZ082713	11f70b01.
c 311	16	28.6	670	9	BZ088554	BZ088554	1kx82d09.	c 384	16	28.6	678	9	BZ087785	BZ087785	1kx30e03.
c 312	16	28.6	671	9	AQ962141	AQ962141	LERGDS6TR	c 385	16	28.6	679	9	BH934749	BH934749	od618f07.
c 313	16	28.6	671	9	BH962712	BH962712	odh09d04.	c 386	16	28.6	679	9	BH942512	BH942512	odf49e07.
c 314	16	28.6	671	9	BH962712	BH962712	odh09d04.	c 387	16	28.6	679	9	BH942512	BH942512	odf49e07.



C 388	16	28.6	679	9	BH957152	BH957152	odh45b10.	C 461	16	28.6	683	9	BZ083643	BZ083643	1kx95e02.
C 389	16	28.6	679	9	BH957669	BH957669	odf78a05.	C 462	16	28.6	684	9	BH931148	BH931148	od187n11.
C 390	16	28.6	679	9	BH980447	BH980447	odf81f03.	C 463	16	28.6	684	9	BH936364	BH936364	odg58a01.
C 391	16	28.6	679	9	BZ038566	BZ038566	1j138e04.	C 464	16	28.6	684	9	BH966575	BH966575	odj32f12.
C 392	16	28.6	679	9	BZ044526	BZ044526	1k152f02.	C 465	16	28.6	684	9	BH968226	BH968226	odh53n04.
C 393	16	28.6	679	9	BZ051247	BZ051247	1jnr61e01.	C 466	16	28.6	684	9	BH970854	BH970854	odf64g11.
C 394	16	28.6	679	9	BZ080386	BZ080386	11f75f03.	C 467	16	28.6	684	9	BH972994	BH972994	odf83d08.
C 395	16	28.6	680	9	BH950043	BH950043	odj27f09.	C 468	16	28.6	684	9	BZ038552	BZ038552	1j138a09.
C 396	16	28.6	680	9	BH951811	BH951811	odh77e04.	C 469	16	28.6	684	9	BZ052990	BZ052990	11f45f01.
C 397	16	28.6	680	9	BH958990	BH958990	od144f09.	C 470	16	28.6	684	9	BZ063896	BZ063896	11c86f04.
C 398	16	28.6	680	9	BH959797	BH959797	od149a01.	C 471	16	28.6	684	9	BZ074683	BZ074683	1k114d01.
C 399	16	28.6	680	9	BH963746	BH963746	odf98f12.	C 472	16	28.6	684	9	BZ080323	BZ080323	11f75a12.
C 400	16	28.6	680	9	BH965998	BH965998	odf80e07.	C 473	16	28.6	684	9	BZ087862	BZ087862	1k122b10.
C 401	16	28.6	680	9	BH975029	BH975029	odf99e12.	C 474	16	28.6	684	9	BZ088506	BZ088506	1kx82d08.
C 402	16	28.6	680	9	BZ038492	BZ038492	1j1u4d07.	C 475	16	28.6	685	9	BH938359	BH938359	odf67e08.
C 403	16	28.6	680	9	BZ038564	BZ038564	1j1u4d07.	C 476	16	28.6	685	9	BH948364	BH948364	odh06e12.
C 404	16	28.6	680	9	BZ041998	BZ041998	1k119d09.	C 477	16	28.6	685	9	BH949547	BH949547	odh79b01.
C 405	16	28.6	680	9	BZ045179	BZ045179	1k1f53f06.	C 478	16	28.6	685	9	BH955432	BH955432	od152e03.
C 406	16	28.6	680	9	BZ048235	BZ048235	1k174b11.	C 479	16	28.6	685	9	BH958942	BH958942	od144c08.
C 407	16	28.6	680	9	BZ050823	BZ050823	1jnr64c01.	C 480	16	28.6	685	9	BH959532	BH959532	odh52f06.
C 408	16	28.6	680	9	BZ061528	BZ061528	1k1h08b01.	C 481	16	28.6	685	9	BH970717	BH970717	od129b11.
C 409	16	28.6	680	9	BZ066562	BZ066562	11f13e02.	C 482	16	28.6	685	9	BH973488	BH973488	odf67c05.
C 410	16	28.6	680	9	BZ088215	BZ088215	11e40b04.	C 483	16	28.6	685	9	BH979522	BH979522	odf52g02.
C 411	16	28.6	680	9	BZ088313	BZ088313	1kx38b02.	C 484	16	28.6	685	9	BZ025930	BZ025930	odh52f06.
C 412	16	28.6	681	9	BH949785	BH949785	odg90a04.	C 485	16	28.6	685	9	BZ043682	BZ043682	odh52f06.
C 413	16	28.6	681	9	BH966915	BH966915	odh13b01.	C 486	16	28.6	685	9	BZ048271	BZ048271	od129b11.
C 414	16	28.6	681	9	BH967797	BH967797	odh56e10.	C 487	16	28.6	685	9	BZ049361	BZ049361	1jnr50a05.
C 415	16	28.6	681	9	BZ043127	BZ043127	1kx94f10.	C 488	16	28.6	685	9	BZ052203	BZ052203	1jnr69b01.
C 416	16	28.6	681	9	BZ043662	BZ043662	1kx28e08.	C 489	16	28.6	685	9	BZ075074	BZ075074	1kx95f02.
C 417	16	28.6	681	9	BZ044100	BZ044100	1k159f08.	C 490	16	28.6	685	9	BZ080174	BZ080174	11a58e07.
C 418	16	28.6	681	9	BZ047981	BZ047981	1k1h1b01.	C 491	16	28.6	685	9	BZ080522	BZ080522	od165d07.
C 419	16	28.6	681	9	BZ052342	BZ052342	1jnr68d01.	C 492	16	28.6	686	9	BH930544	BH930544	od165d11.
C 420	16	28.6	681	9	BZ055553	BZ055553	1jnr27h01.	C 493	16	28.6	686	9	BH930933	BH930933	od110g07.
C 421	16	28.6	681	9	BZ076574	BZ076574	1k1h87h06.	C 494	16	28.6	686	9	BH942864	BH942864	odf19c10.
C 422	16	28.6	681	9	BZ084479	BZ084479	11b61f06.	C 495	16	28.6	686	9	BH948379	BH948379	odh06d10.
C 423	16	28.6	681	9	BZ088299	BZ088299	1kx77b02.	C 496	16	28.6	686	9	BH957628	BH957628	odf178d02.
C 424	16	28.6	681	9	BZ088546	BZ088546	1kx82a04.	C 497	16	28.6	686	9	BH958989	BH958989	odf14h07.
C 425	16	28.6	682	9	BH242876	BH242876	AUTW50TF	C 498	16	28.6	686	9	BH960380	BH960380	odg99d03.
C 426	16	28.6	682	9	BH928741	BH928741	odh29a02.	C 499	16	28.6	686	9	BH963395	BH963395	odh63f04.
C 427	16	28.6	682	9	BH959894	BH959894	od108e07.	C 500	16	28.6	686	9	BH969014	BH969014	odh46912.
C 428	16	28.6	682	9	BH964661	BH964661	odj22d03.	C 501	16	28.6	686	9	BH974869	BH974869	odh59a06.
C 429	16	28.6	682	9	BH974882	BH974882	odh59e11.	C 502	16	28.6	686	9	BZ048419	BZ048419	1jnr55b12.
C 430	16	28.6	682	9	BZ043640	BZ043640	1kx8c10.	C 503	16	28.6	686	9	BZ050692	BZ050692	1jnr55d02.
C 431	16	28.6	682	9	BZ046630	BZ046630	1kx60f01.	C 504	16	28.6	686	9	BZ051082	BZ051082	1jnr62b04.
C 432	16	28.6	682	9	BZ050405	BZ050405	1jnr41a03.	C 505	16	28.6	686	9	BZ051132	BZ051132	1jnr62h03.
C 433	16	28.6	682	9	BZ051223	BZ051223	1jnr61b04.	C 506	16	28.6	686	9	BZ080377	BZ080377	11f75f06.
C 434	16	28.6	682	9	BZ051372	BZ051372	1jnr60b03.	C 507	16	28.6	686	9	BZ080525	BZ080525	11b94b10.
C 435	16	28.6	682	9	BZ066608	BZ066608	11x13g06.	C 508	16	28.6	686	9	BZ080568	BZ080568	11b94f05.
C 436	16	28.6	682	9	BZ067320	BZ067320	1kx20f01.	C 509	16	28.6	686	9	BZ080664	BZ080664	11b94f05.
C 437	16	28.6	682	9	BZ080508	BZ080508	11b94a05.	C 510	16	28.6	686	9	BZ503136	BZ503136	BONQ60TF
C 438	16	28.6	682	9	BZ080563	BZ080563	11b94e12.	C 511	16	28.6	687	9	BH9227704	BH9227704	odh34h07.
C 439	16	28.6	683	9	BH924659	BH924659	odh76b04.	C 512	16	28.6	687	9	BH949767	BH949767	odg90a05.
C 440	16	28.6	683	9	BH928525	BH928525	odg92a06.	C 513	16	28.6	687	9	BH969152	BH969152	odg08e11.
C 441	16	28.6	683	9	BH948776	BH948776	od157f10.	C 514	16	28.6	687	9	BH974990	BH974990	od133c07.
C 442	16	28.6	683	9	BH951797	BH951797	odh77d08.	C 515	16	28.6	687	9	BZ077543	BZ077543	1kx79d12.
C 443	16	28.6	683	9	BH954412	BH954412	od166c02.	C 516	16	28.6	687	9	BZ080552	BZ080552	11b94e01.
C 444	16	28.6	683	9	BH956749	BH956749	odh04g12.	C 517	16	28.6	688	7	CK119945	CK119945	210c03.p1
C 445	16	28.6	683	9	BH957233	BH957233	odh45c03.	C 518	16	28.6	688	9	BH9227963	BH9227963	od182c04.
C 446	16	28.6	683	9	BH963406	BH963406	odh66b03.	C 519	16	28.6	688	9	BH961890	BH961890	odh97d11.
C 447	16	28.6	683	9	BH964372	BH964372	odh66b03.	C 520	16	28.6	688	9	BH964240	BH964240	od105e06.
C 448	16	28.6	683	9	BH964735	BH964735	odj09g09.	C 521	16	28.6	688	9	BH967167	BH967167	odh689b03.
C 449	16	28.6	683	9	BH970856	BH970856	odf68a08.	C 522	16	28.6	688	9	BH974522	BH974522	odh06a04.
C 450	16	28.6	683	9	BZ038479	BZ038479	1j1u4c12.	C 523	16	28.6	688	9	BZ038550	BZ038550	1j1u76f11.
C 451	16	28.6	683	9	BZ038502	BZ038502	1j1u42h07.	C 524	16	28.6	688	9	BZ042734	BZ042734	11a93e12.
C 452	16	28.6	683	9	BZ040842	BZ040842	1kx33f08.	C 525	16	28.6	688	9	BZ057350	BZ057350	11a93e12.
C 453	16	28.6	683	9	BZ045859	BZ045859	1k1h1f01.	C 526	16	28.6	688	9	BZ060480	BZ060480	1kx16d07.
C 454	16	28.6	683	9	BZ051097	BZ051097	1jnr62d03.	C 527	16	28.6	688	9	BZ072521	BZ072521	1kx37g01.
C 455	16	28.6	683	9	BZ053224	BZ053224	1jnr6e01.	C 528	16	28.6	688	9	BZ072619	BZ072619	1kx46f11.
C 456	16	28.6	683	9	BZ054270	BZ054270	1jnr36b03.	C 529	16	28.6	688	9	BZ078164	BZ078164	11g02h09.
C 457	16	28.6	683	9	BZ057336	BZ057336	11a93c06.	C 530	16	28.6	688	9	BZ080376	BZ080376	11f75f05.
C 458	16	28.6	683	9	BZ064392	BZ064392	1kx17b06.	C 531	16	28.6	688	9	BZ080560	BZ080560	11b94e09.
C 459	16	28.6	683	9	BZ079049	BZ079049	1kx94h05.	C 532	16	28.6	688	9	BH921587	BH921587	odh38g10.
C 460	16	28.6	683	9	BZ080565	BZ080565	11b94f02.	C 533	16	28.6	689	9			



C 534	15	28.6	689	9	BH921623	odt38c02.	C 607	16	28.6	692	9	BH953557	odt184d02.
C 535	16	28.6	689	9	BH923081	odt07c07.	C 608	16	28.6	692	9	BH954570	odt91e09.
C 536	16	28.6	689	9	BH925561	odt159f10.	C 609	16	28.6	692	9	BH957246	odt45f06.
C 537	16	28.6	689	9	BH933800	odt54f11.	C 610	16	28.6	692	9	BH965030	BH965546
C 538	16	28.6	689	9	BH936398	odt58c06	C 611	16	28.6	692	9	BH966546	odt132e02.
C 539	16	28.6	689	9	BH945477	odt14g05.	C 612	16	28.6	692	9	BH967105	odt125a04.
C 540	16	28.6	689	9	BH946260	odt09f09.	C 613	16	28.6	692	9	BH969134	odt61e05.
C 541	16	28.6	689	9	BH962681	odt09f08.	C 614	16	28.6	692	9	BH974896	odt59a10.
C 542	16	28.6	689	9	BH973624	odt124d02.	C 615	16	28.6	692	9	BH979174	odt95d03.
C 543	16	28.6	689	9	BH979147	odt95a05.	C 616	16	28.6	692	9	BZ047352	BZ047352
C 544	16	28.6	689	9	BH980585	odt82g11.	C 617	16	28.6	692	9	BZ052687	odt14a03.
C 545	16	28.6	689	9	BH984135	odt42f03.	C 618	16	28.6	692	9	BZ055241	odt29a03.
C 546	16	28.6	689	9	BZ044325	1k177b04.	C 619	16	28.6	692	9	BZ072388	odt69b05.
C 547	16	28.6	689	9	BZ047935	BZ047935	C 620	16	28.6	692	9	BZ073367	1k672b12.
C 548	16	28.6	689	9	BZ054411	1jnr35d03.	C 621	16	28.6	692	9	BZ078159	1j1g02h04.
C 549	16	28.6	689	9	BZ055095	1jnr30a01.	C 622	16	28.6	692	9	BZ080375	1j1f5f04.
C 550	16	28.6	689	9	BZ068407	1j1c09g04.	C 623	16	28.6	692	9	BZ080534	odt08c07.
C 551	16	28.6	689	9	BZ075546	1k537d11.	C 624	16	28.6	692	9	BZ080540	11b94d01.
C 552	16	28.6	689	9	BZ077501	11h41c10.	C 625	16	28.6	693	2	BG497523	BG497523
C 553	16	28.6	689	9	BZ080511	11b94a08.	C 626	16	28.6	693	9	BH925124	odt03g09.
C 554	16	28.6	689	9	BZ080584	11b94a09.	C 627	16	28.6	693	9	BH927719	odt24f08.
C 555	16	28.6	689	9	BZ080594	11b94a07.	C 628	16	28.6	693	9	BH928649	odt96b08.
C 556	16	28.6	689	9	BZ084478	11b61f05.	C 629	16	28.6	693	9	BH929632	odt170a04.
C 557	16	28.6	689	9	BZ086984	1k985h10.	C 630	16	28.6	693	9	BH935140	odt169e04.
C 558	16	28.6	690	2	BH613400	BH613400	C 631	16	28.6	693	9	BH952365	odt185b03.
C 559	16	28.6	690	7	CK123493	BES182410	C 632	16	28.6	693	9	BH959190	odt10d07.
C 560	16	28.6	690	9	BH921586	odt38c04.	C 633	16	28.6	693	9	BH960036	odt06e04.
C 561	16	28.6	690	9	BH930663	BH930663	C 634	16	28.6	693	9	BH964383	odt09a05.
C 562	16	28.6	690	9	BH952325	odt185a08.	C 635	16	28.6	693	9	BH976464	odt02a07.
C 563	16	28.6	690	9	BH954587	odt91f01.	C 636	16	28.6	693	9	BH976667	odt11b08.
C 564	16	28.6	690	9	BH965879	odt51a12.	C 637	16	28.6	693	9	BH977504	odt46h04.
C 565	16	28.6	690	9	BH969385	odt94e09.	C 638	16	28.6	693	9	BZ044980	odt46h04.
C 566	16	28.6	690	9	BZ0093970	odt974a12.	C 639	16	28.6	693	9	BZ053197	1j1c37e07.
C 567	16	28.6	690	9	BZ052586	1jnr20e05.	C 640	16	28.6	693	9	BZ057305	BZ057305
C 568	16	28.6	690	9	BZ052602	1jnr20g06.	C 641	16	28.6	693	9	BZ073588	1k638g11.
C 569	16	28.6	690	9	BZ052979	1jnr12f04.	C 642	16	28.6	693	9	BZ079379	11g32f04.
C 570	16	28.6	690	9	BZ053102	1jnr12f04.	C 643	16	28.6	693	9	BZ080143	11a58b12.
C 571	16	28.6	690	9	BZ057294	1k66f6f07.	C 644	16	28.6	693	9	BZ080333	11f57b10.
C 572	16	28.6	690	9	BZ073954	1k669g02.	C 645	16	28.6	693	9	BZ080566	11b94f03.
C 573	16	28.6	690	9	BZ073616	1k638g11.	C 646	16	28.6	693	9	BZ086746	11g30g12.
C 574	16	28.6	690	9	BZ073694	1k950e12.	C 647	16	28.6	693	9	BZ087241	11f44h10.
C 575	16	28.6	690	9	BZ077502	11h41d09.	C 648	16	28.6	693	9	BZ088145	11e40d04.
C 576	16	28.6	690	9	BZ080316	11f75a05.	C 649	16	28.6	693	9	BZ088549	1k982b01.
C 577	16	28.6	690	9	BZ080316	11f75a05.	C 650	16	28.6	693	9	BZ088914	11e72d02.
C 578	16	28.6	690	9	BZ080516	11b94b01.	C 651	16	28.6	694	2	BR219474	601881847
C 579	16	28.6	690	9	BZ080529	BZ080529	C 652	16	28.6	694	6	CF418322	USD8-PP-1
C 580	16	28.6	690	9	BZ087294	1k995b03.	C 653	16	28.6	694	9	BH920828	odt93f05.
C 581	16	28.6	691	9	BH927736	odt24d09.	C 654	16	28.6	694	9	BH935903	odt69f07.
C 582	16	28.6	691	9	BH933010	odt98d05.	C 655	16	28.6	694	9	BH936481	odt60g04.
C 583	16	28.6	691	9	BH943987	ma3195h02.	C 656	16	28.6	694	9	BH948588	odt167d12.
C 584	16	28.6	691	9	BH947042	odt912s01.	C 657	16	28.6	694	9	BH952238	odt91h11.
C 585	16	28.6	691	9	BH952393	odt185h04.	C 658	16	28.6	694	9	BH957887	odt185g12.
C 586	16	28.6	691	9	BH957660	odt178h05.	C 659	16	28.6	694	9	BH963756	odt198c12.
C 587	16	28.6	691	9	BH957945	odt63f05.	C 660	16	28.6	694	9	BH965957	odt90f01.
C 588	16	28.6	691	9	BH960922	odt310h07.	C 661	16	28.6	694	9	BH969966	odt11f12.
C 589	16	28.6	691	9	BH961394	odt665b04.	C 662	16	28.6	694	9	BH970043	odt150a10.
C 590	16	28.6	691	9	BH963293	odt07d06.	C 663	16	28.6	694	9	BH975988	odt85e10.
C 591	16	28.6	691	9	BZ038571	1j1u38f11.	C 664	16	28.6	694	9	BZ044462	1k158h02.
C 592	16	28.6	691	9	BZ040808	1kx33a04.	C 665	16	28.6	694	9	BZ048574	1jnr28f03.
C 593	16	28.6	691	9	BZ046539	1kH45b09.	C 666	16	28.6	694	9	BZ0505672	1jnr65a06.
C 594	16	28.6	691	9	BZ048047	1k983b01.	C 667	16	28.6	694	9	BZ051116	1jnr62f04.
C 595	16	28.6	691	9	BZ049536	1jnr19e10.	C 668	16	28.6	694	9	BZ052591	1jnr20f01.
C 596	16	28.6	691	9	BZ051414	1jnr60h03.	C 669	16	28.6	694	9	BZ053358	1jnr01f07.
C 597	16	28.6	691	9	BZ073436	1k972f10.	C 670	16	28.6	694	9	BZ054030	1jnr38f03.
C 598	16	28.6	691	9	BZ080320	11f75h09.	C 671	16	28.6	694	9	BZ054823	1jnr32b05.
C 599	16	28.6	691	9	BZ080404	11f75h09.	C 672	16	28.6	694	9	BZ054969	1jnr31c01.
C 600	16	28.6	691	9	BZ080585	11b94g10.	C 673	16	28.6	694	9	BZ055524	1jnr27d06.
C 601	16	28.6	691	9	BZ080591	11b94h04.	C 674	16	28.6	694	9	BZ055539	1jnr27f01.
C 602	16	28.6	692	5	BH106610	BH106610	C 675	16	28.6	694	9	BZ055557	1jnr27h06.
C 603	16	28.6	692	9	BH926397	odt117e01.	C 676	16	28.6	694	9	BZ057380	11a93h10.
C 604	16	28.6	692	9	BH929799	odt198g06.	C 677	16	28.6	694	9	BZ073431	1k972e07.
C 605	16	28.6	692	9	BH939333	odt95d601.	C 678	16	28.6	694	9	BZ074071	1k613d06.
C 606	16	28.6	692	9	BH948668	odt183b12.	C 679	16	28.6	694	9	BZ075927	1k993d10.



C 680	16	28.6	694	9	BZ079944	11h40b05.	C 753	16	28.6	697	9	BZ043849	BZ043849	1k09d02.
C 681	16	28.6	694	9	BZ080148	BZ080148	C 754	16	28.6	697	9	BZ044568	BZ044568	1k152h12.
C 682	16	28.6	694	9	BZ080178	BZ080178	C 755	16	28.6	697	9	BZ047836	BZ047836	1k152h12.
C 683	16	28.6	694	9	BZ080341	11f75c06.	C 756	16	28.6	697	9	BZ053382	BZ053382	1nc98c04.
C 684	16	28.6	694	9	BZ086777	BZ086777	C 757	16	28.6	697	9	BZ055401	BZ055401	1nr54e03.
C 685	16	28.6	694	9	BZ088557	1k982901.	C 758	16	28.6	697	9	BZ057306	BZ057306	1k83a10.
C 686	16	28.6	695	9	BZ086335	BH926335	C 759	16	28.6	697	9	BZ072242	BZ072242	1kg37901.
C 687	16	28.6	695	9	BH929600	BH929600	C 760	16	28.6	697	9	BZ072628	BZ072628	1kg33911.
C 688	16	28.6	695	9	BH940489	BH940489	C 761	16	28.6	697	9	BZ080335	BZ080335	11f75b12.
C 689	16	28.6	695	9	BH940845	BH940845	C 762	16	28.6	697	9	BZ087203	BZ087203	11f44c10.
C 690	16	28.6	695	9	BH940885	BH940885	C 763	16	28.6	697	9	BZ087315	BZ087315	1kg95d08.
C 691	16	28.6	695	9	BH949307	BH949307	C 764	16	28.6	698	7	CV171972	CV171972	UCRCS08.0
C 692	16	28.6	695	9	BH954918	BH954918	C 765	16	28.6	698	8	CK638168	CK638168	UCRPT02.3
C 693	16	28.6	695	9	BH957676	BH957676	C 766	16	28.6	698	8	BH920371	BH920371	od112c03.
C 694	16	28.6	695	9	BH961631	BH961631	C 767	16	28.6	698	9	BH925633	BH925633	od159h03.
C 695	16	28.6	695	9	BH964128	BH964128	C 768	16	28.6	698	9	BH925698	BH925698	od984c04.
C 696	16	28.6	695	9	BH974002	BH974002	C 769	16	28.6	698	9	BH925732	BH925732	od984c09.
C 697	16	28.6	695	9	BH975225	BH975225	C 770	16	28.6	698	9	BH926299	BH926299	od158b08.
C 698	16	28.6	695	9	BH976945	BH976945	C 771	16	28.6	698	9	BH927984	BH927984	od182c03.
C 699	16	28.6	695	9	BH983887	BH983887	C 772	16	28.6	698	9	BH936249	BH936249	od182c03.
C 700	16	28.6	695	9	BH983948	BH983948	C 773	16	28.6	698	9	BH938725	BH938725	od182c03.
C 701	16	28.6	695	9	BZ054407	BZ054407	C 774	16	28.6	698	9	BH943998	BH943998	od459e09.
C 702	16	28.6	695	9	BZ052328	BZ052328	C 775	16	28.6	698	9	BH960389	BH960389	od499g06.
C 703	16	28.6	695	9	BZ052815	BZ052815	C 776	16	28.6	698	9	BH967557	BH967557	od499g06.
C 704	16	28.6	695	9	BZ055123	BZ055123	C 777	16	28.6	698	9	BH978136	BH978136	od613d09.
C 705	16	28.6	695	9	BZ055429	BZ055429	C 778	16	28.6	698	9	BH983369	BH983369	od613d09.
C 706	16	28.6	695	9	BZ055429	BZ055429	C 779	16	28.6	698	9	BZ051409	BZ051409	od613d09.
C 707	16	28.6	695	9	BZ057295	BZ057295	C 780	16	28.6	698	9	BZ052815	BZ052815	1nr13a06.
C 708	16	28.6	695	9	BZ057777	BZ057777	C 781	16	28.6	698	9	BZ052845	BZ052845	1nr13a08.
C 709	16	28.6	695	9	BZ072570	BZ072570	C 782	16	28.6	698	9	BZ052885	BZ052885	1nr12g02.
C 710	16	28.6	695	9	BZ078028	BZ078028	C 783	16	28.6	698	9	BZ052985	BZ052985	1nr12g02.
C 711	16	28.6	695	9	BZ080315	BZ080315	C 784	16	28.6	698	9	BZ054132	BZ054132	1nr12g02.
C 712	16	28.6	695	9	BZ080326	BZ080326	C 785	16	28.6	698	9	BZ063789	BZ063789	1kx72h05.
C 713	16	28.6	696	9	BH927427	BH927427	C 786	16	28.6	698	9	BZ067263	BZ067263	1kx12g02.
C 714	16	28.6	696	9	BH928638	BH928638	C 787	16	28.6	698	9	BZ072484	BZ072484	1kx37c04.
C 715	16	28.6	696	9	BH938906	BH938906	C 788	16	28.6	698	9	BZ077450	BZ077450	11h41a11.
C 716	16	28.6	696	9	BH946918	BH946918	C 789	16	28.6	698	9	BZ080382	BZ080382	11f75f11.
C 717	16	28.6	696	9	BH948734	BH948734	C 790	16	28.6	698	9	BZ080399	BZ080399	11f75h04.
C 718	16	28.6	696	9	BH951829	BH951829	C 791	16	28.6	698	9	BZ086596	BZ086596	1kg85h10.
C 719	16	28.6	696	9	BH952536	BH952536	C 792	16	28.6	699	2	BG497589	BG497589	601899489
C 720	16	28.6	696	9	BH954949	BH954949	C 793	16	28.6	699	9	BH926901	BH926901	od189g05.
C 721	16	28.6	696	9	BH955775	BH955775	C 794	16	28.6	699	9	BH938652	BH938652	od189g05.
C 722	16	28.6	696	9	BH958302	BH958302	C 795	16	28.6	699	9	BH948659	BH948659	od189g05.
C 723	16	28.6	696	9	BH963132	BH963132	C 796	16	28.6	699	9	BH949840	BH949840	od189g05.
C 724	16	28.6	696	9	BH963383	BH963383	C 797	16	28.6	699	9	BH949960	BH949960	od137b03.
C 725	16	28.6	696	9	BH964608	BH964608	C 798	16	28.6	699	9	BH956380	BH956380	od494b07.
C 726	16	28.6	696	9	BH967103	BH967103	C 799	16	28.6	699	9	BH960321	BH960321	od494b07.
C 727	16	28.6	696	9	BH967558	BH967558	C 800	16	28.6	699	9	BH960616	BH960616	od494b07.
C 728	16	28.6	696	9	BZ048221	BZ048221	C 801	16	28.6	699	9	BH964965	BH964965	od494b07.
C 729	16	28.6	696	9	BZ050706	BZ050706	C 802	16	28.6	699	9	BH972938	BH972938	od494b07.
C 730	16	28.6	696	9	BZ050724	BZ050724	C 803	16	28.6	699	9	BH979721	BH979721	od494b07.
C 731	16	28.6	696	9	BZ050981	BZ050981	C 804	16	28.6	699	9	BZ038568	BZ038568	1j388e07.
C 732	16	28.6	696	9	BZ055786	BZ055786	C 805	16	28.6	699	9	BZ049124	BZ049124	1nr12a10.
C 733	16	28.6	696	9	BZ069810	BZ069810	C 806	16	28.6	699	9	BZ049381	BZ049381	1nr50d03.
C 734	16	28.6	696	9	BZ075299	BZ075299	C 807	16	28.6	699	9	BZ050554	BZ050554	1nr66b05.
C 735	16	28.6	696	9	BZ075312	BZ075312	C 808	16	28.6	699	9	BZ050728	BZ050728	1nr66b05.
C 736	16	28.6	696	9	BZ082472	BZ082472	C 809	16	28.6	699	9	BZ051258	BZ051258	1nr61f09.
C 737	16	28.6	697	9	BH924761	BH924761	C 810	16	28.6	699	9	BZ052572	BZ052572	1nr20c08.
C 738	16	28.6	697	9	BH931436	BH931436	C 811	16	28.6	699	9	BZ053363	BZ053363	1nr10g04.
C 739	16	28.6	697	9	BH931749	BH931749	C 812	16	28.6	699	9	BZ056801	BZ056801	1kx78n07.
C 740	16	28.6	697	9	BH931889	BH931889	C 813	16	28.6	699	9	BZ072624	BZ072624	1kx78n07.
C 741	16	28.6	697	9	BH936726	BH936726	C 814	16	28.6	699	9	BZ075884	BZ075884	1kg61f07.
C 742	16	28.6	697	9	BH938899	BH938899	C 815	16	28.6	699	9	BZ080334	BZ080334	11f75b11.
C 743	16	28.6	697	9	BH942621	BH942621	C 816	16	28.6	699	9	BH920004	BH920004	1kx70a11.
C 744	16	28.6	697	9	BH949852	BH949852	C 817	16	28.6	700	9	BH920932	BH920932	od494e07.
C 745	16	28.6	697	9	BH949882	BH949882	C 818	16	28.6	700	9	BH925774	BH925774	od494e12.
C 746	16	28.6	697	9	BH954475	BH954475	C 819	16	28.6	700	9	BH928639	BH928639	od494e03.
C 747	16	28.6	697	9	BH963014	BH963014	C 820	16	28.6	700	9	BH928643	BH928643	od494e03.
C 748	16	28.6	697	9	BH964969	BH964969	C 821	16	28.6	700	9	BH930547	BH930547	od494e03.
C 749	16	28.6	697	9	BH965506	BH965506	C 822	16	28.6	700	9	BH936059	BH936059	od494e03.
C 750	16	28.6	697	9	BH971513	BH971513	C 823	16	28.6	700	9	BH943184	BH943184	od494e03.
C 751	16	28.6	697	9	BH977236	BH977236	C 824	16	28.6	700	9	BH943210	BH943210	od494e03.
C 752	16	28.6	697	9	BZ040834	BZ040834	C 825	16	28.6	700	9	BH956562	BH956562	od494e03.



C 826	16	28.6	700	9	BH960839	BH960839	cdj30c11.	C 899	16	28.6	703	9	BZ050581	BZ050581	fnr66e10.
C 827	16	28.6	700	9	BH965886	BH965886	odh51fd3.	C 900	16	28.6	703	9	BZ057346	BZ057346	11a93e06.
C 828	16	28.6	700	9	BH979132	BH979132	cdff95d05.	C 901	16	28.6	703	9	BZ065070	BZ065070	1kz73b07.
C 829	16	28.6	700	9	BZ048859	BZ048859	fnr22g06.	C 902	16	28.6	703	9	BZ065168	BZ065168	11c07b07.
C 830	16	28.6	700	9	BZ053108	BZ053108	fnr11fd6.	C 903	16	28.6	703	9	BZ068463	BZ068463	1Kk31a08.
C 831	16	28.6	700	9	BZ053329	BZ053329	fnr01b03.	C 904	16	28.6	703	9	BZ072443	BZ072443	1Kf48a02.
C 832	16	28.6	700	9	BZ059325	BZ059325	1kz3b03.	C 905	16	28.6	703	9	BZ075376	BZ075376	1kz47c04.
C 833	16	28.6	700	9	BZ087253	BZ087253	11f44b09.	C 906	16	28.6	703	9	BZ080338	BZ080338	11f75c03.
C 834	16	28.6	701	2	BG618692	BG618692	602645139	C 907	16	28.6	703	9	BZ083263	BZ083263	11f02d09.
C 835	16	28.6	701	5	BX847900	BX847900	BX847900	C 908	16	28.6	703	9	BZ084322	BZ084322	11a92b09.
C 836	16	28.6	701	9	BH926897	BH926897	od188a07.	C 909	16	28.6	703	9	BZ086757	BZ086757	11g30a06.
C 837	16	28.6	701	9	BH928500	BH928500	odg92c11.	C 910	16	28.6	703	9	BZ087194	BZ087194	11f44b09.
C 838	16	28.6	701	9	BH931756	BH931756	odh48b05.	C 911	16	28.6	704	7	CO105636	CO105636	GR_Eb003
C 839	16	28.6	701	9	BH934626	BH934626	odff87909.	C 912	16	28.6	704	9	BH925069	BH925069	BH925069
C 840	16	28.6	701	9	BH935287	BH935287	odf75h07.	C 913	16	28.6	704	9	BH929829	BH929829	od198d08.
C 841	16	28.6	701	9	BH936244	BH936244	odf10e10.	C 914	16	28.6	704	9	BH940776	BH940776	odf15h01.
C 842	16	28.6	701	9	BH940475	BH940475	odh80b02.	C 915	16	28.6	704	9	BH943201	BH943201	odd65e05.
C 843	16	28.6	701	9	BH943238	BH943238	odh65a07.	C 916	16	28.6	704	9	BH954523	BH954523	odg91g08.
C 844	16	28.6	701	9	BH950324	BH950324	odh97c08.	C 917	16	28.6	704	9	BH957946	BH957946	odf85c10.
C 845	16	28.6	701	9	BH952113	BH952113	odh19e08.	C 918	16	28.6	704	9	BH960587	BH960587	odh45h05.
C 846	16	28.6	701	9	BH961273	BH961273	odh49g08.	C 919	16	28.6	704	9	BH962165	BH962165	odh86d05.
C 847	16	28.6	701	9	BH965039	BH965039	odj25g09.	C 920	16	28.6	704	9	BH968007	BH968007	odj12h10.
C 848	16	28.6	701	9	BH966704	BH966704	odh17f12.	C 921	16	28.6	704	9	BH969506	BH969506	odh60b11.
C 849	16	28.6	701	9	BH967828	BH967828	odh56g05.	C 922	16	28.6	704	9	BH972822	BH972822	odh62f12.
C 850	16	28.6	701	9	BH978100	BH978100	odh13b04.	C 923	16	28.6	704	9	BH974038	BH974038	odh10b10.
C 851	16	28.6	701	9	BZ031481	BZ031481	odh43e09.	C 924	16	28.6	704	9	BH978726	BH978726	odh94a10.
C 852	16	28.6	701	9	BZ042751	BZ042751	1jg76h06.	C 925	16	28.6	704	9	BH979034	BH979034	odf68e06.
C 853	16	28.6	701	9	BZ054556	BZ054556	fnr34f03.	C 926	16	28.6	704	9	BH979591	BH979591	odf50b06.
C 854	16	28.6	701	9	BZ055246	BZ055246	fnr29a11.	C 927	16	28.6	704	9	BH982422	BH982422	odh93e04.
C 855	16	28.6	701	9	BZ059836	BZ059836	fnr67b07.	C 928	16	28.6	704	9	BZ042711	BZ042711	1jg76d06.
C 856	16	28.6	701	9	BZ074665	BZ074665	1khl4b01.	C 929	16	28.6	704	9	BZ045087	BZ045087	1k114c01.
C 857	16	28.6	701	9	BZ080633	BZ080633	11b94d12.	C 930	16	28.6	704	9	BZ049523	BZ049523	fnr19d03.
C 858	16	28.6	702	7	CK120938	CK120938	205d14.PI	C 931	16	28.6	704	9	BZ050077	BZ050077	fnr44f02.
C 859	16	28.6	702	7	CK122622	CK122622	BES18210	C 932	16	28.6	704	9	BZ052351	BZ052351	fnr68e05.
C 860	16	28.6	702	9	BH925705	BH925705	odg84h11.	C 933	16	28.6	704	9	BZ055981	BZ055981	11g93b10.
C 861	16	28.6	702	9	BH926120	BH926120	odg88b09.	C 934	16	28.6	704	9	BZ057318	BZ057318	11a93b08.
C 862	16	28.6	702	9	BH933421	BH933421	odg71e12.	C 935	16	28.6	704	9	BZ057721	BZ057721	11f21a04.
C 863	16	28.6	702	9	BH935627	BH935627	odf48e03.	C 936	16	28.6	704	9	BZ060655	BZ060655	1kz15f01.
C 864	16	28.6	702	9	BH941271	BH941271	odf05g12.	C 937	16	28.6	704	9	BZ064522	BZ064522	11d83f07.
C 865	16	28.6	702	9	BH954840	BH954840	odh99h06.	C 938	16	28.6	704	9	BZ072856	BZ072856	1kg18h06.
C 866	16	28.6	702	9	BH963387	BH963387	odh66c11.	C 939	16	28.6	704	9	BZ074096	BZ074096	1kz13g10.
C 867	16	28.6	702	9	BH964537	BH964537	odh57a06.	C 940	16	28.6	704	9	BZ079993	BZ079993	11h40f06.
C 868	16	28.6	702	9	BH983652	BH983652	odh20e11.	C 941	16	28.6	704	9	BZ080023	BZ080023	11b40h12.
C 869	16	28.6	702	9	BZ050448	BZ050448	fnr41f04.	C 942	16	28.6	704	9	BZ080551	BZ080551	11b94d12.
C 870	16	28.6	702	9	BZ053104	BZ053104	fnr11e08.	C 943	16	28.6	705	7	CK118011	CK118011	207R15.PI
C 871	16	28.6	702	9	BZ055128	BZ055128	fnr30d12.	C 944	16	28.6	705	9	BH927385	BH927385	odh16h11.
C 872	16	28.6	702	9	BZ065066	BZ065066	1kz73a08.	C 945	16	28.6	705	9	BH928658	BH928658	odh96d01.
C 873	16	28.6	702	9	BZ073439	BZ073439	1kg72g08.	C 946	16	28.6	705	9	BH931959	BH931959	odj16g08.
C 874	16	28.6	702	9	BZ075365	BZ075365	1kf47a06.	C 947	16	28.6	705	9	BH935940	BH935940	odh99f01.
C 875	16	28.6	702	9	BZ075374	BZ075374	1kf47d08.	C 948	16	28.6	705	9	BH948803	BH948803	odh57f03.
C 876	16	28.6	702	9	BZ080160	BZ080160	11a58d05.	C 949	16	28.6	705	9	BH967864	BH967864	odg80e12.
C 877	16	28.6	702	9	BZ080325	BZ080325	11f75b02.	C 950	16	28.6	705	9	BH970146	BH970146	odg901c10.
C 878	16	28.6	702	9	BZ088900	BZ088900	11e72g05.	C 951	16	28.6	705	9	BZ045092	BZ045092	1k114d02.
C 879	16	28.6	703	1	AW188247	AW188247	x194c01.X	C 952	16	28.6	705	9	BZ048585	BZ048585	fnr28g08.
C 880	16	28.6	703	2	BG534588	BG534588	602553439	C 953	16	28.6	705	9	BZ049380	BZ049380	fnr50d01.
C 881	16	28.6	703	7	CK121991	CK121991	211K06.PI	C 954	16	28.6	705	9	BZ049936	BZ049936	fnr45c03.
C 882	16	28.6	703	9	BH933760	BH933760	odh97e10.	C 955	16	28.6	705	9	BZ050212	BZ050212	fnr43f05.
C 883	16	28.6	703	9	BH935063	BH935063	odh89g10.	C 956	16	28.6	705	9	BZ052951	BZ052951	fnr12b03.
C 884	16	28.6	703	9	BH942061	BH942061	odf74g12.	C 957	16	28.6	705	9	BZ053242	BZ053242	fnr02g09.
C 885	16	28.6	703	9	BH952889	BH952889	odf176e11.	C 958	16	28.6	705	9	BZ053621	BZ053621	fnr98h08.
C 886	16	28.6	703	9	BH955444	BH955444	odf152c09.	C 959	16	28.6	705	9	BZ054149	BZ054149	fnr37d02.
C 887	16	28.6	703	9	BH963954	BH963954	odh84d12.	C 960	16	28.6	705	9	BZ057325	BZ057325	11a93c06.
C 888	16	28.6	703	9	BH966241	BH966241	odh96h07.	C 961	16	28.6	705	9	BZ057359	BZ057359	11a93f08.
C 889	16	28.6	703	9	BH966245	BH966245	odh96d02.	C 962	16	28.6	705	9	BZ075007	BZ075007	1kz35a10.
C 890	16	28.6	703	9	BH967004	BH967004	odf411f09.	C 963	16	28.6	705	9	BZ075106	BZ075106	1kz69c11.
C 891	16	28.6	703	9	BH969012	BH969012	odh46c06.	C 964	16	28.6	705	9	BZ075453	BZ075453	1kz86h12.
C 892	16	28.6	703	9	BH970105	BH970105	odg01a04.	C 965	16	28.6	705	10	CM230053	CM230053	104_671_1
C 893	16	28.6	703	9	BH973010	BH973010	odj32g03.	C 966	16	28.6	706	9	BH928796	BH928796	odh25g12.
C 894	16	28.6	703	9	BH976970	BH976970	odh49g05.	C 967	16	28.6	706	9	BH937480	BH937480	odg954d10.
C 895	16	28.6	703	9	BH978751	BH978751	odh94b09.	C 968	16	28.6	706	9	BH939980	BH939980	odf58a04.
C 896	16	28.6	703	9	BZ042761	BZ042761	1kg97a07.	C 969	16	28.6	706	9	BH941997	BH941997	odf46e07.
C 897	16	28.6	703	9	BZ044326	BZ044326	1k177b05.	C 970	16	28.6	706	9	BH942437	BH942437	odf08g07.
C 898	16	28.6	703	9	BZ048811	BZ048811	fnr22a06.	C 971	16	28.6	706	9	BH952271	BH952271	odh91d03.



LOCUS	BE695762	354 bp	mRNA	linear	EST 11-SEP-2000
DEFINITION	OVO-CT0225-280700-307-e06 CT0225 Homo sapiens CDNA, mRNA sequence.				
ACCESSION	BE695762.1	GI:10082974			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 354)				
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcritpome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This entry was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=ct2-QV0-CT0225-280700-307-e06&ts=2000-07-28&ts=1) Seq primer: puc 18 forward High quality sequence start: 68 High quality sequence end: 202. Location/Qualifiers				

## ALIGNMENTS

LOCUS	A0724199	576 bp	DNA	linear	GSS 14-JUL-1999
DEFINITION	HS_2102_A1_C04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2102 Col=7 Row=E, genomic survey sequence.				
ACCESSION	A0724199.1	GI:5483868			
VERSION	GSS.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 576)				
AUTHORS	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Hood, L., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				
PUBMED	10449764				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2102 row: E column: 7 Seq primer: 17 Classes: BAC ends High quality sequence start: 576. Location/Qualifiers				
FEATURES	source				
ORIGIN	1..354 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="taxon:9606" /dev_stage="Adult" /clone_id="CT0225" /note="Organ: colon; Vector: puc18; Site 1: Sma1; Site 2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."				
Query Match	33.9%; Score 19; DB 2; Length 354;				
Best Local Similarity	100.0%; Pred. No. 4.2;				
Matches	19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;				
Qy	19 AATGCTATCGGATCCAG 37       32 AATGCTATCGGATCCAG 50				
Db	32 AATGCTATCGGATCCAG 50				

LOCUS	BE695762	354 bp	mRNA	linear	EST 11-SEP-2000
DEFINITION	OVO-CT0225-280700-307-e06 CT0225 Homo sapiens CDNA, mRNA sequence.				
ACCESSION	BE695762.1	GI:10082974			
VERSION	EST.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
ORGANISM	Homo sapiens (human)				
REFERENCE	1 (bases 1 to 354)				
AUTHORS	Dias Neto, E., Garcia Correa, R., Verjowski-Almeida, S., Briones, M.R., Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.U., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and Simpson, A.J.				
TITLE	Shotgun sequencing of the human transcritpome with ORF expressed sequence tags				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)				
PUBMED	10737800				
COMMENT	Contact: Simpson A.J.G. Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil Tel: +55-11-2704922 Fax: +55-11-2707001 Email: asimpson@ludwig.org.br This entry was derived from the FAPESP/LICR Human Cancer Genome project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?cl=ct2-QV0-CT0225-280700-307-e06&ts=2000-07-28&ts=1) Seq primer: puc 18 forward High quality sequence start: 68 High quality sequence end: 202. Location/Qualifiers				

LOCUS	A0724199	576 bp	DNA	linear	GSS 14-JUL-1999
DEFINITION	HS_2102_A1_C04_T7C CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2102 Col=7 Row=E, genomic survey sequence.				
ACCESSION	A0724199.1	GI:5483868			
VERSION	GSS.				
KEYWORDS	Homo sapiens (human)				
SOURCE	Homo sapiens				
ORGANISM	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae; Homo.				
REFERENCE	1 (bases 1 to 576)				
AUTHORS	Mahairas, G.G., Wallace, J.C., Smith, K., Swartzell, S., Holzman, T., Hood, L., Keller, A., Shaker, R., Furlong, J., Young, J., Zhao, S., Adams, M.D. and Hood, L.				
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome				
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)				
PUBMED	10449764				
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones may be purchased from Research Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 2102 row: E column: 7 Seq primer: 17 Classes: BAC ends High quality sequence start: 576. Location/Qualifiers				
FEATURES	source				
ORIGIN	1..576 /organism="Homo sapiens" /mol_type="genomic DNA" /db_xref="taxon:9606" /clone_id="Plate=2102 Col=7 Row=E" /sex="male" /clone_lib="CIT Approved Human Genomic Sperm Library D" /note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"				
Query Match	33.9%; Score 19; DB 9; Length 576;				
Best Local Similarity	100.0%; Pred. No. 4.2;				



Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 TTCGGTGTATGTTGATG 22  
 |||||  
 Db 503 TTCGGTGTATGTTGATG 485

RESULT 3  
 CA266323 688 bp mRNA linear EST 26-SEP-2003  
 LOCUS SCAGLB2046H03.gb L2 Saccharum officinarum cDNA clone SCAGLB2046H03  
 DEFINITION 5', mRNA sequence.  
 ACCESSION CA266323  
 VERSION CA266323.1 GI:35965079  
 KEYWORDS EST.  
 SOURCE Saccharum officinarum  
 ORGANISM Saccharum officinarum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Saccharum; Saccharum officinarum  
 complex.  
 1 (bases 1 to 688)  
 REFERENCE Vettore,A.L., da Silva,F.R., Kemper,E.L. and Arruda,P.  
 AUTHORS The libraries that made SUCEST  
 TITLE Genet. Mol. Biol. 24 (1-4), 1-7 (2001)  
 JOURNAL Contact: Arruda P  
 COMMENT Centro de Biologia Molecular e Engenharia Genetica  
 Universidade Estadual de Campinas  
 Caixa Postal 6010, 13083-970, Campinas SP, Brazil  
 Tel: 55 19 3788 1137  
 Fax: 55 19 3788 1089  
 Email: parnada@unicamp.br  
 Clone distribution: clone distribution information can be found  
 through the Brazilian Clone Collection Center (BCCC) at  
 http://www.bcccenter.fcav.unesp.br  
 Plate: 046 row: H column: 03  
 Seq primer: T7 Promoter Primer.  
 Location/Qualifiers  
 1..688  
 /organism="Saccharum officinarum"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:4547"  
 /clone="SCAGLB2046H03"  
 /lab\_host="DH10B"  
 /clone\_id="LB2"  
 /note="Organ: Lateral buds from plants adult plants  
 growing in greenhouse; Vector: pSport1; Site 1: SalI;  
 Site 2: NotI; An unidirectional cDNA library generated  
 from lateral buds from plants adult plants growing in  
 greenhouse). cDNA was prepared from polyA+ mRNA using  
 SuperScript Plasmid System Kit (Invitrogen). The  
 double-strand cDNAs were fractionated in a sepharose  
 CL-2B 40cm-columns and fragments siting between 0.8 and  
 1.5 Kb were directionally cloned into the vector. Details  
 of each source of RNA and library construction can be  
 obtained at http://succest.lad.ic.unicamp.br/public"

ORIGIN  
 Query Match 33.9%; Score 19; DB 6; Length 688;  
 Best Local Similarity 100.0%; Pred. No. 4.2;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 GAATGCTCATCCGATCCA 36  
 |||||  
 Db 653 GAATGCTCATCCGATCCA 671

RESULT 4  
 CC239784 1135 bp DNA linear GSS 12-MAY-2003  
 LOCUS CH261-81N2.SP6.1 CH261 Gallus gallus genomic clone CH261-81N2,  
 DEFINITION genomic survey sequence.  
 ACCESSION CC239784

VERSION CC239784.1 GI:30566447  
 KEYWORDS GSS.  
 SOURCE Gallus gallus (chicken)  
 ORGANISM Gallus gallus  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;  
 Phasianinae; Gallus.  
 1 (bases 1 to 1135)  
 REFERENCE Krenitzki,C., Higginbotham,J., Wylie,K., Carter,J., McPherson,J.,  
 AUTHORS Warren,W., Graves,T., Marks,E. and Wilson,R.  
 TITLE Gallus gallus BAC End Reads  
 JOURNAL Unpublished (2003)  
 COMMENT Contact: Richard K. Wilson  
 Genome Sequencing Center  
 Washington University School of Medicine  
 Email: submissions@wustl.edu  
 Insert Length: 18200 Std Error: 0.00  
 Seq primer: SP6 ATTTAGGTGACACTATG  
 Class: BAC ends  
 High quality sequence start: 63  
 High quality sequence stop: 447.  
 Location/Qualifiers  
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 /organism="Gallus gallus"  
 /mol\_type="genomic DNA"  
 /strain="Red Jungle Fowl"  
 /db\_xref="taxon:9031"  
 /clone="CH261-81N2"  
 /sex="female"  
 /cell\_line="UCD001, inbred 256"  
 /clone\_id="CH261"  
 /note="Vector: PTARBAC.1; Site 1: EcoRI; Site 2: EcoRI;  
 CH261 Female Chicken library - For library and clone  
 ordering information: http://www.chori.org/bacpac"

ORIGIN  
 Query Match 33.9%; Score 19; DB 9; Length 1135;  
 Best Local Similarity 100.0%; Pred. No. 4.2;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 30 GGATCCGAGGCAATGAGA 48  
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 Db 283 GGATCCGAGGCAATGAGA 265

RESULT 5  
 CB333333 259 bp mRNA linear EST 11-MAR-2003  
 LOCUS PY43606.y1 Haemonchus contortus whole worm SL1 TOPO v1 Haemonchus  
 DEFINITION contortus cDNA 5', mRNA sequence.  
 ACCESSION CB333333  
 VERSION CB333333.1 GI:28915196  
 KEYWORDS EST.  
 SOURCE Haemonchus contortus  
 ORGANISM Haemonchus contortus  
 Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabdilita; Strongylida;  
 Trichostrongylidae; Haemonchidae; Haemonchinae; Haemonchus.  
 1 (bases 1 to 259)  
 REFERENCE McCarter,J., Clifton,S., Chiapelli,B., Pape,D., Martin,J.,  
 AUTHORS Wylie,T., Dante,M., Marra,M., Hillier,L., Kucaba,T., Theising,B.,  
 Bowers,Y., Gibbons,M., Ritzer,E., Bennett,J., Franklin,C.,  
 Tsagarishevili,R., Ronko,I., Kennedy,S., Maguire,L., Beck,C.,  
 Underwood,K., Steptoe,M., Allen,M., Person,B., Swaller,T.,  
 Harvey,N., Schurk,R., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,  
 McCann,R., Waterston,R. and Wilson,R.  
 TITLE The Washington Univ. Nematode EST Project, 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: McCarter JP  
 The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810



Email: est@watson.wustl.edu  
 The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR11-TOPO(Invitrogen) following the Topo TA cloning protocol. Whole worm RNA was provided by Dr. Douglas Jaamer of Washington State University (djaamer@vetmed.wsu.edu).

## FEATURES

## Source

Location/Qualifiers  
 1..259  
 /organism="Haemophilus contortus"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:6289"  
 /tissue\_type="whole organism"  
 /lab\_host="DH10B"  
 /clone\_lib="Haemophilus contortus whole worm SL1 TOPO v1"  
 /note="Vector: PCR11-TOPO (Invitrogen); Site 1: EcoRI; Site 2: EcoRI; The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. Oligo(dT)-SL1 PCR based library. cDNA PCR products of size >400 nucleotides containing SL1 on the 5' end and oligo(dT) on the 3' end were non-directionally cloned into PCR11-TOPO(Invitrogen) following the Topo TA cloning protocol. Whole worm RNA was provided by Dr. Douglas Jaamer of Washington State University (djaamer@vetmed.wsu.edu)."

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 259;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 8 GTGGTATGTTGATGCTC 25  
 |||||  
 83 GTGGTATGTTGATGCTC 66

## RESULT 6

## CM470659

LOCUS 401 bp DNA linear GSS 02-NOV-2004  
 DEFINITION fdbb001f223p19k0 Sorghum methylation filtered library (LibID: 104)  
 Sorghum bicolor genomic clone fdbb001f223p19, genomic survey  
 sequence.

## ACCESSION

## CM470659

## KEYWORDS

## SOURCE

## ORGANISM

## Sorghum bicolor (sorghum)

## Sorghum bicolor

## Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.

## 1 (bases 1 to 401)

## Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddahon,J.A. and Martienssen,R.A.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## COMMENT

## 15660154

## Contact: Bedell JA

## Orion Genomics, LLC

## 4041 Forest Park Ave, St. Louis, MO 63108, USA

## Tel: 314 615 6979

## Fax: 314 615 5975

## Email: jbedell@oriongenomics.com

## Plate: fdbb001f223 row: p column: 19

## Seq primer: k Reverse

## Class: methylation filtered

## High quality sequence stcp: 401.

## Location/Qualifiers

## 1..401

## FEATURES

## Source

/organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone\_lib="fbb001f223p19"  
 /clone\_lib="Sorghum methylation filtered library (LibID: 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

## ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 401;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## Oy 25

## CM111224

## LOCUS

## CM111224

## DEFINITION

## 104\_484\_11104188\_116\_34530\_040 Sorghum methylation filtered library (LibID: 104) Sorghum bicolor genomic clone 11104188, genomic survey sequence.

## ACCESSION

## CM111224

## KEYWORDS

## Sorghum bicolor (sorghum)

## Sorghum bicolor

## Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD clade; Panicoidae; Andropogoneae; Sorghum.

## 1 (bases 1 to 403)

## Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D., Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K., McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korff,I.F., Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddahon,J.A. and Martienssen,R.A.

## REFERENCE

## AUTHORS

## TITLE

## JOURNAL

## PUBMED

## COMMENT

## 15660154

## Contact: Bedell JA

## Orion Genomics, LLC

## 4041 Forest Park Ave, St. Louis, MO 63108, USA

## Tel: 314 615 6979

## Fax: 314 615 5975

## Email: jbedell@oriongenomics.com

## Plate: 484 row: 1 column: 12

## Seq primer: T3 Reverse

## Class: methylation filtered

## High quality sequence stcp: 403.

## Location/Qualifiers

## 1..403

## /organism="Sorghum bicolor"

## /mol\_type="genomic DNA"

## /cultivar="ATx623"

## /db\_xref="taxon:4558"

## /clone\_lib="11104188"

## /clone\_lib="Sorghum methylation filtered library (LibID: 104)"

## /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

## ORIGIN

## Source



Query Match 32.1%; Score 18; DB 10; Length 403;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 219 CATCCGATCCAGAGCA 236

RESULT 8  
CD811731/c 462 bp mRNA linear EST 10-JUL-2003  
LOCUS BN10.001K12F011207 BN10 Brassica napus cDNA clone BN10001K12, mRNA  
DEFINITION sequence.  
ACCESSION CD811731  
VERSION CD811731.1 GI:32493671  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 462)  
AUTHORS Genoplatte, a major partnership french program in plant genomics  
TITLE Unpublished (2003)  
JOURNAL Contact: Genoplatte

FEATURES  
source 1..462  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jel Neuf"  
/db\_xref="taxon:3708"  
/clone="BN1001K12"  
/tissue\_type="seed"  
/clone\_lib="BN10"  
location/Qualifiers

ORIGIN  
Query Match 32.1%; Score 18; DB 6; Length 462;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 29 CATCCGATCCAGAGCA 12

RESULT 9  
CD822333/c 511 bp mRNA linear EST 10-JUL-2003  
LOCUS BN25.044N12F011129 BN25 Brassica napus cDNA clone BN25044N12, mRNA  
DEFINITION sequence.  
ACCESSION CD822333  
VERSION CD822333.1 GI:32504273  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 511)  
AUTHORS Genoplatte, a major partnership french program in plant genomics  
TITLE Unpublished (2003)  
JOURNAL Contact: Genoplatte  
COMMENT

Genoplatte  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatte' (<http://www.genoplatte.com>  
and <http://genoplatte-info.infobiogen.fr>).  
location/Qualifiers  
1..511  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jel Neuf"  
/db\_xref="taxon:3708"  
/clone="BN25044N12"  
/tissue\_type="seed"  
/clone\_lib="BN25"

ORIGIN  
Query Match 32.1%; Score 18; DB 6; Length 511;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 246 CATCCGATCCAGAGCA 229

RESULT 10  
CD817719/c 516 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.04201F011127 BN20 Brassica napus cDNA clone BN20042017, mRNA  
DEFINITION sequence.  
ACCESSION CD817719  
VERSION CD817719.1 GI:3249659  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
REFERENCE 1 (bases 1 to 516)  
AUTHORS Genoplatte, a major partnership french program in plant genomics  
TITLE Unpublished (2003)  
JOURNAL Contact: Genoplatte  
COMMENT

FEATURES  
source 1..516  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jel Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20042017"  
/tissue\_type="seed"  
/clone\_lib="BN20"  
location/Qualifiers

ORIGIN  
Query Match 32.1%; Score 18; DB 6; Length 516;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 246 CATCCGATCCAGAGCA 229

RESULT 11



BI471522 539 bp mRNA linear EST 21-JUL-2004  
 LOCUS sag21002.Y1 Gm-cl080 glycine max cDNA clone GENOME SYSTEMS CLONE  
 DEFINITION ID: Gm-cl080-1755 5' similar to TR:Q9SHG7 Q9SHG7 F20023.22 PROTEIN.  
 ; mRNA sequence.  
 BI471522.1 GI:15287631  
 EST.  
 VERSION BI471522  
 KEYWORDS  
 SOURCE ORGANISM  
 Glycine max (soybean)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
 rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseolae;  
 Glycine.  
 1 (bases 1 to 539)  
 Sheemaker, R., Keim, P., Vodkin, L., Eipelting, J., Corryell, V.,  
 Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,  
 Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,  
 Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N.,  
 Schurk, R., Ralter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,  
 McCann, R., Waterston, R. and Wilson, R.  
 Unpublished (1999)  
 TITLE  
 JOURNAL  
 COMMENT  
 CONTACT: Sheemaker R/Public Soybean EST Project  
 Public Soybean EST Project  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: esheemaker.wustl.edu  
 When it has been determined, an EST from the other end of this  
 clone is listed in the 'Other ESTs on clone' field. This clone is  
 available through: Biogenetic Services, 801 32nd Ave. Brookings, SD  
 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
 High quality sequence stop: 421.  
 Location/Qualifiers  
 1..539  
 /organism="Glycine max"  
 /mol\_type="mRNA"  
 /cultivar="Bragg NTS382"  
 /db\_xref="taxon:3847"  
 /clone="GENOME SYSTEMS CLONE ID: Gm-cl080-1755"  
 /tissue\_type="Roots of 8 day old 'Bragg' supernodulating  
 mutant NTS382 seedlings"  
 /dev\_stage="8 days old"  
 /lab\_host="PH10B"  
 /clone\_lib="Gm-cl080"  
 /note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2:  
 XhoI; The mRNA was isolated from roots of 8 day old  
 'Bragg' supernodulating mutant NTS382 seedlings that were  
 infected with Bradyrhizobium japonicum, strain USDA 110, 72  
 hours prior to harvest. Dr. Gary Stacey generously donated  
 the tissue. The roots were flash-frozen in liquid  
 nitrogen. Stratagene's cDNA Synthesis Kit (catalog number  
 200401) was used to synthesize the cDNA. First-strand  
 synthesis was performed with 5-methyl dCTP, hence the  
 ligated cDNA was hemimethylated. A modification of  
 Stratagene's first-strand synthesis primer was used. An  
 anchor nucleotide (V=A, C, or G) was added to the 3' end  
 of the primer (GAGAGAGAGAGAGAGACTGTCGAG(T)18V) to  
 anchor the primer at the 5' end of the poly(A) tract.  
 After second-strand synthesis, the cDNA ends were filled  
 in with cloned Pfu DNA, ligated to EcoRI adapters and  
 subsequently phosphorylated. The cDNA was then  
 precipitated and redissolved in sterile, RNase-,  
 DNase-free water. The XhoI site within the first-strand  
 synthesis primer was then restricted by digestion with  
 XhoI from Promega (40U/ul); all XhoI sites in the cDNA  
 would be protected by their hemimethylated status. The  
 cDNA constructs were size-fractionated with a 500bp  
 cutoff, using Sephacryl S-500 High Resolution (Pharmacia  
 Biotech) in a 2-mm diameter column and a bed volume of  
 approximately 1ml. The column eluent was precipitated,

redissolved, and ligated into Stratagene's pBluescript II  
 XR Pridigested vector (pBluescript II SK(+)) vector that  
 has been digested with EcoRI and XhoI, and phosphorylated  
 by Stratagene). This library was constructed in the  
 laboratory of Dr. Paul Keim and Dr. Virginia H. Corryell at  
 Northern Arizona University."

ORIGIN  
 Query Match 32.1%; Score 18; DB 3; Length 539;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 GCATTCGCGTATGTTG 18  
 |||||||  
 DB 394 GCATTCGCGTATGTTG 411

RESULT 12  
 Cw493595/c  
 LOCUS  
 DEFINITION  
 Cw493595 545 bp DNA linear GSS 03-NOV-2004  
 fsbb001f284g24f0 Sorghum methylation filtered library (libid: 104)  
 Sorghum bicolor genomic clone fsbb001f284g24, genomic survey  
 sequence.  
 Cw493595  
 Cw493595.1 GI:55264835  
 GSS.  
 Sorghum bicolor (sorghum)  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 545)  
 Bedell, J. A., Budiman, M. A., Nunberg, A., Citek, R. W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McNamey, J., Smith, M., Holman, H., Roe, B. A., Wiley, G., Korff, I. F.,  
 Radlowski, P. D., Lakey, N., McCombie, W. R., Jeddalon, J. A. and  
 Martiniussen, R. A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154  
 TITLE  
 JOURNAL  
 PUBMED  
 COMMENT  
 CONTACT: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@origenomics.com  
 Plate: fsbb001f284 row: 9 column: 24  
 Seq primer: F Forward  
 Class: methylation filtered  
 High quality sequence stop: 545.  
 Location/Qualifiers  
 1..545  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
 /cultivar="ATx623"  
 /db\_xref="taxon:4558"  
 /clone="fsbb001f284g24"  
 /clone\_lib="Sorghum methylation filtered library (libid:  
 104)"  
 /note="Organ: leaf; Vector: pBSK(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBSK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."

ORIGIN  
 Query Match 32.1%; Score 18; DB 10; Length 545;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 25 CATCGGATCGAGAGCA 42  
 |||||||



Db 338 CATCCGATCCAGAGCA 321

RESULT 13  
LOCUS CD818845/c 563 bp mRNA linear EST 10-JUL-2003  
DEFINITION BN20.047A04F011226 BN20 Brassica napus cDNA clone BN20047A04, mRNA sequence.

ACCESSION CD818845  
VERSION CD818845.1 GI:32500785  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 563)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french plant genomics programme 'Genoplante' (http://www.genoplante.com and http://genoplante-info.inbioigen.fr).

FEATURES  
source  
1..563  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jct Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20047A04"  
/tissue\_type="seed"  
/clone\_lib="BN20"

ORIGIN  
Query Match 32.1%; Score 18; DB 6; Length 563;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 246 CATCCGATCCAGAGCA 229  
|||||

RESULT 14  
LOCUS B1701634 572 bp mRNA linear EST 08-JUL-2004  
DEFINITION sail81812.y1 Gm-cl053 glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-cl053-3528 5' similar to TR:Q9SH67 Q9SH67 F20023.22 PROTEIN.  
; mRNA sequence.

ACCESSION B1701634  
VERSION B1701634.1 GI:15664263  
KEYWORDS EST.  
SOURCE Glycine max (soybean)  
ORGANISM Glycine max  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids I; Fabales; Fabaceae; Papilionoidae; Phaseoleae; Glycine.

REFERENCE 1 (bases 1 to 572)  
AUTHORS Shoemaker, R., Keim, P., Vodkin, L., Expelting, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Pearson, B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
TITLE Public Soybean EST Project  
JOURNAL Unpublished (1999)  
COMMENT Contact: Shoemaker R./Public Soybean EST Project

Public Soybean EST Project  
Washington University School of Medicine  
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
Tel: 314 286 1800  
Fax: 314 286 1810  
Email: est@watson.wustl.edu  
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)  
Seq primer: -40RP from Glibco  
High quality sequence stop: 425.

FEATURES  
source  
1..572  
/organism="Glycine max"  
/mol\_type="mRNA"  
/cultivar="Harosoy"  
/db\_xref="taxon:3847"  
/clone="GENOME SYSTEMS CLONE ID: Gm-cl053-3528"  
/tissue\_type="Whole seedling, 3 week old, greenhouse grown"  
/lab\_host="DH10B"  
/clone\_lib="Gm-cl053"  
/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site 2: XhoI; The Harosoy NIL was constructed and seed was provided by Dr. J. Specht, University of Nebraska (Shoemaker and Specht, 1995). The cDNA library was constructed from mRNA isolated from whole seedlings of 3 week old greenhouse grown plants. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site and a 3' anchor. EcoRI adapters were ligated to the blunt-ended cDNA fragments. Followed by XhoI digestion. The cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcoBRL). This library was constructed in cooperation with Dr. Paul Keim's laboratory at Northern Arizona University."

ORIGIN  
Query Match 32.1%; Score 18; DB 3; Length 572;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GCATTCGGTGTATGTTG 18  
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Db 374 GCATTCGGTGTATGTTG 391  
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RESULT 15  
LOCUS CD816121/c 615 bp mRNA linear EST 10-JUL-2003  
DEFINITION BN15.028J22F020327 BN15 Brassica napus cDNA clone BN15028J22, mRNA sequence.

ACCESSION CD816121  
VERSION CD816121.1 GI:32498061  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 615)  
AUTHORS Genoplante.  
TITLE Genoplante, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplante  
Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french



plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr/>).  
Location/Qualifiers

## FEATURES

## source

1..615  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jec Neuf"  
/db\_xref="taxon:3708"  
/clone="BN15028U22"  
/issue\_type="seed"  
/clone\_lib="BN15"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 615;  
Best Local Similarity 100.0%; Pred.No.16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 246 CATCCGATCCAGAGCA 229

RESULT 16  
CD817335/c 629 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.041122F011221 BN20 Brassica napus cDNA clone BN20041122, mRNA  
DEFINITION  
sequence.

ACCESSION CD817335  
VERSION CD817335.1 GI:32499275  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 629)  
AUTHORS Genoplatne.  
TITLE Genoplatne, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatne

Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr/>).  
Location/Qualifiers

## FEATURES

## source

1..629  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jec Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20041122"  
/issue\_type="seed"  
/clone\_lib="BN20"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 629;  
Best Local Similarity 100.0%; Pred.No.16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 245 CATCCGATCCAGAGCA 228

RESULT 17  
CD820120/c 631 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.051E04F011221 BN20 Brassica napus cDNA clone BN20051E04, mRNA  
DEFINITION  
sequence.  
ACCESSION CD820120

VERSION CD820120.1 GI:32502060  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 631)  
AUTHORS Genoplatne.  
TITLE Genoplatne, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatne

Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr/>).  
Location/Qualifiers

## FEATURES

## source

1..631  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jec Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20051E04"  
/issue\_type="seed"  
/clone\_lib="BN20"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 631;  
Best Local Similarity 100.0%; Pred.No.16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 246 CATCCGATCCAGAGCA 229

RESULT 18  
CD818923/c 639 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.047E17F011221 BN20 Brassica napus cDNA clone BN20047E17, mRNA  
DEFINITION  
sequence.

ACCESSION CD818923  
VERSION CD818923.1 GI:32500863  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE 1 (bases 1 to 639)  
AUTHORS Genoplatne.  
TITLE Genoplatne, a major partnership french program in plant genomics  
JOURNAL Unpublished (2003)  
COMMENT Contact: Genoplatne

Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr/>).  
Location/Qualifiers

## FEATURES

## source

1..639  
/organism="Brassica napus"  
/mol\_type="mRNA"  
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/db\_xref="taxon:3708"  
/clone="BN20047E17"  
/issue\_type="seed"  
/clone\_lib="BN20"







/db\_xref="taxon:3708"  
/clone="BN10020M17"  
/issue\_type="seed"  
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## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 648;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 245 CATCCGATCCAGAGCA 228

RESULT 22  
CD888947/c 653 bp mRNA linear EST 14-JUL-2003  
LOCUS G118.110J22F010723 G118 Triticum aestivum cDNA clone G118110J22,  
DEFINITION mRNA sequence.  
ACCESSION CD888947 GI:32656828  
VERSION CD888947.1 GI:32656828  
KEYWORDS EST.  
SOURCE Triticum aestivum (bread wheat)  
ORGANISM Triticum aestivum  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Poideae; Triticeae; Triticum.  
1 (bases 1 to 653)  
Genoplatne.  
Genoplatne, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatne

REFERENCE  
AUTHORS 93, rue Henri Rochefort 91025 EVRY CEDEX France  
TITLE Tel: 33 1 69 47 54 00  
JOURNAL Fax: 33 1 69 47 54 10  
COMMENT This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr>).  
Location/Qualifiers

FEATURES  
source 1..653  
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/mol\_type="mRNA"  
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/clone="G118110J22"  
/issue\_type="grain (118 degrees per day after  
pollination)"  
/clone\_lib="G118"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 653;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 TGAATGCTCATCCGATC 34  
|||||  
Db 430 TGAATGCTCATCCGATC 473

RESULT 23  
CD819000/c 660 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.047122F011226 BN20 Brassica napus cDNA clone BN20047122, mRNA  
DEFINITION sequence.  
ACCESSION CD819000  
VERSION CD819000.1 GI:32500940  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

REFERENCE  
AUTHORS 1 (bases 1 to 660)  
TITLE Genoplatne.  
JOURNAL Genoplatne, a major partnership french program in plant genomics  
COMMENT Unpublished (2003)  
Contact: Genoplatne

Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr>).  
Location/Qualifiers

## FEATURES

source 1..660  
/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jct Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20047122"  
/issue\_type="seed"  
/clone\_lib="BN20"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 660;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGAGCA 42  
|||||  
Db 252 CATCCGATCCAGAGCA 235

RESULT 24  
CD817887/c 685 bp mRNA linear EST 10-JUL-2003  
LOCUS BN20.043121F01127 BN20 Brassica napus cDNA clone BN20043121, mRNA  
DEFINITION sequence.  
ACCESSION CD817887  
VERSION CD817887.1 GI:32499827  
KEYWORDS EST.  
SOURCE Brassica napus (rape)  
ORGANISM Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
Rosids; eurosids II; Brassicales; Brassicaceae; Brassica.  
1 (bases 1 to 685)  
Genoplatne.  
Genoplatne, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplatne

## COMMENT

Genoplatne  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplatne' (<http://www.genoplatne.com>  
and <http://genoplatne-info.infobiogen.fr>).  
Location/Qualifiers

## FEATURES

source 1..685  
/organism="Brassica napus"  
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/cultivar="Jct Neuf"  
/db\_xref="taxon:3708"  
/clone="BN20043121"  
/issue\_type="seed"  
/clone\_lib="BN20"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 685;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



QY 25 CATCCGATCCAGAGCA 42  
 |||||  
 Db 246 CATCCGATCCAGAGCA 229

RESULT 25  
 LOCUS CM473221  
 DEFINITION CM473221 691 bp DNA linear GSS 02-NOV-2004  
 feb001f228105f0 Sorghum methylation filtered library (libid: 104)  
 Sorghum bicolor genomic clone feb001f228105, genomic survey  
 sequence.

ACCESSION CM473221  
 VERSION CM473221  
 KEYWORDS GI:55221182  
 SOURCE GSS.  
 ORGANISM Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 691)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
 15660154

REFERENCE  
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 4041 Forest Park Ave, St. Louis, MO 63108, USA  
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 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: feb001f228 row: 1 column: 05  
 Seq primer: f Forward  
 Class: methylation filtered  
 High quality sequence stop: 691.  
 Location/Qualifiers  
 1. 691  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"  
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 /db\_xref="taxon:4559"  
 /clone="feb001f228105"  
 /clone\_lib="Sorghum methylation filtered library (libid:  
 104)"  
 /note="Organ: leaf; Vector: pBCSK(-); Site 1: HincII; DNA  
 prepared from purified nuclei was randomly sheared,  
 end-repaired, size fractionated to enrich for the 0.5 to 5  
 kb fraction, ligated into HincII-digested pBCSK(-) vector  
 and electroporated into E. coli cells. This is a  
 methylation filtered library."

ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 691;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CATCCGATCCAGAGCA 42  
 |||||  
 Db 137 CATCCGATCCAGAGCA 154

RESULT 26  
 LOCUS CD861812  
 DEFINITION CD861812 696 bp mRNA linear EST 11-JUL-2003  
 AZ01.003006F010109 AZ01 Triticum aestivum cDNA AZ01003006,  
 mRNA sequence.  
 ACCESSION CD861812  
 VERSION CD861812  
 KEYWORDS GI:32545628  
 SOURCE EST.  
 Triticum aestivum (bread wheat)

ORGANISM Triticum aestivum  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
 Poideae; Triticeae; Triticum.  
 1 (bases 1 to 696)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
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REFERENCE  
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 Email: jbedell@oriongenomics.com  
 Plate: 588 row: m column: 24  
 Seq primer: SMfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 707.  
 Location/Qualifiers  
 1. 707  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"

FEATURES  
 source

QY 17 TGATGCTCATCCGATC 34  
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 Db 33 TGATGCTCATCCGATC 16

RESULT 27  
 LOCUS CM175990/c  
 DEFINITION CM175990 707 bp DNA linear GSS 29-OCT-2004  
 104 588 11158248 148 36576 084 Sorghum methylation filtered library  
 (libid: 104) Sorghum bicolor genomic clone 11158248, genomic survey  
 sequence.

ACCESSION CM175990  
 VERSION CM175990  
 KEYWORDS GI:54868557  
 SOURCE GSS.  
 ORGANISM Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 707)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
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 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: 588 row: m column: 24  
 Seq primer: SMfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 707.  
 Location/Qualifiers  
 1. 707  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"

FEATURES  
 source

Query Match 32.1%; Score 18; DB 6; Length 696;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGATGCTCATCCGATC 34  
 |||||  
 Db 33 TGATGCTCATCCGATC 16

RESULT 27  
 LOCUS CM175990/c  
 DEFINITION CM175990 707 bp DNA linear GSS 29-OCT-2004  
 104 588 11158248 148 36576 084 Sorghum methylation filtered library  
 (libid: 104) Sorghum bicolor genomic clone 11158248, genomic survey  
 sequence.

ACCESSION CM175990  
 VERSION CM175990  
 KEYWORDS GI:54868557  
 SOURCE GSS.  
 ORGANISM Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 707)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
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REFERENCE  
 AUTHORS  
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 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: 588 row: m column: 24  
 Seq primer: SMfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 707.  
 Location/Qualifiers  
 1. 707  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"

FEATURES  
 source

Query Match 32.1%; Score 18; DB 6; Length 696;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 17 TGATGCTCATCCGATC 34  
 |||||  
 Db 33 TGATGCTCATCCGATC 16

RESULT 27  
 LOCUS CM175990/c  
 DEFINITION CM175990 707 bp DNA linear GSS 29-OCT-2004  
 104 588 11158248 148 36576 084 Sorghum methylation filtered library  
 (libid: 104) Sorghum bicolor genomic clone 11158248, genomic survey  
 sequence.

ACCESSION CM175990  
 VERSION CM175990  
 KEYWORDS GI:54868557  
 SOURCE GSS.  
 ORGANISM Sorghum bicolor (sorghum)  
 Sorghum bicolor  
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
 clade; Panicoideae; Andropogoneae; Sorghum.  
 1 (bases 1 to 707)  
 Bedell, J.A., Budiman, M.A., Nunberg, A., Citek, R.W., Robbins, D.,  
 Jones, J., Flick, E., Rohlfing, T., Fries, J., Bradford, K.,  
 McMenamy, J., Smith, M., Holeman, H., Roe, B.A., Wiley, G., Korff, I.F.,  
 Rabinowicz, P.D., Lakey, N., McCombie, W.R., Jeddeloh, J.A. and  
 Martienssen, R.A.  
 Sorghum genome sequencing by methylation filtration  
 PLOS Biol. 3 (1), e13 (2005)  
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REFERENCE  
 AUTHORS  
 CONTACT: Bedell JA  
 Orion Genomics, LLC  
 4041 Forest Park Ave, St. Louis, MO 63108, USA  
 Tel: 314 615 6979  
 Fax: 314 615 5975  
 Email: jbedell@oriongenomics.com  
 Plate: 588 row: m column: 24  
 Seq primer: SMfor Forward  
 Class: methylation filtered  
 High quality sequence stop: 707.  
 Location/Qualifiers  
 1. 707  
 /organism="Sorghum bicolor"  
 /mol\_type="genomic DNA"

FEATURES  
 source



/cultivar="ATx623"  
/db\_xref="taxon:4558"  
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/clone\_lib="Sorghum methylation filtered library (libid:  
104)"  
/note="Organ: leaf; Vector: pBSC(-); Site 1: HincII; DNA  
prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBSC(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

## ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 707;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CATCCGATCCAGAGCA 42  
|||||  
DB 275 CATCCGATCCAGAGCA 258

RESULT 28  
CM029106/c 715 bp DNA linear GSS 28-OCT-2004  
LOCUS 104\_256\_10499487.116\_30400 Sorghum methylation filtered library  
DEFINITION (Libid: 104) Sorghum bicolor genomic clone 10499487, genomic survey  
sequence.

ACCESSION  
CM029106  
VERSION  
CM029106.1 GI:54705839  
KEYWORDS  
GSS  
ORGANISM  
Sorghum bicolor (sorghum)

Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 715)  
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korff,I.F.,  
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and  
Marienassen,R.A.  
Sorghum genome sequencing by methylation filtration  
PLOS Biol. 3 (1), e13 (2005)

TITLE  
JOURNAL  
PUBMED  
COMMENT  
Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 256 row: 3 column: 13  
Seq primer: T3 Reverse  
Class: methylation filtered  
High quality sequence stop: 715.

FEATURES  
source  
Location/Qualifiers  
1..715

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/db\_xref="taxon:4558"  
/clone="10499487"  
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104)"  
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prepared from purified nuclei was randomly sheared,  
end-repaired, size fractionated to enrich for the 0.5 to 5  
kb fraction, ligated into HincII-digested pBSC(-) vector  
and electroporated into E. coli cells. This is a  
methylation filtered library."

## ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 715;

Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CATCCGATCCAGAGCA 42  
|||||  
DB 700 CATCCGATCCAGAGCA 683

RESULT 29  
CD823726/c 724 bp mRNA linear EST 10-JUL-2003  
LOCUS BN25.049M09F020118 BN25 Brassica napus cDNA clone BN25049M09, mRNA  
DEFINITION sequence.

ACCESSION  
CD823726  
VERSION  
CD823726.1 GI:32505666  
KEYWORDS  
EST.  
SOURCE  
Brassica napus (rape)

Brassica napus  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

1 (bases 1 to 724)  
Genoplante.  
Genoplante, a major partnership french program in plant genomics  
Unpublished (2003)  
Contact: Genoplante

Genoplante  
93, rue Henri Rochefort 91025 EVRY CEDEX France  
Tel: 33 1 69 47 54 00  
Fax: 33 1 69 47 54 10  
This sequence has been generated in the framework of the french  
plant genomics programme 'Genoplante' (<http://www.genoplante.com>  
and <http://genoplante-info.infobiogen.fr>).

FEATURES  
source  
Location/Qualifiers  
1..724

/organism="Brassica napus"  
/mol\_type="mRNA"  
/cultivar="Jef Neuf"  
/db\_xref="taxon:3708"  
/clone="BN25049M09"  
/tissue\_type="seed"  
/clone\_lib="BN25"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 724;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CATCCGATCCAGAGCA 42  
|||||  
DB 247 CATCCGATCCAGAGCA 230

RESULT 30  
CM029105 724 bp DNA linear GSS 28-OCT-2004  
LOCUS 104\_256\_10499487.114\_30399 Sorghum methylation filtered library  
DEFINITION (Libid: 104) Sorghum bicolor genomic clone 10499487, genomic survey  
sequence.

ACCESSION  
CM029105  
VERSION  
CM029105.1 GI:54705838  
KEYWORDS  
GSS  
ORGANISM  
Sorghum bicolor (sorghum)

Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.

1 (bases 1 to 724)  
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
McMenamy,J., Smith,M., Holeman,H., Roe,B.A., Wiley,G., Korff,I.F.,  
Rabinowicz,P.D., Lakey,N., McCombie,W.R., Jeddeloh,J.A. and  
Marienassen,R.A.



TITLE Sorghum genome sequencing by methylation filtration  
JOURNAL PLOS Biol. 3 (1), e13 (2005)  
COMMENT 15660154  
Contact: Bedell JA  
Orion Genomics, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: 256 row: 1 column: 13  
Seq primer: M13/pUC Forward  
Class: methylation filtered  
High quality sequence stop: 724.

## FEATURES

SOURCE

Location/Qualifiers  
1..724  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
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/db\_xref="taxon:4558"  
/clone="10499487"  
/clone\_lib="Sorghum methylation filtered library (libID: 104)"  
/note="Organ: leaf; Vector: pBCSK(-); Site: 1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBCSK(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

## ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 724;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGGAGCA 42

Db 470 CATCCGATCCAGGAGCA 487

RESULT 31  
CD824516/c

LOCUS BN25.053N08F020328 BN25 Brassica napus cdna clone BN25053N08, mRNA

DEFINITION

CD824516 729 bp mRNA linear EST 10-JUL-2003

sequence.

ACCESSION

CD824516

VERSION

CD824516.1 GI:32506456

KEYWORDS

EST.

SOURCE

Brassica napus (rape)

ORGANISM

Brassica napus

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; rosids; eurosids II; Brassicales; Brassicaceae; Brassica.

REFERENCE

1 (bases 1 to 729)

Genoplane.

Genoplane, a major partnership french program in plant genomics

Unpublished (2003)

Contact: Genoplane

Genoplane

93, rue Henri Rochefort 91025 EVRY CEDEX France

Tel: 33 1 69 47 54 00

Fax: 33 1 69 47 54 10

This sequence has been generated in the framework of the french

plant genomics programme 'Genoplane' (<http://www.genoplane.com>and <http://genoplane-info.infobiogen.fr>).

Location/Qualifiers

1..729

/organism="Brassica napus"

/mol\_type="mRNA"

/cultivar="Jei Neuf"

/db\_xref="taxon:3708"

/clone="BN25053N08"

/issue\_type="seed"

/clone\_lib="BN25"

## FEATURES

SOURCE

Location/Qualifiers  
1..729  
/organism="Brassica napus"

## ORIGIN

Query Match 32.1%; Score 18; DB 6; Length 729;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 CATCCGATCCAGGAGCA 42

Db 245 CATCCGATCCAGGAGCA 228

RESULT 32  
CW831094/c

LOCUS OP\_Ba0088F16.f OP\_Ba Oryza punctata genomic clone OP\_Ba0088F16

DEFINITION

5', genomic survey sequence.

ACCESSION

CW831094

VERSION

CW831094.1 GI:56072321

KEYWORDS

GSS.

SOURCE

Oryza punctata

ORGANISM

Oryza punctata

Eukaryote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

REFERENCE

1 (bases 1 to 747)

Bharatolideae; Oryzaceae; Oryza.

SanMiguel, P., Westerman, R., Kim, H., Yu, Y., Wisotski, M., Yost, D.,

Stum, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C.,

Hartfield, J., Soderlund, C., Wang, R. and Jackson, S.A.

OMAP Project - Purdue University

Unpublished (2004)

Contact: Scott A. Jackson

Jackson Laboratory

Purdue University

915 W. State St., West Lafayette, IN 47907, USA

Tel: 7654963621

Fax: 7654967255

Email: sjackson@purdue.edu

Basecalling by phred version 0.020425.c. This sequence was derived

from the raw sequence read by clipping with Lucy version 1.19s.

Bases 121-867 of the raw sequence (length 1004) were retained after

clipping.

Plate: 008 row: F column: 16

Seq primer: TAA TAC GAC TCA CTA TAG CG

Class: BAC ends.

Location/Qualifiers

1..747

/organism="Oryza punctata"

/mol\_type="genomic DNA"

/db\_xref="taxon:4537"

/clone="OP\_Ba0088F16"

/issue\_type="young leaves"

/lab\_host="DH10B-T1 phage resistant"

/clone\_lib="OP\_Ba"

/note="Vector: pAGIBAC1, Site\_1: HindIII, Site\_2: HindIII"

## FEATURES

SOURCE

Location/Qualifiers  
1..747  
/organism="Oryza punctata"

## ORIGIN

Query Match 32.1%; Score 18; DB 10; Length 747;

Best Local Similarity 100.0%; Pred. No. 16;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 GTATGTTGATGCTCAGC 28

Db 559 GTATGTTGATGCTCAGC 542

RESULT 33  
CV203057/c

LOCUS CV203057 755 bp mRNA linear EST 16-SEP-2004

DEFINITION

EST862767 non-normalized T1 cdna library Trichomonas vaginalis cdna

clone TVFA121, mRNA sequence.

ACCESSION

CV203057

VERSION

CV203057.1 GI:52150037

KEYWORDS

EST.



SOURCE Trichomonas vaginalis  
ORGANISM Trichomonas vaginalis  
Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.

REFERENCE 1 (bases 1 to 755)  
AUTHORS Carleton,J.M., Dyall,S., Johnson,P.J. and Fraser,C.M.  
TITLE The complete genome sequence of the sexually transmitted parasite Trichomonas vaginalis  
JOURNAL Unpublished (2004)  
COMMENT Other\_ESTs: EST862766 EST862768  
Contact: Jane Carleton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carleton@tigr.org.  
Location/Qualifiers

FEATURES  
source 1..755  
/organism="Trichomonas vaginalis"  
/mol\_type="mRNA"  
/strain="T1"  
/db\_xref="taxon:5722"  
/clone="VTVA121"  
/note="Vector: Lambda TriplEx2; Site\_1: SfiI; Site\_2: SfiI; T. vaginalis strain T1 library constructed from unidirectionally in the SfiI and SfiI sites. Mass excision of library produced inserts in pTriplEx2 plasmid. Inserts sequenced from both 5' and 3' ends using TriplEx2 sequencing primer and polydT 24 bp primer respectively."

ORIGIN  
Query Match 32.1%; Score 18; DB 7; Length 755;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AGCAATGAGATTACACG 56  
|||||  
Db 382 AGCAATGAGATTACACG 365

RESULT 34  
LOCUS CW493596 762 bp DNA linear GSS 03-NOV-2004  
DEFINITION fdbb001f284g24k0 Sorghum methylation filtered library (LibID: 104)  
Sorghum bicolor genomic clone fdbb001f284g24, genomic survey sequence.  
ACCESSION CW493596  
VERSION CW493596.1 GI:55264836  
KEYWORDS GSS.  
SOURCE Sorghum bicolor (sorghum)  
ORGANISM Sorghum bicolor  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD  
clade; Panicoideae; Andropogoneae; Sorghum.  
1 (bases 1 to 762)  
Bedell,J.A., Budiman,M.A., Nunberg,A., Citek,R.W., Robbins,D.,  
Jones,J., Flick,E., Rohlfing,T., Fries,J., Bradford,K.,  
Mcmenamy,J., Smith,M., Holman,H., Roe,B.A., Wiley,G., Korf,I.F.,  
Rabinowicz,P.D., Lakey,N., McComble,W.R., Jeddeloh,J.A. and  
Martensen,R.A.  
Sorghum genome sequencing by methylation filtration  
PLoS Biol. 3 (1), e13 (2005)  
15660154  
Contact: Bedell JA  
Orion Genomic, LLC  
4041 Forest Park Ave, St. Louis, MO 63108, USA  
Tel: 314 615 6979  
Fax: 314 615 5975  
Email: jbedell@oriongenomics.com  
Plate: fdbb001f284 row: g column: 24

Seq primer: k Reverse  
Class: methylation filtered  
High quality sequence stop: 762.  
Location/Qualifiers

FEATURES  
source 1..762  
/organism="Sorghum bicolor"  
/mol\_type="genomic DNA"  
/cultivar="ATx623"  
/db\_xref="taxon:4558"  
/clone="fdbb001f284g24"  
/clone\_lib="Sorghum methylation filtered library (LibID: 104)"  
/note="Organ: leaf; Vector: pBSC(-); Site\_1: HincII; DNA prepared from purified nuclei was randomly sheared, end-repaired, size fractionated to enrich for the 0.5 to 5 kb fraction, ligated into HincII-digested pBSC(-) vector and electroporated into E. coli cells. This is a methylation filtered library."

ORIGIN  
Query Match 32.1%; Score 18; DB 10; Length 762;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 CATCCGATCCAGAGCA 42  
|||||  
Db 469 CATCCGATCCAGAGCA 486

RESULT 35  
LOCUS CA493148 831 bp mRNA linear EST 09-MAR-2004  
DEFINITION AGENCOURT 10842545 NIH MGC 154 Mus musculus CDNA clone  
IMAGE:6763539 5', mRNA sequence.  
ACCESSION CA493148  
VERSION CA493148.1 GI:24956171  
KEYWORDS EST.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Muridae; Murinae; Mus.  
1 (bases 1 to 831)  
NIH-MGC http://mgc.ncl.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Bradfield Laboratory  
CDNA Library Preparation: Mark Bittinger  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: LNM00130 row: h column: 02  
High quality sequence stop: 456.  
Location/Qualifiers

FEATURES  
source 1..831  
/organism="Mus musculus"  
/mol\_type="mRNA"  
/db\_xref="taxon:10090"  
/clone="IMAGE:6763539"  
/lab\_host="DH10B (phage-resistant)"  
/clone\_lib="NIH MGC\_154"  
/note="Organ: Kidney; TCDD (DMSO vehicle) Treated 48  
Hours IP injections; Vector: pOONR201; Site\_1: attP2;  
Site\_2: attP1; cDNA made by oligo-dT with attB2 site and  
directionally cloned. Priming sequence:  
5'-TTTCTGAGCGCGCGACACATTTGTACAAAGCTGGTTTCTTTT  
TTTT-3'. Full-length enriched library was constructed  
using the Genescreen kit by invivoegen, library  
amplification 16 cycles. Library constructed by Mark







REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

COMMENT

Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
1 (bases 1 to 931)  
Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M.  
The complete genome sequence of the sexually transmitted parasite  
Trichomonas vaginalis  
Unpublished (2004)  
Other ESTs: EST870402  
Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlton@tigr.org  
Seq primer: polydT 24 base.  
Location/Qualifiers

FEATURES  
source

1..931  
/organism="Trichomonas vaginalis"  
/mol\_type="rRNA"  
/strain="T1"  
/db\_xref="taxon:5722"  
/clone\_lib="non-normalized T1 cDNA library"  
/note="Vector: Lambda Triplex2; Site 1: SfiA; Site 2:  
SfiB; T. vaginalis strain T1 library constructed from  
cDNA, made in lambda Triplex2. Inserts cloned  
unidirectionally in the SfiA and SfiB sites. Mass excision  
of library produced inserts in pTriplex2 plasmid. Inserts  
sequenced from both 5' and 3' ends using Triplex2  
sequencing primer and polydT 24 bp primer respectively."

ORIGIN

Query Match 32.1%; Score 18; DB 7; Length 931;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AGCAATGAGATTACACG 56  
DB 355 AGCAATGAGATTACACG 338

RESULT 39

LOCUS CV203058 941 bp mRNA linear EST 16-SEP-2004  
DEFINITION EST862768 non-normalized T1 cDNA library Trichomonas vaginalis cDNA  
clone TVTA121 3' end, mRNA sequence.  
ACCESSION CV203058  
VERSION CV203058.1 GI:52150038

KEYWORDS  
SOURCE  
ORGANISM

EST  
Trichomonas vaginalis  
Trichomonas vaginalis  
Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
1 (bases 1 to 941)  
Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M.  
The complete genome sequence of the sexually transmitted parasite  
Trichomonas vaginalis  
Unpublished (2004)  
Other ESTs: EST862766 EST862767  
Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlton@tigr.org  
Seq primer: polydT 24 base.  
Location/Qualifiers

FEATURES

source  
1..941  
/organism="Trichomonas vaginalis"  
/mol\_type="rRNA"  
/strain="T1"

ORIGIN

/db\_xref="taxon:5722"  
/clone\_lib="non-normalized T1 cDNA library"  
/note="Vector: Lambda Triplex2; Site 1: SfiA; Site 2:  
SfiB; T. vaginalis strain T1 library constructed from  
cDNA, made in lambda Triplex2. Inserts cloned  
unidirectionally in the SfiA and SfiB sites. Mass excision  
of library produced inserts in pTriplex2 plasmid. Inserts  
sequenced from both 5' and 3' ends using Triplex2  
sequencing primer and polydT 24 bp primer respectively."

Query Match 32.1%; Score 18; DB 7; Length 941;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AGCAATGAGATTACACG 56  
DB 299 AGCAATGAGATTACACG 282

RESULT 40

LOCUS CV210692 958 bp mRNA linear EST 16-SEP-2004  
DEFINITION EST870402 non-normalized T1 cDNA library Trichomonas vaginalis cDNA  
clone TVTB82 5' end, mRNA sequence.  
ACCESSION CV210692  
VERSION CV210692.1 GI:52157672

KEYWORDS  
SOURCE  
ORGANISM

EST  
Trichomonas vaginalis  
Trichomonas vaginalis  
Eukaryota; Parabasalidae; Trichomonada; Trichomonadida;  
Trichomonadidae; Trichomonadinae; Trichomonas.  
1 (bases 1 to 958)  
Carlton, J.M., Dyall, S., Johnson, P.J. and Fraser, C.M.  
The complete genome sequence of the sexually transmitted parasite  
Trichomonas vaginalis  
Unpublished (2004)  
Other ESTs: EST870401  
Contact: Jane Carlton  
Parasite Genomics Group  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850, USA  
Tel: 301-530-9319  
Fax: 301-838-0208  
Email: carlton@tigr.org  
Seq primer: lambda Triplex2.  
Location/Qualifiers

FEATURES

source

1..958  
/organism="Trichomonas vaginalis"  
/mol\_type="rRNA"  
/strain="T1"  
/db\_xref="taxon:5722"  
/clone\_lib="non-normalized T1 cDNA library"  
/note="Vector: Lambda Triplex2; Site 1: SfiA; Site 2:  
SfiB; T. vaginalis strain T1 library constructed from  
cDNA, made in lambda Triplex2. Inserts cloned  
unidirectionally in the SfiA and SfiB sites. Mass excision  
of library produced inserts in pTriplex2 plasmid. Inserts  
sequenced from both 5' and 3' ends using Triplex2  
sequencing primer and polydT 24 bp primer respectively."

ORIGIN

Query Match 32.1%; Score 18; DB 7; Length 958;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 39 AGCAATGAGATTACACG 56  
DB 816 AGCAATGAGATTACACG 833



Search completed: April 11, 2006, 21:44:48  
Job time : 805.045 secs

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GenCore version 5.1.7  
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:22 ; Search time 3440.08 Seconds

(without alignments)  
9253.359 Million cell updates/sec

Title: US-10-712-654-34

Perfect score: 560

Sequence: 1 acaactggtacatctgcgcg.....ggagcatgagaattacacg 560

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 5883141 seqs, 28421725653 residues

Word size : 1

Total number of hits satisfying chosen parameters: 11765110

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: listing first 1000 summaries

Database :

Genembl:\*  
1: gb\_ba:\*  
2: gb\_in:\*  
3: gb\_env:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pr:\*  
9: gb\_ro:\*  
10: gb\_sts:\*  
11: gb\_gy:\*  
12: gb\_un:\*  
13: gb\_vi:\*  
14: gb\_htg:\*  
15: gb\_pl:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result	No.	Score	Query Match	Length	ID	Description
	1	560	100.0	3244	1 BACCAPABC	M24150 B.anthraxis
	2	560	100.0	94829	1 AEO11191	ABO11191 Bacillus
	3	560	100.0	94830	1 AEO17335	ABO17335 Bacillus
	4	560	100.0	96231	1 AF188935	AF188935 Bacillus
	5	32	5.7	32	6 AX743806	AX743806 Sequence
	6	30	5.4	30	6 AX743807	AX743807 Sequence
	7	29	5.2	110000	1 BA000028.02	Continuation (3 of
	8	26	4.6	26	6 AX743817	AX743817 Sequence
	9	25	4.5	25	6 AX743816	AX743816 Sequence
	10	24	4.3	181419	8 AL445984	AL445984 Human DNA
	11	23	4.1	284	15 AY022390	AY022390 Oryza sat
	12	23	4.1	102599	8 AC096951	AC096951 Homo sapi
	13	23	4.1	110000	15 AP008218.250	Continuation (251
	14	23	4.1	121563	15 CNS07YQ4	AL713904 Oryza sat
	15	23	4.1	146686	15 CNS080CBR	AL928754 Oryza sat
	16	23	4.1	152394	14 AC069315	AC069315 Homo sapi
	17	21	3.8	126080	8 AY029472	AY029472 Homo sapi
	18	21	3.8	159791	8 AC009951	AC009951 Homo sapi

C	19	3.8	179984	8	AC016526	AC016526 Homo sapi
	20	3.8	199024	14	AC150721	AC150721 Callithrix
	21	3.8	206630	14	AC150604	AC150604 Callithrix
	22	3.6	2424	15	VFA243461	AJ244461 Vicia fab
	23	3.6	6278	8	HSB806491	BX58250 Homo sapi
	24	3.6	74914	14	AC165169	AC165169 Mus muscu
	25	3.6	79173	8	AC114958	AC114958 Homo sapi
	26	3.6	87302	8	AC027313	AC027313 Homo sapi
	27	3.6	91039	15	AP004491	AP004491 Lotus cor
	28	3.6	110000	1	CP000076.24	Continuation (25 o
	29	3.6	110000	1	CP000076.25	Continuation (26 o
	30	3.6	110000	15	CR382127_03	Continuation (4 of
	31	3.6	110000	15	AP008212_289	Continuation (290
	32	3.6	123778	8	AC069294	AC069294 Homo sapi
	33	3.6	143918	15	AP004278	AP004278 Oryza sat
	34	3.6	152963	5	AL929530	AL929530 Zebrafish
	35	3.6	167536	5	CR848759	CR848759 Zebrafish
	36	3.6	170793	8	AC044907	AC044907 Homo sapi
	37	3.6	171184	8	AC108733	AC108733 Homo sapi
	38	3.6	171403	9	AC124423	AC124423 Mus muscu
	39	3.6	173031	8	AL359853	AL359853 Human DNA
	40	3.6	173602	8	AC090226	AC090226 Homo sapi
	41	3.6	173683	14	AC053542	AC053542 Homo sapi
	42	3.6	174832	8	AF280107	AF280107 Homo sapi
	43	3.6	174869	14	AP001840	AP001840 Homo sapi
	44	3.6	174874	9	AC123054	AC123054 Mus muscu
	45	3.6	175786	8	AC105339	AC105339 Homo sapi
	46	3.6	178764	9	AC137849	AC137849 Mus muscu
	47	3.6	178779	14	AC162816	AC162816 Bos tauru
	48	3.6	181222	14	AP001530	AP001530 Homo sapi
	49	3.6	187362	9	AC124593	AC124593 Mus muscu
	50	3.6	198524	14	AC109554	AC109554 Rattus no
	51	3.6	199030	14	AC111324	AC111324 Rattus no
	52	3.6	202260	14	AC166605	AC166605 Oryctolag
	53	3.6	204785	9	AC124605	AC124605 Mus muscu
	54	3.6	210993	14	AC152100	AC152100 Bos tauru
	55	3.6	214658	9	AC133509	AC133509 Mus muscu
	56	3.6	221775	14	AC092992	AC092992 Homo sapi
	57	3.6	226673	9	AC107786	AC107786 Mus muscu
	58	3.6	228302	9	AC107711	AC107711 Mus muscu
	59	3.6	248587	14	CR626889	CR626889 Dantio rer
	60	3.6	300092	14	AC106230	AC106230 Rattus no
	61	3.4	581	10	BV454344	BV454344 BOP38C12.
	62	3.4	624	10	BV434902	BV434902 S237P6354
	63	3.4	694	10	BV555733	BV555733 S222P6370
	64	3.4	701	10	BV532649	BV532649 G591P6210
	65	3.4	830	10	BV542708	BV542708 G591P5847
	66	3.4	901	10	BV454344	BV454344 BOP38C12.
	67	3.4	1134	6	CO716409	CO716409 Sequence
	68	3.4	1776	6	BD127726	BD127726 Primer fo
	69	3.4	1776	6	CQ783580	CQ783580 Sequence
	70	3.4	1776	6	AK074683	AK074683 Homo sapi
	71	3.4	1863	6	AR396447	AR396447 Sequence
	72	3.4	1914	6	AX540481	AX540481 Sequence
	73	3.4	2316	8	DQ023507	DQ023507 Homo sapi
	74	3.4	2537	8	AK025649	AK025649 Homo sapi
	75	3.4	2655	5	AB032416	AB032416 Dantio rer
	76	3.4	2873	5	BC045561	BC045561 Dantio rer
	77	3.4	2896	5	BC056327	BC056327 Dantio rer
	78	3.4	3028	6	CO845964	CO845964 Sequence
	79	3.4	3028	6	AK131463	AK131463 Homo sapi
	80	3.4	3055	5	BC066380	BC066380 Dantio rer
	81	3.4	3087	8	AB168347	AB168347 Macaca fa
	82	3.4	3671	8	DQ023505	DQ023505 Homo sapi
	83	3.4	4661	6	CS080604	CS080604 Sequence
	84	3.4	4661	6	AB007896	AB007896 Homo sapi
	85	3.4	4959	8	AX540479	AX540479 Sequence
	86	3.4	5656	8	DQ023503	DQ023503 Homo sapi
	87	3.4	6272	8	DQ023504	DQ023504 Homo sapi
	88	3.4	9772	1	AE010159	AE010159 Pyrococcu
	89	3.4	10431	1	AE010287	AE010287 Pyrococcu
	90	3.4	10872	6	AX251989	AX251989 Sequence
	91	3.4	10872	6	AX344385	AX344385 Sequence



C 92	19	3.4	10872	6	AX348768	Sequence	C 165	19	3.4	172753	8	AL359259	19	3.4	172753	8	AL359259
C 93	19	3.4	13311	1	STAF001386	AF001386 Salmonella	C 166	19	3.4	172611	1	AF001386	19	3.4	172611	1	AF001386
C 94	19	3.4	13311	6	AX191732	Sequence	C 167	19	3.4	173693	14	AC142422	19	3.4	173693	14	AC142422
C 95	19	3.4	17817	8	BS000221	Pan trogl	C 168	19	3.4	173967	8	AC147338	19	3.4	173967	8	AC147338
C 96	19	3.4	22108	1	AEO08819	Salmonell	C 169	19	3.4	175961	9	AC124705	19	3.4	175961	9	AC124705
C 97	19	3.4	32768	6	BD193805	Enterococ	C 170	19	3.4	176545	1	AEO16957	19	3.4	176545	1	AEO16957
C 98	19	3.4	41461	8	AC010646	Homo sapi	C 171	19	3.4	176671	14	AC080419	19	3.4	176671	14	AC080419
C 99	19	3.4	62027	1	AEO08743	Salmonell	C 172	19	3.4	178494	14	AC080819	19	3.4	178494	14	AC080819
C 100	19	3.4	68673	14	AC124071	Homo sapi	C 173	19	3.4	178544	9	AC128943	19	3.4	178544	9	AC128943
C 101	19	3.4	76228	14	AC016338	Homo sapi	C 174	19	3.4	179357	14	AC009665	19	3.4	179357	14	AC009665
C 102	19	3.4	76581	8	AL355304	Human DNA	C 175	19	3.4	181557	14	AC072055	19	3.4	181557	14	AC072055
C 103	19	3.4	78607	8	AC145092	Human DNA	C 176	19	3.4	182437	8	AC148875	19	3.4	182437	8	AC148875
C 104	19	3.4	93134	15	BX908807	Neutropor	C 177	19	3.4	182906	14	AC131221	19	3.4	182906	14	AC131221
C 105	19	3.4	101021	14	AC161017	Pan trogl	C 178	19	3.4	183846	14	AC159840	19	3.4	183846	14	AC159840
C 106	19	3.4	104829	9	AEO14175_3	Continuatio	C 179	19	3.4	183980	14	AC011081	19	3.4	183980	14	AC011081
C 107	19	3.4	106730	15	ATP12M12	Continuatio (4 of	C 180	19	3.4	184477	9	AC117638	19	3.4	184477	9	AC117638
C 108	19	3.4	106769	14	AP007725	AL355775 Arabidops	C 181	19	3.4	184767	14	AC084363	19	3.4	184767	14	AC084363
C 109	19	3.4	107895	9	ALB85448	Mouse DNA	C 182	19	3.4	184818	8	AC148937	19	3.4	184818	8	AC148937
C 110	19	3.4	109830	14	CR955007	Medicago	C 183	19	3.4	184818	8	AC148937	19	3.4	184818	8	AC148937
C 111	19	3.4	110000	1	AEO05174_20	Continuatio (21 o	C 184	19	3.4	185385	8	AC155319	19	3.4	185385	8	AC155319
C 112	19	3.4	110000	1	CR626927_34	Continuatio (35 o	C 185	19	3.4	185551	8	HSU171K17	19	3.4	185551	8	HSU171K17
C 113	19	3.4	110000	1	CR626927_35	Continuatio (36 o	C 186	19	3.4	185824	14	AC156317	19	3.4	185824	14	AC156317
C 114	19	3.4	110000	1	ABO17220_10	Continuatio (11 o	C 187	19	3.4	186334	8	AL158073	19	3.4	186334	8	AL158073
C 115	19	3.4	110000	1	ABO17220_37	Continuatio (28 o	C 188	19	3.4	186528	9	ALB08024	19	3.4	186528	9	ALB08024
C 116	19	3.4	110000	1	AP006841_35	Continuatio (36 o	C 189	19	3.4	186534	14	AC142442	19	3.4	186534	14	AC142442
C 117	19	3.4	110000	1	AP006841_35	Continuatio (37 o	C 190	19	3.4	188314	14	AC162289	19	3.4	188314	14	AC162289
C 118	19	3.4	110000	1	BA000007_20	Continuatio (21 o	C 191	19	3.4	188746	14	CR925714	19	3.4	188746	14	CR925714
C 119	19	3.4	110000	15	CR382135_13	Continuatio (14 o	C 192	19	3.4	189158	8	AC147666	19	3.4	189158	8	AC147666
C 120	19	3.4	110000	15	AP008207_372	Continuatio (37.3	C 193	19	3.4	190860	5	AL923344	19	3.4	190860	5	AL923344
C 121	19	3.4	110000	15	AP008208_005	Continuatio (6 of	C 194	19	3.4	190898	5	AL923344	19	3.4	190898	5	AL923344
C 122	19	3.4	110000	15	AP008209_348	Continuatio (349	C 195	19	3.4	191064	14	AL161745	19	3.4	191064	14	AL161745
C 123	19	3.4	110000	15	AP008209_349	Continuatio (350	C 196	19	3.4	192819	9	AC114585	19	3.4	192819	9	AC114585
C 124	19	3.4	110000	15	AP008211_140	Continuatio (141	C 197	19	3.4	192952	14	AC026966	19	3.4	192952	14	AC026966
C 125	19	3.4	110001	8	AC084880	Homo sapi	C 198	19	3.4	195487	14	AC162270	19	3.4	195487	14	AC162270
C 126	19	3.4	111252	15	AC148404	Medicago	C 199	19	3.4	196311	9	AC159644	19	3.4	196311	9	AC159644
C 127	19	3.4	113075	8	AL512353	Human DNA	C 200	19	3.4	196468	14	AC111065	19	3.4	196468	14	AC111065
C 128	19	3.4	115956	15	AC146566	Medicago	C 201	19	3.4	196501	14	AC163922	19	3.4	196501	14	AC163922
C 129	19	3.4	117751	8	AC020913	AL512353 Human DNA	C 202	19	3.4	196501	14	AC163922	19	3.4	196501	14	AC163922
C 130	19	3.4	118068	8	AL356798	Human DNA	C 203	19	3.4	199052	14	AC122101	19	3.4	199052	14	AC122101
C 131	19	3.4	126152	8	HS433M19	295703 Human DNA	C 204	19	3.4	203914	14	AC148941	19	3.4	203914	14	AC148941
C 132	19	3.4	134865	9	ALB844206	Mouse DNA	C 205	19	3.4	206032	14	AC134799	19	3.4	206032	14	AC134799
C 133	19	3.4	135356	15	AP004769	Orzya sat	C 206	19	3.4	213310	8	AC147334	19	3.4	213310	8	AC147334
C 134	19	3.4	139788	14	AC024118	Homo sapi	C 207	19	3.4	213365	8	AC147687	19	3.4	213365	8	AC147687
C 135	19	3.4	140077	15	AC136524	Orzya sat	C 208	19	3.4	212556	14	AC134142	19	3.4	212556	14	AC134142
C 136	19	3.4	142225	8	AC110053	AC136524 Orzya sat	C 209	19	3.4	213025	14	AC120278	19	3.4	213025	14	AC120278
C 137	19	3.4	143655	14	AC1010808	AC110053 Homo sapi	C 210	19	3.4	214856	14	AC113738	19	3.4	214856	14	AC113738
C 138	19	3.4	144195	9	AL935297	AC1010808 Homo sapi	C 211	19	3.4	216424	14	AC161783	19	3.4	216424	14	AC161783
C 139	19	3.4	145413	14	CR762474	Mouse DNA	C 212	19	3.4	218013	14	AC097255	19	3.4	218013	14	AC097255
C 140	19	3.4	150817	8	BS000220	CR762474 Dantio ter	C 213	19	3.4	218986	14	AC111652	19	3.4	218986	14	AC111652
C 141	19	3.4	152149	15	AP003611	BS000220 Pan trogl	C 214	19	3.4	218986	14	AC111652	19	3.4	218986	14	AC111652
C 142	19	3.4	152149	2	AC159448	AP003611 Orzya sat	C 215	19	3.4	219991	14	BS000547	19	3.4	219991	14	BS000547
C 143	19	3.4	153666	15	AP003287	AC159448 Trypanoso	C 216	19	3.4	226270	14	CR388062	19	3.4	226270	14	CR388062
C 144	19	3.4	154968	8	AL596342	AP003287 Orzya sat	C 217	19	3.4	223667	14	AC127058	19	3.4	223667	14	AC127058
C 145	19	3.4	155173	15	AL530952	AL596342 Human DNA	C 218	19	3.4	226493	14	AC162220	19	3.4	226493	14	AC162220
C 146	19	3.4	155369	8	AL160058	AL530952 Zea mays	C 219	19	3.4	236007	14	AC107559	19	3.4	236007	14	AC107559
C 147	19	3.4	156603	15	AP004752	AL160058 Human DNA	C 220	19	3.4	232840	14	AC155191	19	3.4	232840	14	AC155191
C 148	19	3.4	158193	14	AC010828	AP004752 Orzya sat	C 221	19	3.4	239200	14	AC133848	19	3.4	239200	14	AC133848
C 149	19	3.4	158485	8	AP001608	AC010828 Homo sapi	C 222	19	3.4	240732	14	AC131694	19	3.4	240732	14	AC131694
C 150	19	3.4	159305	8	AL355384	AP001608 Homo sapi	C 223	19	3.4	242577	14	AC121694	19	3.4	242577	14	AC121694
C 151	19	3.4	159453	2	AC159451	AL355384 Human DNA	C 224	19	3.4	244105	14	AC098897	19	3.4	244105	14	AC098897
C 152	19	3.4	161266	14	AC148285	AC159451 Trypanoso	C 225	19	3.4	247189	14	AC109910	19	3.4	247189	14	AC109910
C 153	19	3.4	161507	8	AC046195	AC148285 Rhinoloph	C 226	19	3.4	249867	14	AC127704	19	3.4	249867	14	AC127704
C 154	19	3.4	162608	8	AC009478	AC046195 Homo sapi	C 227	19	3.4	252394	14	AC096112	19	3.4	252394	14	AC096112
C 155	19	3.4	162755	14	AC128922	AC009478 Homo sapi	C 228	19	3.4	260492	14	AC133228	19	3.4	260492	14	AC133228
C 156	19	3.4	164352	15	AC092557	AC128922 Rattus no	C 229	19	3.4	260953	14	AC135479	19	3.4	260953	14	AC135479
C 157	19	3.4	164529	14	AC079975	AC092557 Orzya sat	C 230	19	3.4	263942	14	AC161418	19	3.4	263942	14	AC161418
C 158	19	3.4	164933	14	AC074231	AC079975 Homo sapi	C 231	19	3.4	269921	14	AC160310	19	3.4	269921	14	AC160310
C 159	19	3.4	168364	9	AC116507	AC074231 Homo sapi	C 232	19	3.4	283992	14	AC099286	19	3.4	283992	14	AC099286
C 160	19	3.4	168813	8	AC013717	AC116507 Mus muscu	C 233	19	3.4	304018	14	AC161133	19	3.4	304018	14	AC161133
C 161	19	3.4	168909	14	AC118862	AC013717 Homo sapi	C 234	19	3.4	304143	1	AEO15926	19	3.4	304143	1	AEO15926
C 162	19	3.4	168991	8	AC073958	AC118862 Rattus no	C 235	19	3.4	340000	8	AE001700	19	3.4	340000	8	AE001700
C 163	19	3.4	169131	8	AC147127	AC073958 Homo sapi	C 236	19	3.4	345980	6	AX344569	19	3.4	345980	6	AX344569
C 164	19	3.4	169938	14	AC146023	AC147127 Pan trogl	C 237	19	3.2	18	6	AX743805	19	3.2	18	6	AX743805



C 238	18	3.2	323	13	AF516027	AF516027 Hepatitis	311	18	3.2	3521	1	MESCPHAB	L26487 Methanosarc
C 239	18	3.2	339	13	AF516032	AF516032 Hepatitis	312	18	3.2	3550	6	CO577316	CO577316 Sequence
C 240	18	3.2	391	13	AY632173	AY632173 Hepatitis	313	18	3.2	3786	5	BC044014	BC044014 Xenopus 1
C 241	18	3.2	391	13	AY632174	AY632174 Hepatitis	C 314	18	3.2	3994	5	EX511070	EX511070 Zebrafish
C 242	18	3.2	392	13	AY632175	AY632175 Hepatitis	C 315	18	3.2	4050	9	BX322535	BX322535 Mouse DNA
C 243	18	3.2	401	13	AY265427	AY265427 Hepatitis	C 316	18	3.2	4176	9	BC057009	BC057009 Mus muscu
C 244	18	3.2	483	2	AY857434	AY857434 Subtelom	C 317	18	3.2	4291	5	AJ851535	AJ851535 Gallus ga
C 245	18	3.2	517	1	AY471587	AY471587 Subtelom	C 318	18	3.2	4342	6	I41349	I41349 Sequence 1
C 246	18	3.2	534	15	AF130171	AF130171 Aegilops	C 319	18	3.2	4342	9	MUSHTK	L38847 Mus musculu
C 247	18	3.2	571	10	BV411680	BV411680 S229P6304	C 320	18	3.2	4438	15	AF168391	AF168391 Arabidops
C 248	18	3.2	583	10	BV395032	BV395032 S243P6117	C 321	18	3.2	4440	6	CQ493282	CQ493282 Sequence
C 249	18	3.2	586	10	BV424207	BV424207 S237P621R	C 322	18	3.2	4668	14	AC014532	AC014532 Drosophi1
C 250	18	3.2	623	10	BV560748	BV560748 qf127F09.	C 323	18	3.2	5600	15	AF188485	AF188485 Arabidops
C 251	18	3.2	627	10	BV380471	BV380471 S245P638F	C 324	18	3.2	6319	15	SCYOR291W	Z75199 S.cerevisia
C 252	18	3.2	628	2	AY707372	AY707372 Thekabaladi	C 325	18	3.2	6444	15	RCPPRAS	Z32849 R.communis
C 253	18	3.2	628	2	AY707373	AY707373 An1solabi	C 326	18	3.2	6480	15	LP049498	LP049498 Legionella
C 254	18	3.2	687	6	AX404802	AX404802 Sequence	C 327	18	3.2	7722	13	DQ092436	DQ092436 Banana st
C 255	18	3.2	687	6	AX404804	AX404804 Sequence	C 328	18	3.2	10029	1	AE013449	AE013449 Methanosa
C 256	18	3.2	712	10	BV649644	BV649644 S216P6101	C 329	18	3.2	10127	1	AE010077	AE010077 Streptococ
C 257	18	3.2	713	10	BV582600	BV582600 GS91P6222	C 330	18	3.2	10129	1	AE006595	AE006595 Streptococ
C 258	18	3.2	745	10	BV583581	BV583581 GS91P6263	C 331	18	3.2	10771	1	AB011422	AB011422 Lepospiir
C 259	18	3.2	751	10	BV498166	BV498166 S217P6052	C 332	18	3.2	11275	1	AE015596	AE015596 Shewanell
C 260	18	3.2	767	10	BV574271	BV574271 GS91P6080	C 333	18	3.2	11964	6	AX458510	AX458510 Sequence
C 261	18	3.2	785	10	BV557183	BV557183 qj132F07.	C 334	18	3.2	13809	1	AE007857	AE007857 Clostridi
C 262	18	3.2	797	10	BV630442	BV630442 S217P6081	C 335	18	3.2	14863	11	AY339820	AY339820 Mx-lox ta
C 263	18	3.2	825	10	BV618443	BV618443 S217P6105	C 336	18	3.2	15048	9	EX465213	EX465213 Mouse DNA
C 264	18	3.2	836	10	BV016177	BV016177 S212P6454	C 337	18	3.2	22143	5	AC151464	AC151464 Xenopus t
C 265	18	3.2	892	10	BV467041	BV467041 GS91P6246	C 338	18	3.2	23103	8	AL3390235	AL3390235 Human DNA
C 266	18	3.2	1002	6	AR173235	AR173235 Sequence	C 339	18	3.2	27200	8	BX545851	BX545851 Human DNA
C 267	18	3.2	1002	6	AR254055	AR254055 Sequence	C 340	18	3.2	28799	2	CEV73F4A	CEV73F4A Caenorhab
C 268	18	3.2	1002	6	AR365260	AR365260 Sequence	C 341	18	3.2	30311	5	AB083364	AB083364 Oryzias 1
C 269	18	3.2	1002	6	AR360877	AR360877 Sequence	C 342	18	3.2	36760	2	CET05F1	CET05F1
C 270	18	3.2	1002	6	AX481412	AX481412 Sequence	C 343	18	3.2	38569	8	AC007793	AC007793 Homo sapi
C 271	18	3.2	1011	9	CT010381	CT010381 Mus muscu	C 344	18	3.2	40681	1	BA000003_6	BA000003_6 Continuati
C 272	18	3.2	1024	6	AX577888	AX577888 Sequence	C 345	18	3.2	40681	6	BD061520_6	BD061520_6 Continuati
C 273	18	3.2	1040	8	BC074856	BC074856 Homo sapi	C 346	18	3.2	40681	6	AR409405_6	AR409405_6 Continuati
C 274	18	3.2	1040	8	BC074857	BC074857 Homo sapi	C 347	18	3.2	41369	2	CER03C1	CER03C1 Caenorhabdi
C 275	18	3.2	1051	6	E11715	E11715 cDNA encodi	C 348	18	3.2	43387	15	ATK10A8	ATK10A8
C 276	18	3.2	1051	6	E12186	E12186 A novel 119	C 349	18	3.2	44088	2	CETC3C5	CETC3C5
C 277	18	3.2	1055	8	BC069342	BC069342 Homo sapi	C 350	18	3.2	44118	8	AC012386	AC012386
C 278	18	3.2	1154	6	MMU30244	MMU30244 Mus musculu	C 351	18	3.2	47518	14	AC020452	AC020452 Drosophi1
C 279	18	3.2	1188	6	AX953527	AX953527 Sequence	C 352	18	3.2	47635	14	AC090180	AC090180 Homo sapi
C 280	18	3.2	1262	9	AF403040	AF403040 Mus muscu	C 353	18	3.2	51385	15	AE014162	AE014162 Streptococ
C 281	18	3.2	1340	6	CO732656	CO732656 Sequence	C 354	18	3.2	55870	15	AC005819	AC005819 Arabidops
C 282	18	3.2	1542	15	AF042333	AF042333 Oryza sat	C 355	18	3.2	59461	14	AC011889	AC011889 Homo sapi
C 283	18	3.2	1542	15	AF042333	AF042333 Oryza sat	C 356	18	3.2	60211	14	AC068685	AC068685 Homo sapi
C 284	18	3.2	1896	15	HSU16797	HSU16797 Human LERK-	C 357	18	3.2	60834	14	AC087472	AC087472 Homo sapi
C 285	18	3.2	1953	8	AK117704	AK117704 Arabidops	C 358	18	3.2	61169	8	AP001433	AP001433
C 286	18	3.2	1953	8	HUMHTR	I41350 Sequence 3	C 359	18	3.2	64596	14	AC165620	AC165620 Bos tauru
C 287	18	3.2	1980	5	CR354279	CR354279 Gallus ga	C 360	18	3.2	66173	5	BX248103	BX248103 Zebrafish
C 288	18	3.2	2000	6	AX510197	AX510197 Sequence	C 361	18	3.2	66492	14	AC090761	AC090761 Homo sapi
C 289	18	3.2	2049	7	B32RGHSEQ	M91810 Bacterioph	C 362	18	3.2	67033	8	AL137008	AL137008 Human DNA
C 290	18	3.2	2145	15	BT001087	BT001087 Arabidops	C 363	18	3.2	67646	14	AC026641	AC026641 Drosophi1
C 291	18	3.2	2216	7	P29G17A	M144001087 Bacteri	C 364	18	3.2	68080	5	BX640591	BX640591 Zebrafish
C 292	18	3.2	2337	15	AX540655	AX540655 Sequence	C 365	18	3.2	70042	8	AP001424	AP001424
C 293	18	3.2	2337	15	AX515563	AX515563 Arabidops	C 366	18	3.2	72638	15	AB007645	AB007645 Arabidops
C 294	18	3.2	2397	15	AY057503	AY057503 Arabidops	C 367	18	3.2	75539	8	AC142336	AC142336 Pan trogl
C 295	18	3.2	2407	6	AR171285	AR171285 Sequence	C 368	18	3.2	76743	2	AC005473	AC005473 Drosophi1
C 296	18	3.2	2407	6	AR236740	AR236740 Sequence	C 369	18	3.2	78849	8	AC008407	AC008407 Homo sapi
C 297	18	3.2	2611	6	AX671060	AX671060 Sequence	C 370	18	3.2	79114	14	AC005475	AC005475 Drosophi1
C 298	18	3.2	2611	9	MMU16819	MMU16819 Mus musculu	C 371	18	3.2	81240	14	AC09862_3	AC09862_3 Continuati
C 299	18	3.2	2857	6	BD159997	BD159997 Primer fo	C 372	18	3.2	83233	15	AB022219	AB022219 Arabidops
C 300	18	3.2	2857	6	AX882904	AX882904 Sequence	C 373	18	3.2	85722	14	AC093210	AC093210 Homo sapi
C 301	18	3.2	2857	8	AK023487	AK023487 Homo sapi	C 374	18	3.2	86497	15	AP004525	AP004525 Lotus cor
C 302	18	3.2	2898	6	AX671058	AX671058 Sequence	C 375	18	3.2	86568	8	AC113613	AC113613 Homo sapi
C 303	18	3.2	2902	6	CO722763	CO722763 Sequence	C 376	18	3.2	87047	8	AC079231	AC079231
C 304	18	3.2	2902	6	CO875340	CO875340 Sequence	C 377	18	3.2	87210	15	AB011485	AB011485 Arabidops
C 305	18	3.2	2902	6	AX577963	AX577963 Sequence	C 378	18	3.2	88249	14	AC164482	AC164482 Bos tauru
C 306	18	3.2	2902	6	AX578102	AX578102 Sequence	C 379	18	3.2	90500	8	AL157889	AL157889 Human DNA
C 307	18	3.2	2902	8	HSU81262	HSU81262 Homo sapien	C 380	18	3.2	92250	9	AL928965	AL928965 Mouse DNA
C 308	18	3.2	2910	15	AK103230	AK103230 Oryza sat	C 381	18	3.2	94826	14	AC146828	AC146828 Carolli
C 309	18	3.2	3053	15	ZRO303361	ZRO303361 Zygosacch	C 382	18	3.2	94867	14	AC166811	AC166811 Bos tauru
C 310	18	3.2	3321	15	SOU23210	SOU23210 Debaryomyce	C 383	18	3.2	96163	14	AP007428	AP007428 Lotus cor



384	18	3.2	98852	9	AL935127	AL935127 Mouse DNA	C 457	18	3.2	140639	15	AC146571	AC146571 Medicago
385	18	3.2	99322	14	OSTG00040	AL733340 Oryza sat	C 458	18	3.2	141329	8	AC146383	AC146383 Pan trogl
386	18	3.2	100000	8	AP000157	AP000157 Homo sapi	C 459	18	3.2	142662	14	AC160241	AC160241 Medicago
387	18	3.2	100549	8	AL138776	AL138776 Human DNA	C 460	18	3.2	143223	8	AL162725	AL162725 Human DNA
388	18	3.2	101123	14	OSIG00054	AL733346 Oryza sat	C 461	18	3.2	143223	8	AC091997	AC091997 Homo sapi
389	18	3.2	101591	14	AP007567	AP007567 Lotus cor	C 462	18	3.2	143257	9	AC151848	AC151848 Mus muscu
390	18	3.2	102234	14	AC116116	AC116116 Mus muscu	C 463	18	3.2	143485	8	AC099678	AC099678 Homo sapi
391	18	3.2	103219	14	AC079745	AC079745 Homo sapi	C 464	18	3.2	143878	14	AL359974	AL359974 Medicago
392	18	3.2	103563	8	AC006979	AC006979 Homo sapi	C 465	18	3.2	143993	8	AC093607	AC093607 Homo sapi
393	18	3.2	103616	8	AL138689	AL138689 Human DNA	C 466	18	3.2	144048	9	AC154782	AC154782 Mus muscu
394	18	3.2	104894	15	AP006863	AP006863 Lotus cor	C 467	18	3.2	144250	14	CR354553	CR354553 Danio rer
395	18	3.2	106508	8	AC005102	AC005102 Homo sapi	C 468	18	3.2	144792	8	AL359649	AL359649 Human DNA
396	18	3.2	106954	8	AC104651	AC104651 Homo sapi	C 469	18	3.2	144793	8	AF202031	AF202031 Homo sapi
397	18	3.2	107066	14	AC138264	AC138264 Homo sapi	C 470	18	3.2	144828	8	AP001577	AP001577 Homo sapi
398	18	3.2	109355	8	AC004857	AC004857 Homo sapi	C 471	18	3.2	145190	8	AC156285	AC156285 Mus muscu
399	18	3.2	109465	8	AL158821	AL158821 Human DNA	C 472	18	3.2	145275	8	AF189745	AF189745 Homo sapi
400	18	3.2	110000	1	AP006878_02	Continuation (3 of	C 473	18	3.2	146198	8	AC040963	AC040963 Homo sapi
401	18	3.2	110000	1	AP008934_23	Continuation (24 o	C 474	18	3.2	146324	14	AC155858	AC155858 Bos tauru
402	18	3.2	110000	1	BA000003_5	Continuation (6 of	C 475	18	3.2	146436	9	AL831763	AL831763 Mouse DNA
403	18	3.2	110000	1	BA000034_05	Continuation (6 of	C 476	18	3.2	146684	9	AL159634	AL159634 Mus muscu
404	18	3.2	110000	1	BX908798_20	Continuation (21 o	C 477	18	3.2	147094	5	AL929543	AL929543 Oryza sat
405	18	3.2	110000	1	BX908798_21	Continuation (22 o	C 478	18	3.2	147102	15	AP005506	AP005506 Oryza sat
406	18	3.2	110000	1	CP000001_39	Continuation (40 o	C 479	18	3.2	147148	14	AP004763	AP004763 Homo sapi
407	18	3.2	110000	1	CP000003_13	Continuation (14 o	C 480	18	3.2	147202	8	AP005526	AP005526 Oryza sat
408	18	3.2	110000	1	CP000017_13	Continuation (14 o	C 481	18	3.2	147382	15	AP005526	AP005526 Oryza sat
409	18	3.2	110000	1	CP000056_13	Continuation (14 o	C 482	18	3.2	147536	8	AF285443	AF285443 Homo sapi
410	18	3.2	110000	6	BD061520_5	Continuation (6 of	C 483	18	3.2	147881	5	BX942831	BX942831 Zebrafish
411	18	3.2	110000	6	AB409405_5	Continuation (6 of	C 484	18	3.2	148011	15	AC134236	AC134236 Oryza sat
412	18	3.2	110000	6	AY958432_0	Continuation (5 of	C 485	18	3.2	148290	14	AC133470	AC133470 Homo sapi
413	18	3.2	110000	14	AC105643_4	Continuation (3 of	C 486	18	3.2	148579	8	AC092274	AC092274 Homo sapi
414	18	3.2	110000	14	AC109410_2	Continuation (10 o	C 487	18	3.2	148640	14	AC154165	AC154165 Medicago
415	18	3.2	110000	14	AC125548_0	Continuation (4 of	C 488	18	3.2	149062	14	AC160904	AC160904 Dasyple n
416	18	3.2	110000	14	AC125733_3	Continuation (26 o	C 489	18	3.2	149277	14	AL627207	AL627207 Homo sapi
417	18	3.2	110000	15	AP008214_025	Continuation (6 of	C 490	18	3.2	150140	8	AC112216	AC112216 Mus muscu
418	18	3.2	110000	15	AE017356_5	Continuation (14 o	C 491	18	3.2	150336	14	AC115043	AC115043 Mus muscu
419	18	3.2	110000	15	AP008207_039	Continuation (40 o	C 492	18	3.2	151923	14	AC164690	AC164690 Homo sapi
420	18	3.2	110000	15	AP008209_008	Continuation (9 of	C 493	18	3.2	152103	14	AC012130	AC012130 Mus muscu
421	18	3.2	110000	15	AP008210_341	Continuation (200	C 494	18	3.2	152489	9	AC139576	AC139576 Mus muscu
422	18	3.2	110000	15	AP008210_341	Continuation (10 o	C 495	18	3.2	152914	9	AC154674	AC154674 Mus muscu
423	18	3.2	110000	15	AP008210_009	Continuation (10 o	C 496	18	3.2	153472	8	AC011179	AC011179 Homo sapi
424	18	3.2	110250	14	AC134022	Continuation (10 o	C 497	18	3.2	154210	14	AC034114	AC034114 Homo sapi
425	18	3.2	111117	14	AL358932	Continuation (10 o	C 498	18	3.2	154618	14	AC094013	AC094013 Homo sapi
426	18	3.2	111244	5	BX640481	Continuation (10 o	C 499	18	3.2	155194	14	AC025231	AC025231 Homo sapi
427	18	3.2	111557	8	HS232N11	Continuation (10 o	C 500	18	3.2	155235	14	AC144679	AC144679 Homo sapi
428	18	3.2	111641	8	HS232N11	Continuation (10 o	C 501	18	3.2	155567	8	AC073492	AC073492 Homo sapi
429	18	3.2	112107	8	AL139320	Continuation (10 o	C 502	18	3.2	155567	8	AC073492	AC073492 Homo sapi
430	18	3.2	112513	14	AL139320	Continuation (10 o	C 503	18	3.2	155567	8	AC073492	AC073492 Homo sapi
431	18	3.2	115137	14	AF252831	Continuation (10 o	C 504	18	3.2	155567	8	AC073492	AC073492 Homo sapi
432	18	3.2	116818	14	AF252831	Continuation (10 o	C 505	18	3.2	155567	8	AC073492	AC073492 Homo sapi
433	18	3.2	117077	14	HS1662M14	Continuation (10 o	C 506	18	3.2	155987	14	CR956623	CR956623 Danio rer
434	18	3.2	117354	14	AC152424	Continuation (10 o	C 507	18	3.2	155987	14	CR956623	CR956623 Danio rer
435	18	3.2	117559	8	AC092279	Continuation (10 o	C 508	18	3.2	159991	9	AC131986	AC131986 Mus muscu
436	18	3.2	118489	8	AP000766	Continuation (10 o	C 509	18	3.2	160034	9	AC131986	AC131986 Mus muscu
437	18	3.2	118787	8	AP000766	Continuation (10 o	C 510	18	3.2	160390	14	AL445244	AL445244 Homo sapi
438	18	3.2	120194	15	AC135319	Continuation (10 o	C 511	18	3.2	160411	14	AC135935	AC135935 Homo sapi
439	18	3.2	120590	15	AC135319	Continuation (10 o	C 512	18	3.2	160748	8	AC021241	AC021241 Homo sapi
440	18	3.2	121469	15	AC137838	Continuation (10 o	C 513	18	3.2	160748	8	AC021241	AC021241 Homo sapi
441	18	3.2	121951	9	BX470145	Continuation (10 o	C 514	18	3.2	161738	14	AC110909	AC110909 Mus muscu
442	18	3.2	124152	9	AC147048	Continuation (10 o	C 515	18	3.2	161940	8	AC090116	AC090116 Homo sapi
443	18	3.2	126846	8	AL359375	Continuation (10 o	C 516	18	3.2	162004	8	AC090116	AC090116 Homo sapi
444	18	3.2	127766	8	AL359375	Continuation (10 o	C 517	18	3.2	162608	8	AC009478	AC009478 Homo sapi
445	18	3.2	128906	15	AP003810	Continuation (10 o	C 518	18	3.2	163353	8	AC069528	AC069528 Homo sapi
446	18	3.2	130431	9	AC140552	Continuation (10 o	C 519	18	3.2	163353	8	AC069528	AC069528 Homo sapi
447	18	3.2	130647	8	AL157385	Continuation (10 o	C 520	18	3.2	163353	8	AC069528	AC069528 Homo sapi
448	18	3.2	131707	5	BX247948	Continuation (10 o	C 521	18	3.2	163866	5	CNS07ED1	CNS07ED1 Homo sapi
449	18	3.2	132290	5	HS1147016	Continuation (10 o	C 522	18	3.2	163866	5	AL929590	AL929590 Homo sapi
450	18	3.2	133877	14	AC138786	Continuation (10 o	C 523	18	3.2	163907	14	BX248134	BX248134 Danio rer
451	18	3.2	135473	14	AC102705	Continuation (10 o	C 524	18	3.2	164055	14	AC130883	AC130883 Mus muscu
452	18	3.2	137127	14	AC113343	Continuation (10 o	C 525	18	3.2	164994	14	AC148183	AC148183 Macaca mu
453	18	3.2	137436	8	AL159986	Continuation (10 o	C 526	18	3.2	164994	14	AC148183	AC148183 Macaca mu
454	18	3.2	138209	8	HSJ444211	Continuation (10 o	C 527	18	3.2	165608	8	AC004492	AC004492 Homo sapi
455	18	3.2	140151	8	AC009804	Continuation (10 o	C 528	18	3.2	165720	8	AC025524	AC025524 Homo sapi
456	18	3.2	140523	15	AC147501	Continuation (10 o	C 529	18	3.2	165880	8	AL136372	AL136372 Human DNA



530	18	3.2	166118	14	AC151016	AC151016	Callithrix	c 603	18	3.2	179901	14	AC011006	AC011006	Homo sapi
531	18	3.2	166385	14	AC074340	AC074340	Homo sapi	c 604	18	3.2	180305	14	CT009681	CT009681	Pan trogl
532	18	3.2	166428	8	AC146879	AC146879	Otolemur	c 605	18	3.2	180348	14	AC120315	AC120315	Rattus no
533	18	3.2	166683	8	AP002980	AP002980	Homo sapi	c 606	18	3.2	180625	8	AL391478	AL391478	Human DNA
534	18	3.2	166759	8	AC007716	AC007716	Homo sapi	c 607	18	3.2	180713	8	AC149286	AC149286	Pan trogl
535	18	3.2	167107	2	AC0093104	AC0093104	Drosophila	c 608	18	3.2	180951	14	AC157665	AC157665	Mus muscu
536	18	3.2	167118	8	AC023385	AC023385	Homo sapi	c 609	18	3.2	181127	14	AC068203	AC068203	Homo sapi
537	18	3.2	167174	8	AC013492	AC013492	Homo sapi	c 610	18	3.2	181437	2	AC008194	AC008194	Drosophila
538	18	3.2	167440	14	AC130346	AC130346	Homo sapi	c 611	18	3.2	181555	9	AC113298	AC113298	Mus muscu
539	18	3.2	167574	14	AC011274	AC011274	Homo sapi	c 612	18	3.2	182155	8	AC104814	AC104814	Homo sapi
540	18	3.2	167791	14	AC120913	AC120913	Rattus no	c 613	18	3.2	182247	5	CR388163	CR388163	Zebrafish
541	18	3.2	167949	14	AC019075	AC019075	Homo sapi	c 614	18	3.2	182618	8	AC095349	AC095349	Homo sapi
542	18	3.2	168108	8	AC104119	AC104119	Homo sapi	c 615	18	3.2	182836	8	AC107029	AC107029	Homo sapi
543	18	3.2	168223	14	AC012042	AC012042	Homo sapi	c 616	18	3.2	182926	8	AC145899	AC145899	Pan trogl
544	18	3.2	168302	5	AL935294	AL935294	Zebrafish	c 617	18	3.2	183273	8	AC093898	AC093898	Homo sapi
545	18	3.2	168346	14	AC036227	AC036227	Homo sapi	c 618	18	3.2	183431	14	AC138788	AC138788	Sus scrof
546	18	3.2	168595	14	AC146354	AC146354	Macaca mu	c 619	18	3.2	183641	14	AC118666	AC118666	Rattus no
547	18	3.2	168673	5	BX470264	BX470264	Zebrafish	c 620	18	3.2	183707	9	AC124384	AC124384	Mus muscu
548	18	3.2	168800	14	AC009467	AC009467	Homo sapi	c 621	18	3.2	184299	14	AL935266	AL935266	Mus muscu
549	18	3.2	168835	8	AC105751	AC105751	Homo sapi	c 622	18	3.2	184648	14	AC017102	AC017102	Homo sapi
550	18	3.2	168873	14	BX537112	BX537112	Homo sapi	c 623	18	3.2	184718	8	AC018646	AC018646	Homo sapi
551	18	3.2	169540	8	AC009248	AC009248	Homo sapi	c 624	18	3.2	184920	14	AC160943	AC160943	Pan trogl
552	18	3.2	169566	8	AC021518	AC021518	Homo sapi	c 625	18	3.2	185084	4	AC147708	AC147708	Canis fam
553	18	3.2	170090	9	AC113593	AC113593	Mus muscu	c 626	18	3.2	185123	14	AC053524	AC053524	Homo sapi
554	18	3.2	170625	14	AC160931	AC160931	Mus muscu	c 627	18	3.2	185550	14	CR354564	CR354564	Danio rer
555	18	3.2	170691	8	AC025253	AC025253	Homo sapi	c 628	18	3.2	185830	14	AC146924	AC146924	Otolemur
556	18	3.2	170936	8	AC147028	AC147028	Pan trogl	c 629	18	3.2	185838	9	AC133177	AC133177	Mus muscu
557	18	3.2	171161	9	AC105980	AC105980	Mus muscu	c 630	18	3.2	186051	14	AC015683	AC015683	Homo sapi
558	18	3.2	171275	14	AC064825	AC064825	Homo sapi	c 631	18	3.2	186058	14	AC112245	AC112245	Homo sapi
559	18	3.2	171423	14	AC025664	AC025664	Homo sapi	c 632	18	3.2	186266	8	AL512782	AL512782	Human DNA
560	18	3.2	171437	8	AC121336	AC121336	Homo sapi	c 633	18	3.2	187045	14	AC073253	AC073253	Homo sapi
561	18	3.2	171474	8	AC130360	AC130360	Homo sapi	c 634	18	3.2	187064	8	AC011476	AC011476	Homo sapi
562	18	3.2	171480	8	AC016542	AC016542	Homo sapi	c 635	18	3.2	187380	8	AC023946	AC023946	Homo sapi
563	18	3.2	171541	8	AC011853	AC011853	Homo sapi	c 636	18	3.2	188048	14	AC141801	AC141801	Apis mell
564	18	3.2	171639	8	AC130365	AC130365	Homo sapi	c 637	18	3.2	188327	14	AC154980	AC154980	Bos tauru
565	18	3.2	171757	8	CNS01DSO	AL121857	Human chr	c 638	18	3.2	188386	9	AL671872	AL671872	Mouse DNA
566	18	3.2	172084	8	AC134683	AC134683	Homo sapi	c 639	18	3.2	188661	14	AC093705	AC093705	Papio anu
567	18	3.2	172485	5	BX005339	BX005339	Zebrafish	c 640	18	3.2	188800	14	AC015846	AC015846	Homo sapi
568	18	3.2	172517	9	AC130716	AC130716	Mus muscu	c 641	18	3.2	188884	8	AC130367	AC130367	Homo sapi
569	18	3.2	172560	8	AP252830	AP252830	Homo sapi	c 642	18	3.2	188978	14	AC148262	AC148262	Callithrix
570	18	3.2	172918	14	AC023366	AC023366	Homo sapi	c 643	18	3.2	189509	14	AC121051	AC121051	Rattus no
571	18	3.2	172918	8	AC008119	AC008119	Homo sapi	c 644	18	3.2	189570	14	AC019120	AC019120	Homo sapi
572	18	3.2	173255	8	AC130339	AC130339	Homo sapi	c 645	18	3.2	189616	14	AC119603	AC119603	Rattus no
573	18	3.2	173414	8	AC012535	AC012535	Homo sapi	c 646	18	3.2	189917	14	AC120606	AC120606	Rattus no
574	18	3.2	173926	14	MM454K24	AL160232	Mus muscu	c 647	18	3.2	189966	8	AC146082	AC146082	Pan trogl
575	18	3.2	174130	5	AL732628	AL732628	Zebrafish	c 648	18	3.2	190031	8	AC131269	AC131269	Homo sapi
576	18	3.2	174133	9	AL732628	AL732628	Mus muscu	c 649	18	3.2	190191	14	AC138784	AC138784	Sus scrof
577	18	3.2	174274	14	AC044905	AC044905	Homo sapi	c 650	18	3.2	190224	9	AC124500	AC124500	Mus muscu
578	18	3.2	174327	14	AC146773	AC146773	Didelphis	c 651	18	3.2	190432	15	OSJN00032	OSJN00032	Oryza sat
579	18	3.2	174415	9	AC129557	AC129557	Mus muscu	c 652	18	3.2	191093	9	AL671765	AL671765	Mouse DNA
580	18	3.2	174427	14	AC152201	AC152201	Bos tauru	c 653	18	3.2	191501	14	AL592113	AL592113	Homo sapi
581	18	3.2	174568	14	AC162263	AC162263	Bos tauru	c 654	18	3.2	191705	14	AC165414	AC165414	Mus muscu
582	18	3.2	174576	8	AC090525	AC090525	Homo sapi	c 655	18	3.2	191805	8	AC027670	AC027670	Homo sapi
583	18	3.2	175303	14	AC158887	AC158887	Bos tauru	c 656	18	3.2	191954	14	AC148260	AC148260	Callithrix
584	18	3.2	175775	14	AC026831	AC026831	Homo sapi	c 657	18	3.2	192663	9	AC134406	AC134406	Mus muscu
585	18	3.2	175157	14	AC013776	AC013776	Homo sapi	c 658	18	3.2	192811	14	AC044896	AC044896	Homo sapi
586	18	3.2	176416	9	AL805906	AL805906	Mouse DNA	c 659	18	3.2	192971	9	AC118012	AC118012	Mus muscu
587	18	3.2	176428	9	AC157094	AC157094	Mus muscu	c 660	18	3.2	193321	8	AC158673	AC158673	Mus muscu
588	18	3.2	176448	4	AC129886	AC129886	Atelestrix	c 661	18	3.2	193927	8	AC098852	AC098852	Homo sapi
589	18	3.2	176466	8	AL161733	AL161733	Human DNA	c 662	18	3.2	194158	8	AC021127	AC021127	Homo sapi
590	18	3.2	176593	14	AC087661	AC087661	Human DNA	c 663	18	3.2	194840	14	AC130489	AC130489	Homo sapi
591	18	3.2	176708	8	DQ145721	DQ145721	Homo sapi	c 664	18	3.2	195252	5	BX547935	BX547935	Zebrafish
592	18	3.2	177014	8	AC004063	AC004063	Homo sapi	c 665	18	3.2	195296	14	AC156652	AC156652	Bos tauru
593	18	3.2	177637	8	AC146037	AC146037	Pan trogl	c 666	18	3.2	195403	14	AC117174	AC117174	Rattus no
594	18	3.2	177756	8	AC034111	AC034111	Homo sapi	c 667	18	3.2	195526	8	AC116274	AC116274	Rattus no
595	18	3.2	178229	14	AC001061	AC001061	Homo sapi	c 668	18	3.2	195646	14	AC093709	AC093709	Pan trogl
596	18	3.2	178403	8	AC134395	AC134395	Homo sapi	c 669	18	3.2	195959	9	AC034143	AC034143	Homo sapi
597	18	3.2	178401	8	HS1115A15	AL096855	Human DNA	c 670	18	3.2	195968	8	AC125224	AC125224	Mus muscu
598	18	3.2	178573	8	AC079452	AC079452	Homo sapi	c 671	18	3.2	196004	8	AC079269	AC079269	Homo sapi
599	18	3.2	179312	9	AC104906	AC104906	Mus muscu	c 672	18	3.2	196013	9	AC114988	AC114988	Mus muscu
600	18	3.2	179321	9	AC101719	AC101719	Mus muscu	c 673	18	3.2	196331	9	AC154319	AC154319	Mus muscu
601	18	3.2	179574	14	AC055783	AC055783	Homo sapi	c 674	18	3.2	196383	14	AC113159	AC113159	Rattus no
602	18	3.2	179757	8	AC006960	AC006960	Homo sapi	c 675	18	3.2	197094	14	AC112061	AC112061	Rattus no



676	18	3.2	198254	14	AC016049	AC016049 Homo sapi	c 749	18	3.2	226128	14	AC136487	AC136487 Rattus no
677	18	3.2	198312	8	AL590422	Human DNA	750	18	3.2	226613	14	AC130127	AC130127 Rattus no
678	18	3.2	198736	5	AL929023	AL929023 Zebrafish	751	18	3.2	226833	2	AB003838	AB003838 Drosophila
679	18	3.2	199294	5	AL589652	Mus muscu	752	18	3.2	227158	14	AC162839	AC162839 Bos tauru
680	18	3.2	199381	9	AC157278	Mus muscu	753	18	3.2	227158	14	AC153822	AC153822 Mus muscu
681	18	3.2	199430	14	AC151034	AC151034 Gallitaxi	754	18	3.2	228657	14	AC112333	AC112333 Rattus no
682	18	3.2	199824	14	AC154815	AC154815 Mus muscu	755	18	3.2	228804	14	AC117318	AC117318 Rattus no
683	18	3.2	199906	14	AC021764	AC021764 Homo sapi	756	18	3.2	229037	14	AC164926	AC164926 Bulemur m
684	18	3.2	200087	8	AL354821	Human DNA	757	18	3.2	229478	14	AC151871	AC151871 Lemur cat
685	18	3.2	200476	8	AL845433	Human DNA	758	18	3.2	229563	9	AC024957	AC024957 Mus muscu
686	18	3.2	200985	8	AL121787	Human DNA	759	18	3.2	229623	14	AC103107	AC103107 Rattus no
687	18	3.2	201749	5	CR626878	CR626878 Zebrafish	760	18	3.2	229634	14	AC150010	AC150010 Gallitaxi
688	18	3.2	201934	5	AL645504	AL645504 Human DNA	761	18	3.2	230058	14	AC108229	AC108229 Rattus no
689	18	3.2	202327	14	AC158247	AC158247 Gallitaxi	762	18	3.2	231373	14	AC112543	AC112543 Rattus no
690	18	3.2	202356	5	AC145931	AC145931 Gallus ga	763	18	3.2	231373	14	AC151911	AC151911 Ornithoth
691	18	3.2	202838	9	AC113470	AC113470 Mus muscu	764	18	3.2	232060	14	AC154884	AC154884 Mus muscu
692	18	3.2	203266	9	AC140429	AC140429 Mus muscu	765	18	3.2	232066	14	AC133823	AC133823 Rattus no
693	18	3.2	203717	9	AC157658	AC157658 Mus muscu	766	18	3.2	232862	14	AC111682	AC111682 Rattus no
694	18	3.2	204083	14	AC120971	AC120971 Rattus no	767	18	3.2	233569	14	AC098273	AC098273 Rattus no
695	18	3.2	204491	9	AC138368	AC138368 Mus muscu	768	18	3.2	233754	14	AC134226	AC134226 Rattus no
696	18	3.2	204135	14	AC055744	AC055744 Homo sapi	769	18	3.2	233949	14	AC095312	AC095312 Rattus no
697	18	3.2	204142	14	AC159767	AC159767 Bos tauru	770	18	3.2	234602	9	AC102099	AC102099 Mus muscu
698	18	3.2	205592	14	AC150295	AC150295 Gallitaxi	771	18	3.2	234620	14	AC122606	AC122606 Rattus no
699	18	3.2	205651	14	AC106630	AC106630 Rattus no	772	18	3.2	235453	9	AC133910	AC133910
700	18	3.2	206074	9	AL831790	AL831790 Mouse DNA	773	18	3.2	235681	14	AC150045	AC150045 Bos tauru
701	18	3.2	206433	8	AC147978	AC147978 Pan trogl	774	18	3.2	236169	14	AC158076	AC158076 Bos tauru
702	18	3.2	207070	8	CT009632	CT009632 Mus muscu	775	18	3.2	236658	14	AC152441	AC152441 Bos tauru
703	18	3.2	208015	8	AC119424	AC119424 Homo sapi	776	18	3.2	237672	14	AC152441	AC152441 Bos tauru
704	18	3.2	208788	14	AC114152	AC114152 Rattus no	777	18	3.2	237007	9	AL627166	AL627166
705	18	3.2	209108	14	AC097897	AC097897 Rattus no	778	18	3.2	237498	5	BX927077	BX927077 Zebrafish
706	18	3.2	209120	14	AC095998	AC095998 Rattus no	779	18	3.2	239162	14	AC134768	AC134768 Rattus no
707	18	3.2	209531	14	AC133837	AC133837 Rattus no	780	18	3.2	239162	14	AC111965	AC111965 Rattus no
708	18	3.2	209731	8	AC145908	AC145908 Pan trogl	781	18	3.2	239591	14	AC134295	AC134295 Rattus no
709	18	3.2	210086	9	AC105256	AC105256 Mus muscu	782	18	3.2	240142	14	AC133305	AC133305 Rattus no
710	18	3.2	211123	14	AC160969	AC160969 Mus muscu	783	18	3.2	240234	14	AC135010	AC135010 Rattus no
711	18	3.2	211216	9	AC102350	AC102350 Mus muscu	784	18	3.2	240256	14	AC095388	AC095388 Rattus no
712	18	3.2	212470	14	AC162715	AC162715 Bos tauru	785	18	3.2	240594	14	AC137254	AC137254 Rattus no
713	18	3.2	212779	8	AC104031	AC104031 Homo sapi	786	18	3.2	240918	14	AC110658	AC110658 Rattus no
714	18	3.2	213113	8	AC124807	AC124807 Mus muscu	787	18	3.2	241031	14	AC146101	AC146101 Pan trogl
715	18	3.2	213806	8	AC147977	AC147977 Pan trogl	788	18	3.2	242054	14	AC166444	AC166444 Rattus no
716	18	3.2	214302	14	AC157602	AC157602 Mus muscu	789	18	3.2	242195	14	AC162977	AC162977 Bos tauru
717	18	3.2	214305	14	AC156145	AC156145 Bos tauru	790	18	3.2	242764	14	AC156297	AC156297 Rattus no
718	18	3.2	214532	9	AC159468	AC159468 Mus muscu	791	18	3.2	242993	14	AC153029	AC153029 Rattus no
719	18	3.2	214819	9	AC123948	AC123948 Mus muscu	792	18	3.2	244853	14	AC094949	AC094949 Rattus no
720	18	3.2	214906	14	AC162710	AC162710 Bos tauru	793	18	3.2	245258	14	AC121737	AC121737 Rattus no
721	18	3.2	215111	8	AC010255	AC010255 Homo sapi	794	18	3.2	245424	14	AC130069	AC130069 Rattus no
722	18	3.2	215175	9	AL604031	AL604031 Mouse DNA	795	18	3.2	245603	14	AC132997	AC132997 Rattus no
723	18	3.2	215792	14	AC136190	AC136190 Rattus no	796	18	3.2	246434	14	AC121486	AC121486 Rattus no
724	18	3.2	215891	5	AL928692	AL928692 Zebrafish	797	18	3.2	246939	14	AC135656	AC135656 Rattus no
725	18	3.2	216080	14	AC150049	AC150049 Gallus ga	798	18	3.2	248788	14	AC129747	AC129747 Rattus no
726	18	3.2	216493	14	AC013530	AC013530 Homo sapi	799	18	3.2	248980	14	AC164982	AC164982 Mus muscu
727	18	3.2	216735	14	AC107532	AC107532 Rattus no	800	18	3.2	249083	14	AC098753	AC098753 Rattus no
728	18	3.2	218071	9	AC123689	AC123689 Mus muscu	801	18	3.2	250537	14	AC112106	AC112106 Rattus no
729	18	3.2	218085	14	AC094952	AC094952 Rattus no	802	18	3.2	251270	14	AC111234	AC111234 Rattus no
730	18	3.2	218515	8	AC025765	AC025765 Homo sapi	803	18	3.2	252824	14	AC125827	AC125827 Rattus no
731	18	3.2	218657	9	AC110517	AC110517 Mus muscu	804	18	3.2	252839	14	AC095096	AC095096 Rattus no
732	18	3.2	218958	14	CR925753	CR925753 Dario rer	805	18	3.2	254912	14	AC095474	AC095474 Rattus no
733	18	3.2	219558	14	AC117028	AC117028 Rattus no	806	18	3.2	254912	14	AC123482	AC123482 Rattus no
734	18	3.2	220068	14	CR974571	CR974571 Mus muscu	807	18	3.2	255881	14	AC106961	AC106961 Rattus no
735	18	3.2	220169	14	AC148252	AC148252 Otolenur	808	18	3.2	258144	14	AC157164	AC157164 Bos tauru
736	18	3.2	220225	14	AC161954	AC161954 Bos tauru	809	18	3.2	258911	14	AC107548	AC107548 Rattus no
737	18	3.2	220621	5	CR628387	CR628387 Zebrafish	810	18	3.2	259875	14	AC115406	AC115406 Rattus no
738	18	3.2	220932	8	BS000125	BS000125 Pan trogl	811	18	3.2	260162	14	AC127763	AC127763 Rattus no
739	18	3.2	221608	14	AC135934	AC135934 Rattus no	812	18	3.2	260759	14	AC133325	AC133325 Rattus no
740	18	3.2	221649	14	AC137392	AC137392 Rattus no	813	18	3.2	261157	14	AC103330	AC103330 Rattus no
741	18	3.2	221712	4	CR956411	CR956411 Pig DNA s	814	18	3.2	262285	14	AC103016	AC103016 Rattus no
742	18	3.2	221961	9	AC161676	AC161676 Bos tauru	815	18	3.2	262285	14	CR354393	CR354393 Dario rer
743	18	3.2	222946	14	AC124568	AC124568 Mus muscu	816	18	3.2	264464	14	AC097851	AC097851 Rattus no
744	18	3.2	223009	14	BX942812	BX942812 Dario rer	817	18	3.2	264464	14	AC107410	AC107410 Bos tauru
745	18	3.2	223863	14	AC136532	AC136532 Rattus no	818	18	3.2	265486	14	AC156327	AC156327 Bos tauru
746	18	3.2	223955	14	AC163523	AC163523 Bos tauru	819	18	3.2	265875	14	AC162081	AC162081 Bos tauru
747	18	3.2	223958	14	AC127401	AC127401 Rattus no	820	18	3.2	266188	14	AC103296	AC103296 Rattus no
748	18	3.2	225542	14	AC094586	AC094586 Rattus no	821	18	3.2	266533	14	AC155068	AC155068 Bos tauru



822	18	3.2	267760	14	AC160669	AC160669 Bos tauru	895	17	3.0	591	10	BV328663	BV328663 S241P6114
823	18	3.2	272190	14	AC095925	AC095925 Rattus no	896	17	3.0	595	10	BV454469	BV454469 PRB-085P1
824	18	3.2	273445	14	AC157301	AC157301 Bos tauru	897	17	3.0	598	10	BV347420	BV347420 S230P6439
825	18	3.2	274220	14	AC149713	AC149713 Bos tauru	898	17	3.0	619	10	BV406052	BV406052 S229P6425
826	18	3.2	276008	14	AC112310	AC112310 Rattus no	899	17	3.0	622	10	BV437839	BV437839 S237P646R
827	18	3.2	276376	14	AC097979	AC097979 Rattus no	900	17	3.0	623	8	F283327850	
828	18	3.2	276477	14	AC158009	AC158009 Bos tauru	901	17	3.0	625	2	AY702691	AY702691 Serratosp
829	18	3.2	276713	14	AC097881	AC097881 Rattus no	902	17	3.0	629	10	BV273404	BV273404 S235P6412
830	18	3.2	277587	14	AC157344	AC157344 Bos tauru	903	17	3.0	631	6	AX401226	AX401226 Sequence
831	18	3.2	277772	14	AC155660	AC155660 Bos tauru	904	17	3.0	651	10	BV288812	BV288812 S232P6557
832	18	3.2	278712	14	AC158915	AC158915 Mus muscu	905	17	3.0	662	10	BV543833	BV543833 qov49H06.
833	18	3.2	280278	14	AL390201	AL390201 Homo sapi	906	17	3.0	667	10	BV642079	BV642079 S215P6097
834	18	3.2	283531	14	AC161152	AC161152 Bos tauru	907	17	3.0	669	10	BV543674	BV543674 qc192C07.
835	18	3.2	284749	14	AC113251	AC113251 Rattus no	908	17	3.0	672	10	BV069215	BV069215 S212P6336
836	18	3.2	286701	14	AC137276	AC137276 Rattus no	909	17	3.0	687	10	BV065094	BV065094 S212P6867
837	18	3.2	287560	1	AE017274	AE017274 Bacillus	910	17	3.0	698	1	AB195289	AB195289 Staphyloc
838	18	3.2	290061	14	AC161993	AC161993 Bos tauru	911	17	3.0	698	10	BV552279	BV552279 S221P6110
839	18	3.2	292235	14	AL499603	AL499603 Homo sapi	912	17	3.0	702	10	BV672358	BV672358 S217P6076
840	18	3.2	297969	2	AE003511	AE003511 Drosophi1	913	17	3.0	724	10	BV499128	BV499128 S222P6991
841	18	3.2	298978	14	AC152719	AC152719 Mus muscu	914	17	3.0	732	10	BV548913	BV548913 S215P6987
842	18	3.2	299640	14	AC164265	AC164265 Bos tauru	915	17	3.0	738	6	AX621928	AX621928 Sequence
843	18	3.2	301508	1	AE017292	AE017292 Leptospir1	916	17	3.0	739	10	BV534143	BV534143 G591P6220
844	18	3.2	302521	8	AP000014	AP000014 Homo sapi	917	17	3.0	741	6	AR108045	AR108045 Sequence
845	18	3.2	302521	8	AP000014	AP000014 Homo sapi	918	17	3.0	745	10	BV526271	BV526271 G591P6031
846	18	3.2	309677	14	AC128863	AC128863 Rattus no	919	17	3.0	756	10	BV489050	BV489050 S216P6126
847	18	3.2	317210	14	AC112476	AC112476 Rattus no	920	17	3.0	770	10	BV543147	BV543147 bmx83B11.
848	18	3.2	322833	14	AC111863	AC111863 Rattus no	921	17	3.0	788	10	BV594942	BV594942 S215P6163
849	18	3.2	323632	14	AC123432	AC123432 Rattus no	922	17	3.0	789	10	BV485023	BV485023 S215P6143
850	18	3.2	323991	14	AC098512	AC098512 Rattus no	923	17	3.0	795	10	BV518965	BV518965 G591P6909
851	18	3.2	323991	14	AC098512	AC098512 Rattus no	924	17	3.0	803	6	BD149980	BD149980 Primer fo
852	18	3.2	331618	14	AC162485	AC162485 Bos tauru	925	17	3.0	803	6	AX865918	AX865918 Sequence
853	18	3.2	333352	14	AC125577	AC125577 Rattus no	926	17	3.0	810	6	BV657946	BV657946 S217P6082
854	18	3.2	340000	8	AP001730	AP001730 Homo sapi	927	17	3.0	829	6	AR339149	AR339149 Sequence
855	18	3.2	342084	14	AC128752	AC128752 Rattus no	928	17	3.0	832	10	BV503933	BV503933 bow6OE04.
856	18	3.2	344458	14	AC131978	AC131978 Mus muscu	929	17	3.0	844	10	BV647780	BV647780 S215P6141
857	18	3.2	348128	1	CR378668	CR378668 Photobact	930	17	3.0	858	6	BD164473	BD164473 Novel pol
858	18	3.2	348479	14	AL445583	AL445583 Homo sapi	931	17	3.0	858	6	AX122356	AX122356 Sequence
859	17	3.0	125	6	AX934999	AX934999 Sequence	932	17	3.0	862	10	BV175274	BV175274 sqm78011
860	17	3.0	193	6	AR356217	AR356217 Sequence	933	17	3.0	862	10	BV508746	BV508746 qmw73C06.
861	17	3.0	193	6	AR356217	AR356217 Sequence	934	17	3.0	884	10	BV466411	BV466411 G591P6698
862	17	3.0	201	6	AX505342	AX505342 Sequence	935	17	3.0	886	6	AR447685	AR447685 Sequence
863	17	3.0	242	10	AB165308	AB165308 Bos tauru	936	17	3.0	907	10	BV467974	BV467974 G591P6010
864	17	3.0	271	10	G47168	G47168 Z15782.1 Ze	937	17	3.0	910	5	CR352876	CR352876 Gallus ga
865	17	3.0	273	10	G08527	G08527 human STS C	938	17	3.0	924	10	BV550212	BV550212 S215P6033
866	17	3.0	280	10	BV320434	BV320434 S236P6437	939	17	3.0	929	6	AX583740	AX583740 Cucumis s
867	17	3.0	296	10	G05086	G05086 human STS W	940	17	3.0	930	15	AF286650	AF286650 Cucumis s
868	17	3.0	324	10	BV095484	BV095484 RPAMMSBO0	941	17	3.0	941	8	HS4250935	HS4250935 Homo sapi
869	17	3.0	340	6	A50418	A50418 Sequence 73	942	17	3.0	940	15	AF286651	AF286651 Cucumis s
870	17	3.0	340	6	AR127547	AR127547 Sequence	943	17	3.0	940	15	AF286651	AF286651 Cucumis s
871	17	3.0	340	13	HPCNLJ331	L14601 Hepatitis C	944	17	3.0	951	6	AR396178	AR396178 Sequence
872	17	3.0	384	10	BV398754	BV398754 S243P613F	945	17	3.0	991	8	HS4250935	HS4250935 Homo sapi
873	17	3.0	430	6	CO675442	CO675442 Sequence	946	17	3.0	1030	15	AF367005	AF367005 Albizia b
874	17	3.0	451	4	AY509893	AY509893 Sus scrofa	947	17	3.0	1033	6	AR116021	AR116021 Sequence
875	17	3.0	474	6	AX351577	AX351577 Sequence	948	17	3.0	1074	6	AX497216	AX497216 Sequence
876	17	3.0	475	15	AY157815	AY157815 Arachis s	949	17	3.0	1087	15	BT006116	BT006116 Arabidops
877	17	3.0	486	10	G72888	G72888 MARC 3114-3	950	17	3.0	1098	15	AF522946	AF522946 Albizia s
878	17	3.0	526	10	BV392838	BV392838 S243P6107	951	17	3.0	1113	6	BD164581	BD164581 Novel pol
879	17	3.0	527	10	BV240969	BV240969 S234P6228	952	17	3.0	1113	6	AX122464	AX122464 Sequence
880	17	3.0	533	10	BV321847	BV321847 S236P6467	953	17	3.0	1122	2	AF216966	AF216966 Caenorhab
881	17	3.0	541	10	G58977	G58977 SHGC-106751	954	17	3.0	1145	9	BC086355	BC086355 Rattus no
882	17	3.0	549	10	BV292917	BV292917 S232P624F	955	17	3.0	1170	6	AR477697	AR477697 Sequence
883	17	3.0	552	6	AR129204	AR129204 Sequence	956	17	3.0	1170	6	AX066665	AX066665 Sequence
884	17	3.0	558	6	BD103157	BD103157 Human pro	957	17	3.0	1177	5	BX933465	BX933465 Gallus ga
885	17	3.0	558	6	AR534850	AR534850 Sequence	958	17	3.0	1181	6	AR578076	AR578076 Sequence
886	17	3.0	558	13	AF310723	AF310723 Homo sapi	959	17	3.0	1236	6	BD194483	BD194483 Vaccinia a
887	17	3.0	561	13	AY593733	AY593733 Player v1	960	17	3.0	1236	6	AR271293	AR271293 Sequence
888	17	3.0	562	10	BV252360	BV252360 S234P6307	961	17	3.0	1236	6	AR642466	AR642466 Sequence
889	17	3.0	563	10	BV041141	BV041141 S212P6052	962	17	3.0	1243	6	AX813919	AX813919 Sequence
890	17	3.0	566	10	BV214437	BV214437 S233P6156	963	17	3.0	1248	6	AX619886	AX619886 Sequence
891	17	3.0	573	10	BV387409	BV387409 S244P6306	964	17	3.0	1248	15	AX118984	AX118984 Arabidops
892	17	3.0	578	10	HS586F48	AL110020 H. sapiens	965	17	3.0	1271	6	AR004664	AR004664 Sequence
893	17	3.0	586	10	BV095488	BV095488 RPAMMSBO0	966	17	3.0	1271	6	BD175820	BD175820 Human vas
894	17	3.0	586	10	BV278755	BV278755 S232P6318	967	17	3.0	1320	6	AX618074	AX618074 Sequence



C 968	17	3.0	1331	15	AY077866	Phaseolus
C 969	17	3.0	1331	15	AY077867	Phaseolus
C 970	17	3.0	1331	15	AY077868	Phaseolus
C 971	17	3.0	1331	15	AY077869	Phaseolus
C 972	17	3.0	1331	15	AY077870	Phaseolus
C 973	17	3.0	1331	15	AY077871	Phaseolus
C 974	17	3.0	1331	15	AY077872	Phaseolus
C 975	17	3.0	1331	15	AY077873	Phaseolus
C 976	17	3.0	1331	15	AY077874	Phaseolus
C 977	17	3.0	1331	15	AY077875	Phaseolus
C 978	17	3.0	1331	15	AY077876	Phaseolus
C 979	17	3.0	1331	15	AY077877	Phaseolus
C 980	17	3.0	1331	15	AY077878	Phaseolus
C 981	17	3.0	1331	15	AY077879	Phaseolus
C 982	17	3.0	1331	15	AY077880	Phaseolus
C 983	17	3.0	1331	15	AY077881	Phaseolus
C 984	17	3.0	1364	6	AX566077	Sequence
C 985	17	3.0	1366	6	CQ981257	Sequence
C 986	17	3.0	1366	6	CQ981316	Sequence
C 987	17	3.0	1366	6	CS034755	Sequence
C 988	17	3.0	1366	6	CS043707	Sequence
C 989	17	3.0	1366	6	BC010549	Sequence
C 990	17	3.0	1366	6	AX374883	Sequence
C 991	17	3.0	1554	6	BC092650	Sequence
C 992	17	3.0	1555	15	AY088039	Sequence
C 993	17	3.0	1562	9	BC016117	Sequence
C 994	17	3.0	1602	2	AY052012	Sequence
C 995	17	3.0	1611	5	BX950829	Sequence
C 996	17	3.0	1634	6	BC011989	Sequence
C 997	17	3.0	1692	6	CQ725233	Sequence
C 998	17	3.0	1692	6	AB055329	Sequence
C 999	17	3.0	1850	9	BC006934	Sequence
C1000	17	3.0	1854	6	CQ872760	Sequence

ALIGNMENTS

RESULT 1						
LOCUS	BACCPABC	3244 bp	DNA	linear	BCT 26-APR-1993	
DEFINITION	B.anthraxis encapsulation protein genes (capA, capB, and capC), complete cds.					
ACCESSION	M24150	GI:142630				
VERSION	M24150.1	GI:142630				
KEYWORDS	encapsulation protein; membrane-associated protein.					
SOURCE	Bacillus anthracis					
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.					

REFERENCE	1 (bases 1 to 3244)
AUTHORS	Makino,S., Uchida,I., Terakado,N., Sasakawa,C. and Yoshikawa,M.
TITLE	Molecular characterization and protein analysis of the cap region, which is essential for encapsulation in Bacillus anthracis
JOURNAL	J. Bacteriol. 171 (2), 722-730 (1989)
PubMed	2536679
COMMENT	Original source text: B.anthraxis (strain TB702; isolate pCAP1) DNA.

Draht entry and computer-readable sequence for [1] kindly provided by I.Uchida, 01-MAY-1989.  
Location/Qualifiers

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/mol\_type="genomic DNA"  
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282..1475  
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CDS

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TIPNGHLVTISEEYLDYFKFEVBERKTYIVADNSRISEELFKPDYMEPDSILA  
LVAEALGIDEAEFRGLNAPDPGMRITRFADQSPAFVFGFPAAPDSLRITM  
ERYDDRGVSNLAPIVIMNCRPDRVDTRBOFARDLPIYKAEIVAIGETTAPISAE  
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1951..3186  
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NFERVPLEDKNTYQKADKNHLSAKEIYKAVAEAGFTVLANNNMTDYAGKTD  
TIKAFKEADLDYVAGENFQDVKNIVQNVNARVATLGFDAVACALATKEQPSLI  
SMNPDLVLEKQISKADPKKNADLVVNTWGEERYDNKPSRPAALAKWVADADII  
VGHFPHVLOSFDYKQGIIFYSJLNFQDMTSTKDSALVOYHLRNGTALIDVPL  
NIORSPKPVASALDKNRYRQLKDTSKGLAMSKODKLEIKLNHGVLEKMKREK  
QEHDKQEKQNVSEVTT"

CDS

ORIGIN 748 bp upstream of HindIII site.  
Query Match 100.0%; Score 560; DB 1; Length 3244;  
Best Local Similarity 100.0%; Pred. No. 1.5e-299;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	ACAACTGCTACATCTGCGCGAATGATATATTTGTTTACTGACGAGAGCAACCGATTAA	60
DB	471	ACAACTGCTACATCTGCGCGAATGATATATTTGTTTACTGACGAGAGCAACCGATTAA	530
QY	61	CGCGGTAAAGAGGTCCTAATATGCGTGAAGCAAGCGGAGTAAAGAGGCTGCTAT	120
DB	531	CGCGGTAAAGAGGTCCTAATATGCGTGAAGCAAGCGGAGTAAAGAGGCTGCTAT	590
QY	121	TTAGAGCAGAGCACTTATTGTGAATGTATGACAGTTCAACCGATTATCAATATATC	180
DB	591	TTAGAGCAGAGCACTTATTGTGAATGTATGACAGTTCAACCGATTATCAATATATC	650
QY	181	TTCCAAATTAATGATTCAGCAAAAGTTGAGTATTTAAATGTTTAAAGATCAT	240
DB	651	TTCCAAATTAATGATTCAGCAAAAGTTGAGTATTTAAATGTTTAAAGATCAT	710
QY	241	ATGATGTTAAGGACCTACACCTTGAAGCAAGTACGTAAGTTTCACTGCTACCATTC	300
DB	711	ATGATGTTAAGGACCTACACCTTGAAGCAAGTACGTAAGTTTCACTGCTACCATTC	770
QY	301	TATAATGACATTTAGTCACTATTGAAGTAATCTGATTAATTAAAGAGGTTGCA	360
DB	771	TATAATGACATTTAGTCACTATTGAAGTAATCTGATTAATTAAAGAGGTTGCA	830
QY	361	GAAGAGAAATACAAAGATGATTTGCGATTAATCTGAAATTTCAAGAAATTTCTTA	420
DB	831	GAAGAGAAATACAAAGATGATTTGCGATTAATCTGAAATTTCAAGAAATTTCTTA	890
QY	421	CGAAATTTGATATACATGCTCTCCCAATATATGATGCTGTTGCGGTACAGAG	480
DB	891	CGAAATTTGATATACATGCTCTCCCAATATATGATGCTGTTGCGGTACAGAG	950
QY	481	GCTCTTGGAATGATGAGAAACAGCATTCGTGTATGTGAATGCTCATCCGATCCA	540
DB	951	GCTCTTGGAATGATGAGAAACAGCATTCGTGTATGTGAATGCTCATCCGATCCA	1010
QY	541	GGAGCAATGAGAAATTAACG	560



db	1011	GGAGCATGAGATTACACG	1030	
RESULT 2				
AB011191/c	94829 bp	DNA	circular BCT 14-JUN-2002	
LOCUS	AB011191	Bacillus anthracis str. A2012	plasmid pXO2, complete sequence.	
DEFINITION	AB011191	Bacillus anthracis str. A2012	plasmid pXO2, complete sequence.	
ACCESSION	AB011191	Bacillus anthracis str. A2012	plasmid pXO2, complete sequence.	
VERSION	AB011191.1	GI:20520280		
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS	Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L., Holtzapfle, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D., Keim, P. and Fraser, C.M.			
TITLE	Comparative genome sequencing for discovery of novel polymorphisms in Bacillus anthracis			
JOURNAL	Science	296 (5575)	2028-2033 (2002)	
PUBMED	12004073			
REFERENCE	2 (bases 1 to 94829)			
AUTHORS	Read, T.D., Salzberg, S.L., Pop, M., Shumway, M., Umayam, L., Jiang, L., Holtzapfle, E., Busch, J.D., Smith, K.L., Schupp, J.M., Solomon, D., Keim, P. and Fraser, C.M.			
TITLE	Direct Submission			
JOURNAL	Submitted (09-MAY-2002)	The Institute for Genomic Research, 9712		
FEATURES				
Source	1..94829			
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	EYKSEIASVYTKSEKGRPRVTRKPIBENYQEHQRIQREYKTTSPVKPLPMITTDV			
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	/complement(1151..1438)			
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	ENRYIKQNNVTKYRASDNTYVSENVPBPGVSSVYKREYIHPRLQNDVDL			
	KESMKRYVLENKTLRELKKSKSDPYREBYLAFSQALAKKEIKEMDESSAMKOL			
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	KGRRNRLKTYLTKKQVVDIVAPNTDDIGDNPFSHVKAIAIYINSEGDVSKCTALLD			
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	IYQTYNFGNRYVHMLAANNKTHSIQTDADYSLTVVAPAGNRNGTITGYQOPAVAA			
	NGYRYINGNIFFAEMVKQYLSFDGAGTSGQIPGSGETPRKQADBYLAKYNGPYWG			
	KGSSQSGPDCSLTWYAKYTAGITIPISATQYDPTFVYVPPKQAPQDLVFPRTYGS			
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EKMEBGQDDVSLKKEVKDLKOSVMTKQOMVLIILAMELIAQSGSNLSLEKLB  
EKSEIASVYKSEKGPRTYKREPIENYQHQRIQREYKTSFYKKPLPMITDDV  
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IAQNYAQQVYVFKQKEWQTLTPASDYQLEIVGVKSGYPLPSNKIIEFGIPNHQDLK  
DPKGIYAGTSTGAFILIDPFSTGTSFSGFIPTGMAKSKTLKQLEBGLVAKDC  
FIRGPDKARDYVTVQOOGGKILDSGVDSSEVECTMINPLEVPATKITVYKAVDEK  
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Best Local Similarity 100.0%; Pred. No. 1,le-299;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 ACAACTGGTACATCTCCCGGGAATGATATATGGTTACTGACGAGACCAACCGATTAAAG 60  
DB 5603 ACAACTGGTACATCTCCCGGGAATGATATATGGTTACTGACGAGACCAACCGATTAAAG 56544  
QY 61 CGCCGTAAGAAGGTCTAATATCGGTGAGCAACGAGGTGTTAAAGAGCTCTGAT 120  
DB 56543 CGCCGTAAGAAGGTCTAATATCGGTGAGCAACGAGGTGTTAAAGAGCTCTGAT 56484  
QY 121 TTAGAAGCAGAAAGCACTTATTTGGATGTATGGCAGTTCAACCGATTATCAAAATTATC 180  
DB 56483 TTAGAAGCAGAAAGCACTTATTTGGATGTATGGCAGTTCAACCGATTATCAAAATTATC 56424  
QY 181 TTCGAAATTAATATGATTCACGAAATGTTGAGAGTATGTTAAAGTTTGAAGATATCAT 240  
DB 56423 TTCGAAATTAATATGATTCACGAAATGTTGAGAGTATGTTAAAGTTTGAAGATATCAT 56364  
QY 241 ATGAGATGTAAGGACCTTACCTGACGAAAGTACGAAAGCTTCACTGCTACATTCACA 300  
DB 56364 ATGAGATGTAAGGACCTTACCTGACGAAAGTACGAAAGCTTCACTGCTACATTCACA 56304  
QY 301 TATAATGACATTTAGTACTATTTGAAAGTGAATCTTGATTAACCTTTAAAGAGGTTGCA 360  
DB 56303 TATAATGACATTTAGTACTATTTGAAAGTGAATCTTGATTAACCTTTAAAGAGGTTGCA 56244  
QY 361 GAAGAGAAATACAAATATGTTGGGGAATTTCTAGAAATTCAGAAATTCCTTA 420  
DB 56243 GAAGAGAAATACAAATATGTTGGGGAATTTCTAGAAATTCAGAAATTCCTTA 56184  
QY 421 CGAAATTTGATTACATGCTTCCAGATTAATGATCGCTTGCTTAGCGGTAGCAGAG 480  
DB 56183 CGAAATTTGATTACATGCTTCCAGATTAATGATCGCTTGCTTAGCGGTAGCAGAG 56124  
QY 481 GCTCTTGGATTGATGAGAAACAGCATTCGCTGTATGTAATGCTCATCCGATTCGA 540  
DB 56123 GCTCTTGGATTGATGAGAAACAGCATTCGCTGTATGTAATGCTCATCCGATTCGA 56064  
QY 541 GGAGCAATGAGAAATTACAGC 560  
DB 56063 GGAGCAATGAGAAATTACAGC 56044

RESULT 4  
AF188935/c 96231 bp DNA circular BCT 01-OCT-2003  
LOCUS AF188935  
DEFINITION Bacillus anthracis plasmid pX02, complete sequence.  
ACCESSION AF188935  
VERSION AF188935.1 GI:6470151  
KEYWORDS  
SOURCE Bacillus anthracis  
ORGANISM Bacillus anthracis  
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus  
cereus group.  
REFERENCE 1 (bases 1 to 96231)

AUTHORS  
Okimaka,R.T., Cloud,K., Hampton,O., Hill,K.K., Keim,P., Lanke,G.,  
Kumano,S., Manter,D., Martinez,Y., Svensson,R., Tatum,L.R.,  
Brown,A.E. and Jackson,P.J.  
TITLE  
JOURNAL  
Direct Submission  
Submitted (01-NOV-1999) Bioscience Division, Los Alamos National  
Laboratory, M888, Los Alamos, NM 87545, USA  
location/Qualifiers  
FEATURES  
source  
1..96231  
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SGSVLSLEKLEQVKSRIASVTKSKSGKPRVTKRPIENVQEHORIOREVTTSF  
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EKMEKGQDVSLKKEVKDLKQSVNTMKQMDVLIKLMEILIAQSGSNLSLEKLEQ  
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KERSMKTVLENKILNRELKKSQDFPBERYLAISQALKEIEKKEBDSNAKQI  
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EKKTI"



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complement (3449..4057)  
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/evidence=not\_experimental  
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MAIRGGSGSTGPNWGISGRTAVKRLPPEWRQAMVEQBCAAGVBLVPYVAILIM  
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GGRYINGNPFYAEVYKQYLSIPDAGSTGQILPGSETFEKMMDEVLKNGNYYWG  
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PRGIYLGOTSGAFLDPFSTGTRTSFGSFLPGKAGAGSLTLKQLEBGLADCF  
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NHYDLEDFYKYSNLKLBAGATPQRHDLBAITQYEDMITYYGDMFNHTTKANE  
NBQIVPFDIGISKIDKSVFRCQLFTALTILWSALNKGOMKTLREKNUSEIDVY  
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WEKRLKELAFPIVYVGNKTELEIKNVDMKRYGGRQFNILQNMKAKEVKILFRLQNM  
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KKNRPAISSTDSKPKNGMKDIFKQQLGDVYTPYTIEMLTQOKDIPKREYIVYKI  
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Query Match 100.0%; Score 560; DB 1; Length 96231;  
Best Local Similarity 100.0%; Pred. No. 1.1e-299;  
Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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61 CGCGTAAAGAGTCTATATCGGAGCAACGAGGGTAGTTAAAGGGCGTCGAT 120  
57033 CGCGTAAAGAGTCTATATCGGAGCAACGAGGGTAGTTAAAGGGCGTCGAT 56974  
121 TTGAAGCAGACGACTTATTTGATGATGATGAGGACGTTCAACCGATTATCAATTATC 180  
56973 TTGAAGCAGACGACTTATTTGATGATGATGAGGACGTTCAACCGATTATCAATTATC 56914  
181 TTCCAAATTAATTAATGATTCAGACGAATGTTGAGAGTATGTTAAATGTTTGAAGATCAT 240  
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301 TATTAATGACATTTAAGTCACTATTTGAAGAGTAATCTTGATTAATTAAAGAGTTGCA 360  
56793 TATTAATGACATTTAAGTCACTATTTGAAGAGTAATCTTGATTAATTAAAGAGTTGCA 56734



QY 361 GAAGAGAAATACAAAGATGTTGCGGTAATTTCTAGATTTGAGAAATCTTA 420  
DB 56733 GAAGAGAAATACAAAGATGTTGCGGTAATTTCTAGAAATTTGAGAAATCTTA 56674  
QY 421 CGAAATTTGATTAACATGCTCTCCAGATTAATGATCGCTTGTAGCCGATGACAG 480  
DB 56673 CGAAATTTGATTAACATGCTCTCCAGATTAATGATCGCTTGTAGCCGATGACAG 56614  
QY 481 GCTCTGGGATTTGATGAGAAACAGCATTCGGTGTATGTAATGCTCATCCGATCCA 540  
DB 56613 GCTCTGGGATTTGATGAGAAACAGCATTCGGTGTATGTAATGCTCATCCGATCCA 56554  
QY 541 GGAGCAATGAGATTAACAG 560  
DB 56553 GGAGCAATGAGATTAACAG 56534

RESULT 5  
AX743806 32 bp DNA linear PAT 14-MAY-2003  
LOCUS AX743806  
DEFINITION Sequence 3 from Patent EP1304387.  
ACCESSION AX743806  
VERSION AX743806.1 GI:30722558  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
TITLE Detection of Bacillus anthracis  
JOURNAL Patent: BP 1304387-A 23-APR-2003;  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
FEATURES  
source 1..32  
Location/Qualifiers  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:32630"  
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ORIGIN  
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Best Local Similarity 100.0%; Pred.No.9.2e-06;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 53 CGATTAGCCCGCTAAAGAAAGTCTTAATATC 84  
DB 1 CGATTAGCCCGCTAAAGAAAGTCTTAATATC 32

RESULT 6  
AX743807 30 bp DNA linear PAT 14-MAY-2003  
LOCUS AX743807  
DEFINITION Sequence 4 from Patent EP1304387.  
ACCESSION AX743807  
VERSION AX743807.1 GI:30722559  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
TITLE Detection of Bacillus anthracis  
JOURNAL Patent: BP 1304387-A 23-APR-2003;  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
FEATURES  
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Location/Qualifiers  
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ORIGIN

Query Match 5.4%; Score 30; DB 6; Length 30;  
Best Local Similarity 100.0%; Pred.No.0.00012;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 86 GTGAGCAACGACGAGTGTAAAGAGCTG 115  
DB 1 GTGAGCAACGACGAGTGTAAAGAGCTG 30

RESULT 7  
BA000028\_02  
WPCOMMENT  
Sequence split into 37 fragments LOCUS BA000028 Accession BA000028  
Fragment Name Begin End  
BA000028\_00 1 110000  
BA000028\_01 100001 210000  
BA000028\_02 200001 310000  
BA000028\_03 300001 410000  
BA000028\_04 400001 510000  
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BA000028\_33 3300001 3410000  
BA000028\_34 3400001 3510000  
BA000028\_35 3500001 3610000  
BA000028\_36 3600001 3630528  
Continuation (3 of 37) of BA000028 from base 200001 (BA000028 Oceanobacillus thelyensis)

Query Match 5.2%; Score 29; DB 1; Length 110000;  
Best Local Similarity 100.0%; Pred.No.0.00021;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 217 ATTGTAATGTTTGAAGATCATATGGA 245  
DB 21157 ATTGTAATGTTTGAAGATCATATGGA 21185

RESULT 8  
AX743817 26 bp DNA linear PAT 14-MAY-2003  
LOCUS AX743817  
DEFINITION Sequence 14 from Patent EP1304387.  
ACCESSION AX743817  
VERSION AX743817.1 GI:30722569  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Bell,C.A., Uhl,J.R. and Cockerill,F.R.  
TITLE Detection of Bacillus anthracis  
JOURNAL Patent: BP 1304387-A 23-APR-2003;  
Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education  
and Research (US)  
FEATURES  
source 1..26  
Location/Qualifiers  
/organism="synthetic construct"  
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/note="Oligonucleotide"

ORIGIN



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REFERENCE      1
AUTHORS        Bell,C.A., Unl,J.R. and Cockerill,F.R.
TITLE          Detection of Bacillus anthracis
JOURNAL        Patent: EP 1304387-A 14-23-APR-2003;
                Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education
                and Research (US)
FEATURES
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                /db_xref="taxon:32630"
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Query Match    4.6%; Score 26; DB 6; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             87 TGAGCAAGCAGGAGTATTAAAGAG 112
Db             1 TGAGCAAGCAGGAGTATTAAAGAG 26

RESULT 9
AX743816       25 bp      DNA      linear      PAT 14-MAY-2003
LOCUS          AX743816
DEFINITION     Sequence 13 from Patent EP1304387.
ACCESSION      AX743816
VERSION        AX743816.1 GI:30722568
KEYWORDS
SOURCE         synthetic construct
ORGANISM       other sequences; artificial sequences.
REFERENCE      1
AUTHORS        Bell,C.A., Unl,J.R. and Cockerill,F.R.
TITLE          Detection of Bacillus anthracis
JOURNAL        Patent: BP 1304387-A 13-23-APR-2003;
                Roche Diagnostics GmbH (DE) ; Mayo Foundation for Medical Education
                and Research (US)
FEATURES
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                /note="Oligonucleotide"
ORIGIN
Query Match    4.5%; Score 25; DB 6; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.073;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             61 CGCCGTAAGAGGTCTCAATATCG 85
Db             1 CGCCGTAAGAGGTCTCAATATCG 25

RESULT 10
AL445984       181419 bp   DNA      linear      PRI 18-MAY-2005
LOCUS          AL445984
DEFINITION     Human DNA sequence from clone RP11-360A9 on chromosome 13 Contains
                a novel gene, complete sequence.
ACCESSION      AL445984
VERSION        AL445984.6 GI:11545107
KEYWORDS       HTG; MTND5.
SOURCE         Homo sapiens (human)
ORGANISM       Homo sapiens
                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                Homiidae; Homo.
REFERENCE      1 (bases 1 to 181419)
AUTHORS        Kay,M.
TITLE          Direct Submission
JOURNAL        Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,

```

```

COMMENT
Cambridgehire, CB10 1SA, UK. E-mail enquiries: vega@sanger.ac.uk
Clone requests: clonerequest@sanger.ac.uk
On Dec 4, 2000 this sequence version replaced gi:111414669.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
Chromosome 13, constructed by the Sanger Centre Chromosome 13
Mapping Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr13
RP11-360A9 is from the library RPCI-11.2 constructed by the group
of Pieter de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: PBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vega@sanger.ac.uk
-----
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest,
except on the rare occasion of the clone being a YAC.
Location/Qualifiers
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/locus_tag="RP11-360A9.1-002"
/note="match: ESTs: AW664858"
7754..7759
/locus_tag="RP11-360A9.1-001"
7777
/locus_tag="RP11-360A9.1-001"
50263
/note="Clone_right_end: RP11-478H12"
80606
/note="Clone_left_end: RP11-27D9"
117391..117491
/note="sequence from overlapping clone AL157763 Assembly
confirmed by restriction digest"
181419
/note="Clone_right_end: RP11-360A9"

ORIGIN
Query Match    4.3%; Score 24; DB 8; Length 181419;
Best Local Similarity 100.0%; Pred. No. 0.12;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy             268 GAAGTAGCTGAAGCTTCACTGCT 291
Db             17994 GAAGTAGCTGAAGCTTCACTGCT 18017

```



RESULT 11  
AY022390 284 bp DNA linear PLN 07-FEB-2001  
LOCUS Oryza sativa microsatellite MRC4715 containing (AAT)X28, closest to  
DEFINITION marker C454, genomic sequence.  
ACCESSION AY022390  
VERSION AY022390.1 GI:12705606  
KEYWORDS  
SOURCE  
ORGANISM  
Oryza sativa  
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
Ehharididae; Oryzaceae; Oryza.  
REFERENCE  
AUTHORS 1 (bases 1 to 284)  
TITLE Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.  
JOURNAL Simple sequence repeats from Monsanto rice genomic sequences  
REFERENCE 2 (bases 1 to 284)  
AUTHORS Tao, N., Barbazuk, W.B., Liu, J., Wu, K. and Barry, G.F.  
JOURNAL Direct Submission  
TITLE Submitted (10-JAN-2001) Genomics, Monsanto, 800 North Lindbergh  
Blvd., Creve Coeur, MO 63167, USA  
COMMENT Rice Genome Sequencing project. Please see  
http://www.rice-research.org for more information. The sequence  
data were produced primarily in the laboratories of Dr. Leroy Hood  
at the University of Washington in Seattle.  
Location/Qualifiers  
source 1..284  
/organism="Oryza sativa"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:4530"  
1..284  
/note="microsatellite MRC4715"  
/rpt\_type=tandem  
/rpt\_unit="aat"  
repeat\_region  
ORIGIN  
Query Match 4.1%; Score 23; DB 15; Length 284;  
Best Local Similarity 100.0%; Pred. No. 0.77;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 350 AAGAGTTCAGAGAGAGAAAT 372  
DB 63 AAGAGTTCAGAGAGAGAAAT 85  
RESULT 12  
AC096951/c 102599 bp DNA linear PRI 19-JAN-2002  
LOCUS AC096951  
DEFINITION Homo sapiens chromosome 1 clone RP4-739M21, complete sequence.  
ACCESSION AC096951 AL356872  
VERSION AC096951.2 GI:18250000  
KEYWORDS HTG.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
REFERENCE 1 (bases 1 to 102599)  
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.  
JOURNAL Direct Submission  
TITLE 2 (bases 1 to 102599)  
AUTHORS Kaul, R.K., Olson, M.V., Raymond, C., Clendenning, J. and Haugen, E.D.  
JOURNAL Direct Submission  
TITLE Submitted (03-OCT-2001) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
REFERENCE 3 (bases 1 to 102599)  
AUTHORS Kaul, R.K., Olson, M.V., Zhou, Y., James, R.A., Rouse, G., Wu, Z.,  
Saenphimmachak, C., Phelps, K.A., Raymond, C. and Haugen, E.D.  
JOURNAL Direct Submission  
TITLE Direct Submission

## JOURNAL COMMENT

Submitted (19-JAN-2002) Genome Center, University of Washington,  
Box 352145, Seattle, WA 98195, USA  
On Jan 19, 2002 this sequence version replaced gi:15887335.  
----- Genome Center  
Center: University of Washington Genome Center  
Center Code: UWGC  
Web site: http://www.genome.washington.edu  
Contact: uwgchc@u.washington.edu  
Drafting Center: SC

## ----- Project Information

Center Project name: chr-1  
Center clone name: RP4-739M21 (sc0561)

## ----- Summary Statistics

Sequencing vector: plasmid; 108752; 58% of reads  
Chemistry: Dye-terminator ET; 80% of reads  
Chemistry: Dye-terminator Big Dye; 20% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 102531 bases at least Q40  
Consensus quality: 102599 bases at least Q30  
Insert size: 102633; sum-of-contigs  
Quality coverage: 7.2x in Q20 bases; sum-of-contigs

## ----- Overlapping Sequences:

5': Mapping in progress  
3': RP11-64N3 (UWGC:sc0365) AC069315

## ----- Sequence Quality Assessment:

This entry has been annotated with sequence quality  
estimates computed by the Phrap assembly program.  
All manually edited bases have been reduced to quality zero.  
Quality levels above 40 are expected to have less than  
1 error in 10,000 bp.  
Base-by-base quality values are not generally visible from the  
GenBank flat file format but are available as part  
of this entry's ASN.1 file.

This sequence was finished as follows unless otherwise noted:  
all regions were either double-stranded or sequenced with an  
alternate chemistry or covered by high quality data (i.e., Phred  
quality >= 30); an attempt was made to resolve all sequencing  
problems, such as compressions and repeats; all regions were  
covered by at least one plasmid subclone or more than one M13  
subclone; and the assembly was confirmed by restriction digest.

## ----- Sequence Validation:

This sequence has been validated by Multiple Complete Digest  
fingerprinting. Comparison of the experimentally derived digest  
fragments with sequence-predicted fragments is given below.  
The electronically-digested sequence consists of both insert and  
vector, in order to accurately represent the entire circular BAC.  
Small fragments below a variable cutoff (approximately 400-800 bp)  
are not resolved in the fingerprint and hence do not appear  
in the table. There are no significant remaining discrepancies  
between the experimental and predicted values. Uniquely ordered  
fragments are separated by dashed lines.

## ECORI

## HindIII

## BglII

SeqDerMap	FingerPrint	SeqDerMap	FingerPrint	SeqDerMap	FingerPrint
3846	3897	2412	2451	12466	12322
2184	2250	449	<800	5671	5724
8065	8115	512	<800	5184	5284
486	<800	2814	2844	3205	3220
106	<800	1247	1219	504	<800



6439	6455	4695	4699	4885
5470	5344	3373	3378	4108
2776	2784	5941	5970	1404
5376	5344	1865	1877	2717
7684	7662	4794	4699	6776
2503	2511	2023	2015	9360
3577	3605	271	<800	34
5721	5716	2450	2451	19063
210	<800	2036	2015	1360
2249	2250	281	<800	4617
1400	1393	5674	5637	745
13	<800	522	<800	320
722	720	8161	8151	3595
7183	7083	705	<800	10457
4287	4320	706	<800	508
1919	1914	4757	4699	210
1779	1766	579	<800	538
3125	3149	2656	2697	3850
3316	3325	28	<800	2000
3784	3729	393	<800	38
5079	4942	2480	2451	2383
4494	4482	1618	1588	5641
1696	1665	289	<800	1006
3137	3149	924	929	4365
942	935	252	<800	509
1716	1766	4757	4699	998
180	<800	352	<800	
2245	2250	7081	7062	
876	873	1872	1877	
1801	1766	981	986	
5287	5344	594	<800	
6928	7083	4117	4041	
		5361	5224	
		1888	1877	
		592	<800	
		540	<800	
		1893	1877	

FEATURES	Location/Qualifiers
source	1..102599
	/organism="Homo sapiens"
	/mol_type="genomic DNA"
	/db_xref="taxon:9606"
	/chromosome="1"
	/clone_lib="RP4-739M21"
	/clone_lib="RPC1 human PAC library 4"
	1..4
misc_feature	/note="Single subclone region"
misc_feature	102596..102599
	/note="Single subclone region"
ORIGIN	
Query Match	4.1%; Score 23; DB 8; Length 102599;
Best Local Similarity	100.0%; Pred. No. 0.46;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	209 TTGGAGTGATTTGAATGTTT 231
Db	14988 TTGGAGTGATTTGAATGTTT 14966
RESULT 13	
AP008218_250/c	
WPCOMMENT	
Sequence split into 276 fragments LOCUS AP008218 Accession AP008218	
Fragment Name	Begin End
AP008218_000	1 110000
AP008218_001	100001 210000
AP008218_002	200001 310000
AP008218_003	300001 410000
AP008218_004	400001 510000
AP008218_005	500001 610000
AP008218_006	600001 710000
AP008218_007	700001 810000
AP008218_008	800001 910000
AP008218_009	900001 1010000
AP008218_010	1000001 1110000
AP008218_011	1100001 1210000
AP008218_012	1200001 1310000
AP008218_013	1300001 1410000
AP008218_014	1400001 1510000
AP008218_015	1500001 1610000
AP008218_016	1600001 1710000
AP008218_017	1700001 1810000
AP008218_018	1800001 1910000
AP008218_019	1900001 2010000
AP008218_020	2000001 2110000
AP008218_021	2100001 2210000
AP008218_022	2200001 2310000
AP008218_023	2300001 2410000
AP008218_024	2400001 2510000
AP008218_025	2500001 2610000
AP008218_026	2600001 2710000
AP008218_027	2700001 2810000



AP008218\_028 2800001 2910000  
AP008218\_029 2800001 3010000  
AP008218\_030 3000001 3110000  
AP008218\_031 3100001 3210000  
AP008218\_032 3200001 3310000  
AP008218\_033 3300001 3410000  
AP008218\_034 3400001 3510000  
AP008218\_035 3500001 3610000  
AP008218\_036 3600001 3710000  
AP008218\_037 3700001 3810000  
AP008218\_038 3800001 3910000  
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```

AP008218_174 17400001 17510000
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AP008218_186 18600001 18710000
AP008218_187 18700001 18810000
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AP008218_189 18900001 19010000
AP008218_190 19000001 19110000
AP008218_191 19100001 19210000
AP008218_192 19200001 19310000
AP008218_193 19300001 19410000
AP008218_194 19400001 19510000
AP008218_195 19500001 19610000
AP008218_196 19600001 19710000

```

```

Query Match 4.1%; Score 23; DB 15; Length 110000;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 350 AAGAGTTGCAGAGAGAGAAAT 372
Db 67878 AAGAGTTGCAGAGAGAGAAAT 67856

```

```

RESULT 14
CNS07YQ4 121563 bp DNA linear PLN 21-NOV-2003
LOCUS Oryza sativa chromosome 12, . BAC OJ1306_H03 of library Monsanto
DEFINITION from chromosome 12 of cultivar Nipponbare of ssp. japonica of Oryza
sativa (rice), complete sequence.
AL713904.3 GI:20513132
HTG.

```

```

ACCESSION Oryza sativa (japonica cultivar-group)
VERSION Oryza sativa (japonica cultivar-group)
KEYWORDS Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

ORGANISM Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE Erihartoideae; Oryzaceae; Oryza.
1 (bases 1 to 121563)
Choisme,N., Orjeda,G., Cattojico,L., Demange,N., Wincker,P.,

```

```

AUTHORS Segurens,B., Pelletier,B., Scarpell,C., Salanoubat,M.,
Weissenbach,J., and Queletier,F.
Oryza sativa chromosome 12 sequencing
Unpublished
2 (bases 1 to 121563)
Genoscope.

```

```

TITLE Direct Submission
JOURNAL Submitted (20-NOV-2003) Genoscope - Centre National de Sequencage :
REFERENCE BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
AUTHORS - Web : www.genoscope.cns.fr)
JOURNAL On May 8, 2002 this sequence version replaced gi:20160268.

```

```

COMMENT Center: Genoscope / Centre National de Sequencage
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----
The following sequence is oriented from the T7 to the SP6 end. The
nucleotide sequence of this BAC clone was generated by combining
Monsanto and Genoscope sequencing data.
Upstream BAC (overlapping the T7 end) : OSUNBa0056D07 (AC=AL928754)
Downstream BAC (overlapping the SP6 end) : OSUNBa0001B02
(AC=AL7131743) ----- Finishing boundaries
FINISHED SEGMENT STARTS AT BASE 1
FINISHED SEGMENT ENDS AT BASE 121563

```

```

FEATURES
Source Location/Qualifiers
1. 121563
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:39947"
/chromosome="12"
/clone="OJ1306_H03"
/clone_1lb="Monsanto"

```

```

ORIGIN
Query Match 4.1%; Score 23; DB 15; Length 121563;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 350 AAGAGTTGCAGAGAGAGAAAT 372
Db 63601 AAGAGTTGCAGAGAGAGAAAT 63623

```

```

RESULT 15
CNS08CBR 146686 bp DNA linear PLN 21-NOV-2003
LOCUS Oryza sativa chromosome 12, . BAC OSUNBa0056D07 of library OSUNBa
DEFINITION from chromosome 12 of cultivar Nipponbare of ssp. japonica of Oryza
sativa (rice), complete sequence.
AL928754.2 GI:23897123
HTG.

```

```

ACCESSION Oryza sativa (japonica cultivar-group)
VERSION Oryza sativa (japonica cultivar-group)
KEYWORDS Bukarjota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

```

```

SOURCE Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
REFERENCE Erihartoideae; Oryzaceae; Oryza.
1 (bases 1 to 146686)
Choisme,N., Orjeda,G., Cattojico,L., Demange,N., Wincker,P.,

```

```

AUTHORS Segurens,B., Pelletier,B., Scarpell,C., Salanoubat,M.,
Weissenbach,J., and Queletier,F.
Oryza sativa chromosome 12 sequencing
Unpublished
2 (bases 1 to 146686)
Genoscope.

```

```

REFERENCE Direct Submission
JOURNAL Submitted (20-NOV-2003) Genoscope - Centre National de Sequencage :
AUTHORS BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
JOURNAL - Web : www.genoscope.cns.fr)

```

```

COMMENT On Oct 12, 2002 this sequence version replaced gi:23094372.
Center: Genoscope / Centre National de Sequencage
Web site: http://www.genoscope.cns.fr/
Contact: SeqRef@genoscope.cns.fr
-----

```

```

The following sequence is oriented from the T7 to the SP6 end.
Upstream BAC (overlapping the T7 end) : OSUNBa0010M16 (AC=AL811797)
Downstream BAC (overlapping the SP6 end) : OJ1306_H03 (AC=AL713904)
----- Finishing boundaries
FINISHED SEGMENT STARTS AT BASE 95026
FINISHED SEGMENT ENDS AT BASE 144326

```

```

FEATURES
Source Location/Qualifiers
1. 146686
/organism="Oryza sativa (japonica cultivar-group)"
/mol_type="genomic DNA"
/cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:39947"
/chromosome="12"
/clone="OSUNBa0056D07"
/clone_1lb="OSUNBa"

```

ORIGIN



Query Match 4.1%; Score 23; DB 15; Length 146686;  
 Best Local Similarity 100.0%; Pred. No. 0.45; Indels 0; Gaps 0;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 350 AAGAGTTGCAGAGAGAGAAAT 372  
 |||||  
 Db 39290 AAGAGTTGCAGAGAGAGAAAT 39312

RESULT 16  
 AC069315  
 LOCUS AC069315  
 DEFINITION Homo sapiens chromosome 1 clone RP11-64N3, WORKING DRAFT SEQUENCE,  
 25 unordered pieces.  
 AC069315  
 VERSION AC069315.2 GI:8979963  
 KEYWORDS HTG; HTGS PHASE1; HTGS\_DRAFT.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Bunkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 1 (bases 1 to 152394)  
 Waterston,R.H.  
 The sequence of Homo sapiens clone  
 2 (bases 1 to 152394)  
 Waterston,R.H.  
 Direct Submission  
 Submitted (26-MAY-2000) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 On Jul 8, 2000 this sequence version replaced gi:8099082.

COMMENT  
 ----- Genome Center -----  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: <http://genome.wustl.edu/gsc/index.shtml>  
 Project Information -----  
 Center project name: H.NH0064N03  
 ----- Summary Statistics -----  
 Sequencing vector: MJ3; 100%  
 Chemistry: Dye-terminator ET; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 142192 bases at least Q40  
 Consensus quality: 145231 bases at least Q30  
 Consensus quality: 146710 bases at least Q20  
 Insert size: 158000; agarose-fp  
 Insert size: 149994; sum-of-Contigs  
 Quality coverage: 3.84 in Q20 bases; sum-of-Contigs  
 Quality coverage: 4.11 in Q20 bases; sum-of-Contigs  
 ----- NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 25 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of 'N', but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.  
 \* 1 1957: contig of 1957 bp in length  
 \* 1958 2057: gap of unknown length  
 \* 2058 4549: contig of 2492 bp in length  
 \* 4550 4649: gap of unknown length  
 \* 4650 6847: contig of 2198 bp in length  
 \* 6848 6947: gap of unknown length  
 \* 6948 9685: contig of 2738 bp in length  
 \* 9686 13846: gap of unknown length  
 \* 13847 13946: contig of 4061 bp in length  
 \* 13947 17429: gap of unknown length  
 \* 17429 17429: contig of 3483 bp in length

17430 17529: gap of unknown length  
 \* 17530 20686: contig of 3157 bp in length  
 \* 20687 20786: gap of unknown length  
 \* 20787 23153: contig of 2367 bp in length  
 \* 23154 23253: gap of unknown length  
 \* 23254 26778: contig of 3525 bp in length  
 \* 26779 26878: gap of unknown length  
 \* 26879 30575: contig of 3697 bp in length  
 \* 30576 30676: gap of unknown length  
 \* 30677 34743: contig of 4068 bp in length  
 \* 34744 34843: gap of unknown length  
 \* 34844 38654: contig of 3811 bp in length  
 \* 38655 38754: gap of unknown length  
 \* 38755 42676: contig of 3922 bp in length  
 \* 42677 42776: gap of unknown length  
 \* 42777 45544: contig of 3768 bp in length  
 \* 45545 46644: gap of unknown length  
 \* 46645 51531: contig of 4887 bp in length  
 \* 51532 51632: gap of unknown length  
 \* 51633 57546: contig of 5915 bp in length  
 \* 57547 57647: gap of unknown length  
 \* 57648 62201: contig of 4555 bp in length  
 \* 62202 62301: gap of unknown length  
 \* 62302 68854: contig of 6553 bp in length  
 \* 68855 68954: gap of unknown length  
 \* 68955 75633: contig of 6679 bp in length  
 \* 75634 75733: gap of unknown length  
 \* 75734 83467: contig of 7734 bp in length  
 \* 83468 83567: gap of unknown length  
 \* 83568 94159: contig of 10592 bp in length  
 \* 94160 94259: gap of unknown length  
 \* 94260 107976: contig of 13717 bp in length  
 \* 107977 108076: gap of unknown length  
 \* 108077 120546: contig of 12470 bp in length  
 \* 120547 120646: gap of unknown length  
 \* 120647 135897: contig of 15250 bp in length  
 \* 135897 152394: gap of unknown length  
 \* 152394 152394: contig of 16398 bp in length.

FEATURES  
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 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9606"  
 /chromosome="1"  
 /clone="RP11-64N3"  
 1..1957  
 /note="assembly\_name:Contig7"  
 1958..2057  
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 2058..4549  
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 4550..4649  
 /estimated\_length=unknown  
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 4650..6847  
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 6848..6947  
 /estimated\_length=unknown  
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 6948..9685  
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 9686..9785  
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 gap  
 9786..13846  
 /note="assembly\_name:Contig11"  
 13847..13946  
 /estimated\_length=unknown  
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 13947..17429  
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 17430..17529  
 /estimated\_length=unknown  
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 17530..20686  
 /note="assembly\_name:Contig13"  
 20687..20786  
 /estimated\_length=unknown



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gap 23154..23253  
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misc\_feature 23254..26778  
/note="assembly\_name:Contig15"  
gap 26779..26878  
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/note="assembly\_name:Contig16"  
gap 30576..30675  
/estimated\_length=unknown  
misc\_feature 30676..34743  
/note="assembly\_name:Contig17"  
gap 34744..34843  
/estimated\_length=unknown  
misc\_feature 34844..38654  
/note="assembly\_name:Contig18"  
gap 38655..38754  
/estimated\_length=unknown  
misc\_feature 38755..42676  
/note="assembly\_name:Contig19  
clone\_end:T7  
vector\_side:right"  
gap 42677..42776  
/estimated\_length=unknown  
misc\_feature 42777..46544  
/note="assembly\_name:Contig20"  
gap 46545..46644  
/estimated\_length=unknown  
misc\_feature 46645..51531  
/note="assembly\_name:Contig21"  
gap 51532..51631  
/estimated\_length=unknown  
misc\_feature 51632..57546  
/note="assembly\_name:Contig22"  
gap 57547..57646  
/estimated\_length=unknown  
misc\_feature 57647..62201  
/note="assembly\_name:Contig23"  
gap 62202..62301  
/estimated\_length=unknown  
misc\_feature 62302..66854  
/note="assembly\_name:Contig24"  
gap 66855..66954  
/estimated\_length=unknown  
misc\_feature 66955..75633  
/note="assembly\_name:Contig25"  
gap 75634..75733  
/estimated\_length=unknown  
misc\_feature 75734..83467  
/note="assembly\_name:Contig26"  
gap 83468..83567  
/estimated\_length=unknown  
misc\_feature 83568..94159  
/note="assembly\_name:Contig27"  
gap 94160..94259  
/estimated\_length=unknown  
misc\_feature 94260..107976  
/note="assembly\_name:Contig28"  
gap 107977..108076  
/estimated\_length=unknown  
misc\_feature 108077..120546  
/note="assembly\_name:Contig29"  
gap 120547..120646

Query Match 4.1%; Score 23; DB 14; Length 152394;  
Best Local Similarity 100.0%; Pred. No. 0.45; Indels 0; Gaps 0;  
Matches 23; Conservative 0; Mismatches 0;  
OY 209 TTGAGTGATGTGAATGTTTA 231  
DB 48137 TTGAGTGATGTGAATGTTTA 48159

RESULT 17  
LOCUS AY029472  
DEFINITION Homo sapiens smad-interacting protein-1 gene, partial cds.  
ACCESSION AY029472  
VERSION AY029472.1 GI:14717818  
KEYWORDS  
SOURCE  
ORGANISM  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL PUBMED  
REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
FEATURES  
SOURCE  
1.126080  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="2"  
/map="between KXNU and ACVR2"  
join(125..499,3015..3156,71825..72082,76984..77055,  
96827..97015,97721..97935,100544..100652,101581..103550,  
105259..105439,111823..112400)  
/product="smad-interacting protein-1"  
join(3084..3156,71825..72082,76984..77055,96827..97015,  
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111823..112400)  
/codon\_start=1  
/product="smad-interacting protein-1"  
/protein\_id="AAKS2081.1"  
/db\_xref="GI:14717819"  
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HIADGIANPLDQETSPVPHNESPVSQALLPREBEDERREGVHPHNNELI  
LQASVGPSEEMKEDVDPMGEATIGTAINNQTGANNCTSDPEYFAKRLBERDGA  
VSI EYLGQSDTAIIYPAPELSRGTPEANQENBDLPQTPDAQAQLLTQPCDR  
GYRLTSLKSHIKTRHKNEENFSCPLSTYFAVRIQLEHMYTHKGTQDQHLTQG  
AGNRKCTECGKAFFYKHLKELRLHSEKRYECPCCKRFSHSGSYSHISKKC  
IGLISVNGRRNNIKTGSSPNSVSSPTNSAIIQLNKLNGKPLMSBQGLKIKT  
BPLDNDYKVLAMTHGSGTSPNMGGLGATSPISGVPSAQSPHQLGVAEAPLGF  
PTMNSNLSEYQKYLQIVDNTVSRQKDKCAEISLKGKYMKPCQSPREQGVSPNI  
PVGILPVSHNKAITSIIYTLLEKNBAKACLOSUTDSRQISNITKELRTIDIV  
TDKLNENHIISTPFCQCKESFPQPIPLHQBRYICRNNEIKAVLQHENIVPK  
AGVFNKALLISVSLEKMTSPINPYKDMVLAAYVAMNEPNSDELKLSIAG  
LPOEFVWMEFEQRKYQVSNRSRPSLERSKPLAPSNPTKDSLPRSYKPDIST  
SPSIAELHNSVTNCDPPLRLTKPSHFNITKPVKRLDSRNTSPPLNLSSTSKNS  
SSYTPNSFSSEELQAEPLDLSLPRKMKPEPSIATNKTQASSISLDHNSVSSENS  
DEPLNLTFTKESPSNNSNLDNKSNTNYPVSNPPSAKPIYALPQSAFPPTAPPPQ  
TSIPGLRPYFGLDQWSFLPHMATYTPGAATPVDMDQRRYQKQOGQLDCAQDY  
MSGLDWTQSDCLSRKKIKRTSGMYACOLQKTSQKSSLLNKKYKHTGKRPQOQ  
ICKKAPFKHHLIEHRLHSGEKPYQCDKGRKFSHSGSYSHISCKEAEER  
EALREAREREGHLEPTELMMNRAVLOSITFGQSDSEERSMPDQSGSEKHEKEGD  
GYGLKRDQDDEBEFEBSSEKNSMDTDPETIRDEEETGHDHMDSSSDGKMETKSD  
HEEDNMEDMG"

ORIGIN  
Query Match 3.8%; Score 21; DB 8; Length 126080;  
Best Local Similarity 100.0%; Pred. No. 5.9; Indels 0; Gaps 0;  
Matches 21; Conservative 0; Mismatches 0;



QY 173 AAATTATCTCCAAATATAA 193  
 Db 77904 AAATTATCTCCAAATATAA 77924

RESULT 18  
 AC009951/c

LOCUS AC009951 159791 bp DNA linear PRI 16-APR-2005  
 DEFINITION Homo sapiens BAC clone RP11-107B5 from 2, complete sequence.  
 AC009951  
 AC009951.10 GI:18093069  
 HTG.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
 Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 159791)  
 AUTHORS Scott, K., Maupin, R. and Reitz, L.  
 TITLE The sequence of Homo sapiens BAC clone RP11-107B5  
 JOURNAL Unpublished (2001)  
 REFERENCE 2 (bases 1 to 159791)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (08-SEP-1999) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 3 (bases 1 to 159791)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (19-APR-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 4 (bases 1 to 159791)  
 AUTHORS Waterston, R.H.  
 TITLE Direct Submission  
 JOURNAL Submitted (20-APR-2001) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 REFERENCE 5 (bases 1 to 159791)  
 AUTHORS Waterston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 REFERENCE 6 (bases 1 to 159791)  
 AUTHORS Waterston, R.  
 TITLE Direct Submission  
 JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington  
 University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
 REFERENCE 7 (bases 1 to 159791)  
 AUTHORS Wilson, R.K.  
 TITLE Direct Submission  
 JOURNAL Submitted (16-APR-2005) Genome Sequencing Center, Washington  
 University School of Medicine, 4444 Forest Park Parkway, St. Louis,  
 MO 63108, USA  
 COMMENT On Jan 9, 2002 this sequence version replaced gi:11677121.  
 ----- Genome Center  
 Center: Washington University Genome Sequencing Center  
 Center code: WUGSC  
 Web site: http://genome.wustl.edu  
 Contact: submissions@wustl.edu  
 ----- Summary Statistics  
 -----  
 Center project name: H\_NH0107B05

## NOTICE:

This sequence was finished as follows unless otherwise noted:  
 all regions were double stranded, sequenced with an alternate  
 chemistry, or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by sequence  
 from more than one subclone; and the assembly was confirmed by

## restriction digest.

## MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. Mes Warren,  
 Department of Genetics, Washington University, St. Louis MO. For  
 additional information about the map position of this sequence, see  
<http://genome.wustl.edu>

## SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male  
 donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E.,  
 Teleno, M., Cataneese, J.J. and de Jong, P.J. (1998) An improved  
 approach for construction of bacterial artificial chromosome  
 libraries. Genomics 51:1-8. The clone may be obtained either from  
 Research Genetics, Inc. (<http://www.reagen.com>) or Pieter de Jong  
 and coworkers at <http://www.chori.org>  
 VECTOR: pBACe3.6

## NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-294G19, 200 bp overlap;  
 the clone sequenced to the left is RP11-9509. Actual start of this  
 clone is at base position 1 of RP11-107B5; actual end is at base  
 position 159597 of RP11-107B5.

There are polymorphic base differences in the overlap between  
 RP11-107B5 and RP11-294G19.

The sequence from base position 113472 to 113490 is derived from  
 PCR product of RP11-107B5 clone DNA.

FEATURES  
 source

1. 159791

/organism="Homo sapiens"

/mol\_type="genomic DNA"

/db\_xref="taxon:9606"

/chromosome="2"

/clone="RP11-107B5"

/clone\_1lb="RPCI-11"

/complement(17826..113343)

/gene="ZFX1B"

complement(join(17826..17897,22799..23056,110308..110449,

112969..113343))

/gene="ZFX1B"

complement(join(417826..17897,22799..23056,

110308..110380))

/gene="ZFX1B"

/note="Homo sapiens zinc finger homeobox 1b (ZFX1B),

mRNA; H\_NH0107B05.1

This gene was based on gi(7662183)

Continues as H\_NH0095009.1"

/codon\_start=1

/product="unknown"

/protein\_id="AA093269.1"

/db\_xref="GI:62702346"

/translation="MKQPTMDGRCRCRRKQANPRKNVNYDNYTGSTDESDKL

HIAVDGCIANPLDQETSPASVPHNHSFHVQALPREEBDEIRGGVHPHNNKI

LOASVDGPEKMKEDYDTGPRATIGTAINNGT"

86900..87177

/note="CpG\_island (%GC=61.5, o/e=0.74, #CpGs=20)"

108920..110841

/note="CpG\_island (%GC=67.6, o/e=0.89, #CpGs=185)"

117200..117732

/note="CpG\_island (%GC=72.0, o/e=0.89, #CpGs=54)"

## ORIGIN

Query Match 3.8%; Score 21; DB 8; Length 159791;  
 Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 173 AAATTATCTCCAAATATAA 193  
 Db 16977 AAATTATCTCCAAATATAA 16957



RESULT 19  
AC016526/c  
LOCUS  
DEFINITION Homo sapiens chromosome 14 clone RP11-361H10 map 14q24.3, complete  
ACCESSION AC016526  
VERSION AC016526.6  
KEYWORDS GI:11596984  
SOURCE HTG.  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS 1 (bases 1 to 179984)  
Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Kaur,A., Madan,A., Neebitt,R., Traicoff,R. and Hood,L.  
Sequencing of human chromosome 14q24.3 region  
Unpublished  
2 (bases 1 to 179984)  
Rowen,L., Madan,A., Qin,S., Abbasi,N., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., James,R., Kaur,A., Madan,A., Owen,M.P., Ratcliffe,A., Shaffer,T. and Hood,L.  
Direct Submission  
Submitted (02-DEC-1999) Multimegabase Sequencing Center, University of Washington, PO BOX 357730, Seattle, WA 98195, USA  
3 (bases 1 to 179984)  
Rowen,L., Madan,A., Qin,S., Baradarani,L., Birditt,B., Bloom,S., Dors,M., Dickhoff,R., Fleetwood,P., Harrison,G., Neebitt,R., Traicoff,R. and Hood,L.  
Direct Submission  
Submitted (07-DEC-2000) Multimegabase Sequencing Center, Institute for Systems Biology, 4225 Roosevelt Way NE, Suite 200, Seattle, WA 98105, USA  
COMMENT  
On Dec 7, 2000 this sequence version replaced gi:996932.  
----- Genome Center  
Center: Multimegabase Sequencing Center  
Center code: UMWSC  
Web site: http://chroma.mbt.washington.edu/msg\_www  
Contact: leetowen@systemsbiology.org  
----- Summary Statistics  
Sequencing vector: pUC18; 108752  
Chemistry: Dye-terminator Big Dye; 90% of reads  
Chemistry: Dye-primer Big Dye; 10% of reads  
Assembly program: Phrap; version 0.990399  
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/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="14"  
/map="14q24.3"  
/clone.lib="RP11-361H10"  
/note="This clone overlaps RP11-98L12 AC008015 and RP11-516J2 AC016543"  
1..49256  
/note="Overlap with RP11-98L12 AC008015"  
join(37152..37813,49451..49515,54631..54807,56334..56413,59411..59478,60776..60830,63552..63637,78666..78760,84479..84639)  
/note="hypothetical protein; intron-exon boundaries defined in relation to AK00696, mRNA for hypothetical protein FLJ20689"  
1..codon.start=1  
/product="FLJ20689"  
/protein\_id="AAG38637.1"  
/db\_xref="GI:11596985"  
/translation="MDLVHDLASALBOTSHONKLGELMEALSPROQRRLKRRG RKRSDPFLAHEHCYSEASSESIDETKCRVAPYTNFSDDDTVAKRHPLANA IVKSKHSHMSDSFTENAPCRPLRRRRKRVKRVSEVAASIQQLKVDWSEYEGCRF

KSARKLRSWKENTPWTSSGCHGCEAENRTFLKTGRKEMCEETDEOKSGDENM  
SECRETSSVCSSSDTGLFTNDGRQGDQSDMPYEGECVPGFTVNNLPKYAPDHCS  
VERMDSGLDKRSDSTPLPSRPARQGYHTLRNLRGAARCLRGRRRLVCKETSINT  
LGTERRISHITSDPROKKNKALADPHIISCAHEPNPLSLTSLDITADASHRCS  
AHCAQANVHWGPPCSDIRKRRKPVATSLSPSAVHMVAVEPTTASQAPKSPSS  
EMLVTSAAEKATDTATTAFFKMPQKSPGVS"  
42660..42760  
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45270..45360  
/note="low quality data"  
126890..127090  
/note="low quality data"  
139530..139550  
/note="low quality data"  
139850..140410  
/note="Several finishing reads from only one clone in this region"  
139855..139910  
/note="low quality data"  
149450..149550  
/note="low quality data"  
153560..153620  
/note="low quality data"  
156420..156470  
/note="low quality data"  
176340..176580  
/note="single clone coverage"  
177257..179984  
/note="overlap with RP11-516J2 AC016543"  
ORIGIN  
misc\_feature  
Query Match 3.8%; Score 21; DB 8; Length 179984;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 172 CAATTATCTTCCAAATPAA 192  
Db 68425 CAATTATCTTCCAAATPAA 68405  
RESULT 20  
AC150721  
LOCUS  
DEFINITION Callithrix jacchus clone CH259-230J2, WORKING DRAFT SEQUENCE, 4  
ordered pieces.  
ACCESSION AC150721  
VERSION AC150721.3 GI:5411274  
HTG; HTGS PHASE2; HTGS DRAFT.  
KEYWORDS Callithrix jacchus (white-tufted-ear marmoset)  
SOURCE Callithrix jacchus  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Callitrichidae; Callitrich.  
REFERENCE  
AUTHORS 1 (bases 1 to 199024)  
Antonellis,A., Ayele,K., Benjamin,B., Blakesley,R.W., Boakye,A., Bouffard,G.G., Brinkley,C., Brooks,S., Chu,G., Coleman,H., Engle,J., Guan,X., Gupta,J., Haghighi,P., Han,J., Hansen,N., Ho,S.-L., Hu,P., Hurle,B., Idol,J.R., Jones,C., Kwong,P., Latic,P., Larson,S., Lee-Lin,S.-O., Legaspi,R., Madden,M., Maduro,Q.L., Maduro,V.B., Margulies,E.H., Mastello,C., Masferrer,B., McDowell,J., Mullikin,J.C., Oestreich,J.S., Park,M., Portnoy,M.E., Prasad,A., Puri,O., Reddix-Duane,N., Rosas,B., Schandler,K., Schneider,M.G., Shah,K., Sison,C., Stancirpop,S., Stephen,B., Thomas,J.W., Thomas,P.J., Tsipouri,V., Vogt,J.L., Wetherby,K.D., Young,A. and Green,E.D.  
NISC Comparative Sequencing Initiative  
Unpublished  
2 (bases 1 to 199024)  
Green,E.D.  
Direct Submission  
Submitted (04-ANG-2004) NIH Intramural Sequencing Center, 8717  
Groveomont Circle, Gaithersburg, MD 20877, USA  
3 (bases 1 to 199024)



AUTHORS Green, E.D.  
 TITLE Direct Submission  
 JOURNAL Submitted (13-OCT-2004) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 COMMENT On Oct 13, 2004 this sequence version replaced gi:51948562.  
 ----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: ghs  
 Center clone name: 2310J02

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g., human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

#### ----- Summary Statistics

Sequencing vector: plasmid; n/a; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Assembly program: Phrap; version 0.990319  
 Consensus quality: 197043 bases at least Q40  
 Consensus quality: 197785 bases at least Q30  
 Consensus quality: 198372 bases at least Q20  
 Insert size: 200000; agarose-fp  
 Insert size: 198724; sum-of-contigs  
 Quality coverage: 6.89x in Q20 bases; sum-of-contigs  
 Quality coverage: 6.94x in Q20 bases; sum-of-contigs

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 4 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 137567: contig of 137567 bp in length  
 \* 137568 137667: gap of unknown length  
 \* 137668 150803: contig of 13136 bp in length  
 \* 150804 195236: gap of unknown length  
 \* 195237 195336: contig of 44333 bp in length  
 \* 195337 199024: contig of 3688 bp in length.

#### FEATURES

source 1.199024  
 Location/Qualifiers  
 1.199024  
 /organism="Callithrix jacchus"  
 /mol\_type="genomic DNA"  
 /db\_xref="taxon:9483"  
 /clone\_id="CH259-230J2"  
 /clone\_1fb="CH259"  
 /note="BAC resource: <http://bacpac.chori.org/>"  
 1.137567  
 /note="assembly\_fragment"  
 clone\_end:SP6  
 vector\_side:left  
 1.87891  
 /note="clone overlaps with GenBank Accession Number  
 AC150604 clone CH259-231F14 (center project name ghc)."  
 gap 137568..137667  
 /estimated\_length=unknown  
 137668..150803  
 /note="assembly\_fragment"  
 misc\_feature  
 misc\_feature  
 misc\_feature

gap 150804..150903  
 /estimated\_length=unknown  
 misc\_feature 150904..155236  
 /note="assembly\_fragment"  
 gap 195237..195336  
 /estimated\_length=unknown  
 misc\_feature 195337..199024  
 /note="assembly\_fragment"  
 clone\_end:T7  
 vector\_side:right

#### ORIGIN

Query Match 3.8%; Score 21; DB 14; Length 199024;  
 Best Local Similarity 100.0%; Pred. No. 5.7;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 AGAATTTGAGAGAAATTTCTTA 420  
 |||||  
 Db 27849 AGAATTTGAGAGAAATTTCTTA 27869

#### RESULT 21

AC150604 206630 bp DNA linear HTG 22-SEP-2004

#### LOCUS

Callithrix jacchus clone CH259-231F14, WORKING DRAFT SEQUENCE, 5  
 ordered pieces.

#### DEFINITION

AC150604.2 GI:52421366

#### ACCESSION

AC150604.2 GI:52421366

#### VERSION

HTG: HTGS\_PHASE2; HTGS\_DRAFT.

#### KEYWORDS

Callithrix jacchus (white-tufted-ear marmoset)

#### SOURCE

Callithrix jacchus

#### ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini;  
 Callitrichidae; Callitrix.

#### REFERENCE

1 (bases 1 to 206630)

Antoneillis, A., Ayele, K., Benjamin, B., Blakeley, R. W., Boake, A.,  
 Bouffard, G. G., Brinkley, C., Brooks, S., Chu, G., Coleman, H., Daki, N.,  
 Engle, J., Guan, X., Gupta, J., Haghighi, P., Han, J., Hansen, N.,  
 Ho, S.-L., Hu, P., Hulse, B., Idol, J. R., Jones, C., Kwong, P., Latic, P.,  
 Larson, S., Lee-Jin, S.-O., Legaspi, R., Madden, M., Maduro, O. L.,  
 Maduro, V. B., Marzullies, E. H., Masello, C., Maskeri, B., McQuell, J.,  
 Mullikin, J. C., Park, M., Portnoy, M. E., Prasad, A., Puri, O.,  
 Redix-Dugue, N., Roaas, B., Schandler, K., Schuler, M. G., Shah, K.,  
 Sison, C., Stancirpop, S., Stephen, E., Thomas, J. W., Thomas, P. J.,  
 Tsipouri, V., Vogt, J. L., Weherby, K. D., Young, A. and Green, E. D.  
 NISC Comparative Sequencing Initiative

Unpublished  
 2 (bases 1 to 206630)

Green, E.D.  
 Direct Submission  
 Submitted (28-JUL-2004) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 3 (bases 1 to 206630)

Green, E.D.  
 Direct Submission  
 Submitted (22-SEP-2004) NIH Intramural Sequencing Center, 8717  
 Grovemont Circle, Gaithersburg, MD 20877, USA  
 On Sep 22, 2004 this sequence version replaced gi:50726758.

----- Genome Center  
 Center: NIH Intramural Sequencing Center  
 Center code: NISC  
 Web site: <http://www.nisc.nih.gov>  
 Contact: [nisc\\_zoo@nhgri.nih.gov](mailto:nisc_zoo@nhgri.nih.gov)  
 ----- Project Information  
 Center project name: ghc  
 Center clone name: 231F14

The sequence data in this record represents an 'enhanced' version of a Phase 2 submission. Specifically, the indicated order and orientation of each sequence contig has been established using one or more of the following: read-pair data from individual subclones, overlaps with neighboring clones, alignment with available reference sequence (e.g.,



human), and/or confirmation by PCR testing. In addition, the sequence assembly is based on at least 8X average coverage in Q20 bases and has been reviewed to rule out gross misassemblies, the low-quality ends of sequence contigs have been trimmed away, and each base is associated with a Phrap-derived quality score.

## ----- Summary Statistics -----

Sequencing vector: plasmid; n/a; 100% of reads  
Chemistry: Dye-terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 205632 bases at least Q40  
Consensus quality: 206037 bases at least Q30  
Consensus quality: 206186 bases at least Q20  
Insert size: 210000; agarose-fp  
Insert size: 206230; sum-of-contigs  
Quality coverage: 7.85x in Q20 bases; agarose-fp  
Quality coverage: 7.99x in Q20 bases; sum-of-contigs

-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 5 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* provided by the submittor.

\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.

1 15675: contig of 15675 bp in length  
\* 15676 15775: gap of unknown length  
\* 15776 21224: contig of 5449 bp in length  
\* 21225 21324: gap of unknown length  
\* 21325 110980: contig of 89656 bp in length  
\* 110981 111080: gap of unknown length  
\* 111081 142063: contig of 30983 bp in length  
\* 142064 142163: gap of unknown length  
\* 142164 206630: contig of 64467 bp in length.

## FEATURES

## source

1..206630

/organism="Callithrix jacchus"

/mol\_type="genomic DNA"

/db\_xref="taxon:9483"

/clone="CH259-231P14"

/clone\_lib="CH259"

/note="TAC resource: <http://bacpac.choi.org/>"

## misc\_feature

1..15675

/note="assembly\_fragment"

clone end:SP6

vector side:left"

## misc\_feature

1..4071

/note="clone overlaps with GenBank Accession Number  
AC150601 clone CH259-201L23 (center project name gnu)"

## gap

15676..15775

/estimated\_length=unknown

## misc\_feature

15776..21324

/note="assembly\_fragment"

## gap

21225..21324

/estimated\_length=unknown

## misc\_feature

21325..110980

/note="assembly\_fragment"

## gap

110981..111080

/estimated\_length=unknown

## misc\_feature

111081..142063

/note="assembly\_fragment"

## misc\_feature

118711..206630

/note="clone overlaps with GenBank Accession Number  
AC150721 clone CH259-230J2 (center project name gnu)"

## gap

142064..142163

/estimated\_length=unknown

## misc\_feature

142164..206630

/note="assembly\_fragment"

clone end:T7

vector\_side:right"

## ORIGIN

Query Match 3.8%; Score 21; DB 14; Length 206630;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 400 AGAATTCAGAGAAATCTTA 420

Db 146588 AGAATTCAGAGAAATCTTA 146608

## RESULT 22

VFA243461

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

Vicia faba

Bakaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;

rosids; eurosid 1; Fabales; Fabaceae; Papilionoideae; Viciae;

Vicia.

1

Fruehling,M., Albus,U., Hohnjec,N., Geise,G., Puhler,A. and

Perlick,A.M.

A small gene family of broad bean codes for late nodulins

containing conserved cysteine clusters

Plant Sci. 152, 67-77 (2000)

2 (bases 1 to 2424)

Fruehling,M.

Direct Submission

Submitted (02-JUL-1999) Fruehling M., Lehrstuhl fuer Genetiv,

Universitaet Bielefeld, Universitaetsstrasse 25, 33501 Bielefeld,

GERMANY

## FEATURES

## source

1..2424

/organism="Vicia faba"

/mol\_type="genomic DNA"

/cultivar="Kleine Tnreinger"

/db\_xref="taxon:3906"

1777..2073

/gene="nod-CCP1"

join(1777..1852,1952..2073)

/gene="nod-CCP1"

/codon\_start=1

/product="late nodulin"

/protein\_id="CAB96471.1"

/db\_xref="GI:8920397"

/translation="MAKFLNIIVHFMILLISVFIERNMSTIIICKTDADCIKDLNSD

WKCIENQCKFKVAVAPFGTE"

<1777..1852

/gene="nod-CCP1"

/number=1

1853..1951

/gene="nod-CCP1"

/number=1

1952..2073

/gene="nod-CCP1"

/number=2

## ORIGIN

Query Match

Best Local Similarity

Matches 20; Conservative

0; Mismatches

0; Indels

0; Gaps

0;

QY 177 TATCTTCGAAATTAATGA 196

Db 249 TATCTTCGAAATTAATGA 268

## RESULT 23



HSMB06491/c 6278 bp mRNA linear PRI 17-JUN-2003  
LOCUS Homo sapiens mRNA; cDNA DKFZp686A1429 (from clone DKFZp686A1429).  
ACCESSION BX538250  
VERSION BX538250.1 GI:31874723  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.  
1 (bases 1 to 6278)  
Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amd, C., Osanger, A.,  
Fobo, G., Han, M. and Wiemann, S.  
Direct Submission  
Submitted (17-JUN-2003) MIPS, Ingolstaedter Landstr.1, D-85764  
Neuberberg, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;  
sequenced by Oigen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
This clone (DKFZp686A1429) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further  
information about the clone and the sequencing project is available  
at <http://mips.gsf.de/proj/cDNA/>.  
location/Qualifiers  
1. 6278  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/chromosome="15q25.2"  
/clone="DKFZp686A1429"  
/tissue\_type="human testis"  
/clone\_lib="686 (synonym: hicc3). Vector pSport1\_sfi; host  
DH10B; sites SfiI + SfiIb"  
/dev\_stage="adult"  
6227..6232  
polyA\_signal  
polyA\_site  
6247  
ORIGIN  
Query Match 3.6%; Score 20; DB 8; Length 6278;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 170 ATCAATTCTTCCAAAT 189  
DB 3778 ATCAATTCTTCCAAAT 3759  
RESULT 24  
AC165169 74914 bp DNA linear HTG 06-JUL-2005  
LOCUS Mus musculus chromosome 5 clone RP23-9B2, \*\*\* SEQUENCING IN  
DEFINITION  
AC165169  
AC165169.1 GI:68989407  
KEYWORDS HTG; PHASE1.  
SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;  
Sciurognathi; Muridae; Murinae; Mus.  
1 (bases 1 to 74914)  
Wilson, R.K.  
REFERENCE  
AUTHORS Wilson, R.K.  
TITLE The sequence of Mus musculus clone  
JOURNAL Unpublished  
2 (bases 1 to 74914)  
AUTHORS Wilson, R.K.  
TITLE Direct Submission  
Submitted (06-JUL-2005) Genome Sequencing Center, 4444 Forest Park  
Parkway, St. Louis, MO 63108, USA  
COMMENT

----- Genome Center -----  
Center: Washington University Genome Sequencing Center  
Center code: WUGSC  
Web site: <http://genome.wustl.edu>  
----- Project Information -----  
Center project name: M\_BA0009B02  
----- Summary Statistics -----  
Sequencing vector: M13; 0%  
Sequencing vector: plasmid; 100%  
Chemistry: Dye-Primer ET; 0% of reads  
Chemistry: Dye-Terminator Big Dye; 100% of reads  
Assembly program: Phrap; version 0.990319  
Consensus quality: 53745 bases at least Q40  
Consensus quality: 53745 bases at least Q40  
Consensus quality: 63562 bases at least Q20  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 36 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence  
\* as soon as it is available and the accession number will  
\* be preserved.  
1 1278: contig of 1278 bp in length  
1 1279 1378: gap of unknown length  
1 1379 2720: contig of 1342 bp in length  
1 2721 2820: gap of unknown length  
1 2821 4179: contig of 1359 bp in length  
1 4180 4279: gap of unknown length  
1 4280 5559: contig of 1280 bp in length  
1 5560 5660: gap of unknown length  
1 5660 7034: contig of 1375 bp in length  
1 7035 7135: gap of unknown length  
1 7135 8537: contig of 1403 bp in length  
1 8538 8637: gap of unknown length  
1 8638 10100: contig of 1463 bp in length  
1 10101 10201: gap of unknown length  
1 10201 12548: contig of 2348 bp in length  
1 12549 12648: gap of unknown length  
1 12649 14305: contig of 1657 bp in length  
1 14306 14405: gap of unknown length  
1 14406 16052: contig of 1647 bp in length  
1 16053 16152: gap of unknown length  
1 16153 17368: contig of 1216 bp in length  
1 17369 17468: gap of unknown length  
1 17469 19084: contig of 1616 bp in length  
1 19085 19184: gap of unknown length  
1 19185 20459: contig of 1275 bp in length  
1 20460 20559: gap of unknown length  
1 20560 21824: contig of 1265 bp in length  
1 21825 21924: gap of unknown length  
1 21925 23702: contig of 1778 bp in length  
1 23703 23802: gap of unknown length  
1 23803 25810: contig of 2008 bp in length  
1 25811 25910: gap of unknown length  
1 25911 27070: contig of 1160 bp in length  
1 27071 27170: gap of unknown length  
1 27171 29699: contig of 2529 bp in length  
1 29700 29799: gap of unknown length  
1 29800 31529: contig of 1730 bp in length  
1 31530 31629: gap of unknown length  
1 31630 32773: contig of 1144 bp in length  
1 32774 32873: gap of unknown length  
1 32874 34892: contig of 2019 bp in length  
1 34893 34992: gap of unknown length  
1 34993 36169: contig of 1177 bp in length  
1 36170 36269: gap of unknown length  
1 36270 38130: contig of 1861 bp in length  
1 38131 38230: gap of unknown length  
1 38231 39640: contig of 1410 bp in length  
1 39641 39740: gap of unknown length



	*	39741	41679: contig of 1939 bp in length
	*	41680	41779: gap of unknown length
	*	41780	44873: contig of 3094 bp in length
	*	44874	44973: gap of unknown length
	*	44974	47227: contig of 2254 bp in length
	*	47228	47327: gap of unknown length
	*	47328	48763: contig of 1436 bp in length
	*	48764	48863: gap of unknown length
	*	48864	51144: contig of 2281 bp in length
	*	51145	51244: gap of unknown length
	*	51245	54234: contig of 2990 bp in length
	*	54235	54334: gap of unknown length
	*	54335	56123: contig of 1789 bp in length
	*	56124	56223: gap of unknown length
	*	56224	59187: contig of 2364 bp in length
	*	59188	59287: gap of unknown length
	*	59288	62139: contig of 2852 bp in length
	*	62140	62239: gap of unknown length
	*	62240	64021: contig of 1782 bp in length
	*	64022	64121: gap of unknown length
	*	64122	68001: contig of 3880 bp in length
	*	68002	68101: gap of unknown length
	*	68102	74914: contig of 6813 bp in length.
FEATURES			Location/Qualifiers
source		1..74914	
		/organism="Mus musculus"	
		/mol_type="genomic DNA"	
		/db_xref="taxon:10090"	
		/chromosome="5"	
		/clone="RP23-9B2"	
		1..1278	
misc_feature		/note="assembly_name:Contig17"	
gap		1279..1378	
		/estimated_length=unknown	
misc_feature		1379..2720	
gap		/note="assembly_name:Contig24"	
		2721..2820	
		/estimated_length=unknown	
misc_feature		2821..4179	
gap		/note="assembly_name:Contig26"	
		4180..4279	
		/estimated_length=unknown	
misc_feature		4280..5559	
gap		/note="assembly_name:Contig27"	
		5560..5659	
		/estimated_length=unknown	
misc_feature		5660..7034	
gap		/note="assembly_name:Contig39"	
		7035..7134	
		/estimated_length=unknown	
misc_feature		7135..8537	
gap		/note="assembly_name:Contig46"	
		8538..8637	
		/estimated_length=unknown	
misc_feature		8638..10100	
gap		/note="assembly_name:Contig47"	
		10101..10200	
		/estimated_length=unknown	
misc_feature		10201..12548	
gap		/note="assembly_name:Contig50"	
		12549..12648	
		/estimated_length=unknown	
misc_feature		12649..14305	
gap		/note="assembly_name:Contig51"	
		14306..14405	
		/estimated_length=unknown	
misc_feature		14406..16052	
gap		/note="assembly_name:Contig55"	
		16053..16152	
		/estimated_length=unknown	
misc_feature		16153..17368	
gap		/note="assembly_name:Contig58"	
		17369..17468	

---

	misc_feature	/estimated_length=unknown
		17469..19084
		/note="assembly_name:Contig60"
	gap	19085..19184
		/estimated_length=unknown
	misc_feature	19185..20459
		/note="assembly_name:Contig61"
	gap	20460..20559
		/estimated_length=unknown
	misc_feature	20560..21824
		/note="assembly_name:Contig62"
	gap	21825..21924
		/estimated_length=unknown
	misc_feature	21925..23702
		/note="assembly_name:Contig63"
	gap	23703..23802
		/estimated_length=unknown
	misc_feature	23803..25810
		/note="assembly_name:Contig64"
	gap	25811..25910
		/estimated_length=unknown
	misc_feature	25911..27070
		/note="assembly_name:Contig65"
	gap	27071..27170
		/estimated_length=unknown
	misc_feature	27171..29699
		/note="assembly_name:Contig66"
	gap	29700..29799
		/estimated_length=unknown
	misc_feature	29800..31529
		/note="assembly_name:Contig67"
	gap	31530..31629
		/estimated_length=unknown

Query Match 3.6%; Score 20; DB 14; Length 74914;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	176	TTATCTTCCAAAATTAATG	195
Db	22337	TTATCTTCCAAAATTAATG	22356

RESULT 25

AC114958	79173 bp	DNA	linear	PRI 27-MAR-2002
LOCUS				
DEFINITION	Homo sapiens chromosome 5 clone RP11-167018, complete sequence.			
AC114958				
AC114958.2	GI:19747190			
KEYWORDS	HTG.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;			
	Hominidae; Homo			
REFERENCE	1 (bases 1 to 79173)			
AUTHORS	DOE Joint Genome Institute and Stanford Human Genome Center.			
TITLE	Direct Submission			
JOURNAL	Unpublished			
REFERENCE	2 (bases 1 to 79173)			
AUTHORS	DOE Joint Genome Institute.			
TITLE	Direct Submission			
JOURNAL	Submitted (14-MAR-2002) Production Sequencing Facility, DOE Joint			
REFERENCE	Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA			
AUTHORS	3 (bases 1 to 79173)			
TITLE	DOE Joint Genome Institute and Stanford Human Genome Center.			
JOURNAL	Submitted (27-MAR-2002) DOE Joint Genome Institute, 2800 Mitchell			
COMMENT	Drive, Walnut Creek, CA 94598, USA			
	On Mar 27, 2002 this sequence version replaced gi:19424419.			
	Draft Sequence Produced by DOE Joint Genome Institute			
	www.jgi.doe.gov			
	Finishing Completed at Stanford Human Genome Center			



www.shgc.stanford.edu  
Quality: Phrap Quality >=40 99.7% of Sequence;  
Estimated Total Number of Errors is 0.2.

NOTE: This insert is not the entire sequence of the clone (entire sequence is 123kb). It is clipped at the overlap with AC106816. The number of bases overlapped is 65592.

## FEATURES

## SOURCE

Location/Qualifiers  
1..79173  
/organism="Homo sapiens"  
/mol\_type="genomic DNA"  
/db\_xref="taxon:9606"  
/chromosome="5"  
/clone="RP11-167018"

## ORIGIN

Query Match 3.6%; Score 20; DB 8; Length 79173;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

360 AGAAGAGAGAAATACAAAG 379  
13013 AGAAGAGAGAAATACAAAG 13032

RESULT 26  
LOCUS AC027313 87302 bp DNA linear PRI 08-JUN-2001  
DEFINITION Homo sapiens chromosome 5 clone CTC-278L1, complete sequence.

AC027313  
AC027313.4 GI:14329106

## KEYWORDS

## SOURCE

Homo sapiens (human)  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;  
Homidae; Homo.

## REFERENCE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## OY

360 AGAAGAGAGAAATACAAAG 379  
44955 AGAAGAGAGAAATACAAAG 44974

## RESULT 27

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

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## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

AP004491/c 91039 bp DNA linear PLN 22-JUN-2003

Lotus corniculatus var. japonicus genomic DNA, chromosome 1,  
clone:JfT17G08, TM0023, complete sequence.

AP004491  
AP004491.1 GI:17736858

HTG. Lotus corniculatus var. japonicus (Lotus japonicus)

Lotus corniculatus var. japonicus

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;  
rosoids; eurosids I; Fabales; Fabaceae; Papilionoideae; Lotese;

Lotus.

Sato, S., Kaneko, T., Nakamura, Y., Asamizu, E., Kato, T. and Tabata, S.

Structural Analysis of a Lotus japonicus Genome. I. Sequence  
Features and Mapping of Fifty-six TAC Clones which cover the 5.4 Mb  
Regions of the Genome

Unpublished  
2 (bases 1 to 91039)

Nakamura, Y.  
Direct Submission  
Submitted (13-DEC-2001) Yasukazu Nakamura, Kazusa DNA Research  
Institute, Department of Plant Gene Research, 1532-3, Yama,  
Kisarazu, Chiba 292-0812, Japan (E-mail: ynakamu@kazusa.or.jp,  
URL: http://www.kazusa.or.jp, Tel: 81-438-52-3935,  
Fax: 81-438-52-3934)

Location/Qualifiers  
1..91039  
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/variety="japonicus"  
/db\_xref="taxon:34305"  
/chromosome="1"  
/clone="JfT17G08"  
/clone\_id="JfT17G08 library"  
/note="TAC clone: TM0023  
synonym: Lotus japonicus"

Query Match 3.6%; Score 20; DB 15; Length 91039;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

## FEATURES

## SOURCE

## LOCUS

## DEFINITION

## ACCESSION

## VERSION

## KEYWORDS

## SOURCE

## ORGANISM

## REFERENCE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

## AUTHORS

## JOURNAL

## TITLE

Sequence split into 71 fragments LOCUS CP000076 Accession CP000076

## WPCOMMENT

## Fragment Name

## Begin

## End

## CP000076\_00

## CP000076\_01

## CP000076\_02

## CP000076\_03

CP000076\_04

CP000076\_05

CP000076\_06

CP000076\_07

CP000076\_08

CP000076\_09

CP000076\_10

110000

210000

310000

410000

510000

610000

710000

810000

910000

1010000

1110000



CP000076\_11 1100001 1210000  
CP000076\_12 1200001 1310000  
CP000076\_13 1300001 1400000  
CP000076\_14 1400001 1510000  
CP000076\_15 1500001 1610000  
CP000076\_16 1600001 1710000  
CP000076\_17 1700001 1810000  
CP000076\_18 1800001 1910000  
CP000076\_19 1900001 2010000  
CP000076\_20 2000001 2110000  
CP000076\_21 2100001 2210000  
CP000076\_22 2200001 2310000  
CP000076\_23 2300001 2410000  
CP000076\_24 2400001 2510000  
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CP000076\_26 2600001 2710000  
CP000076\_27 2700001 2810000  
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CP000076\_37 3700001 3810000  
CP000076\_38 3800001 3910000  
CP000076\_39 3900001 4010000  
CP000076\_40 4000001 4110000  
CP000076\_41 4100001 4210000  
CP000076\_42 4200001 4310000  
CP000076\_43 4300001 4410000  
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CP000076\_68 6800001 6910000  
CP000076\_69 6900001 7010000  
CP000076\_70 7000001 7074893  
Continuation (25 of 71) of CP000076 from base 2400001 (CP000076 Pseudomonas fluorescens

Query Match 3.6%; Score 20; DB 1; Length 110000;  
Best Local Similarity 10.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 262 CTTGACGAGTAGCTGAAGC 281  
Db 103694 CTTGACGAGTAGCTGAAGC 103713

RESULT 29  
CP000076\_25

WPCOMMENT  
Sequence split into 71 fragments LOCUS CP000076 Accession CP000076  
Fragment Name Begin End  
CP000076\_00 1 110000  
CP000076\_01 100001 210000  
CP000076\_02 200001 310000  
CP000076\_03 300001 410000  
CP000076\_04 400001 510000  
CP000076\_05 500001 610000  
CP000076\_06 600001 710000  
CP000076\_07 700001 810000  
CP000076\_08 800001 910000  
CP000076\_09 900001 1010000  
CP000076\_10 1000001 1110000  
CP000076\_11 1100001 1210000  
CP000076\_12 1200001 1310000  
CP000076\_13 1300001 1410000  
CP000076\_14 1400001 1510000  
CP000076\_15 1500001 1610000  
CP000076\_16 1600001 1710000  
CP000076\_17 1700001 1810000  
CP000076\_18 1800001 1910000  
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CP000076\_20 2000001 2110000  
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CP000076\_22 2200001 2310000  
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CP000076\_67 6700001 6810000  
CP000076\_68 6800001 6910000  
CP000076\_69 6900001 7010000



CP000076 70 700001 7074893  
Continuation (26 of 71) of CP000076 from base 2500001 (CP000076 Pseudomonas fluorescens)

Query Match 3.6%; Score 20; DB 1; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 262 CTTGACGAAGTAGCTGAAGC 281  
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DB 3694 CTTGACGAAGTAGCTGAAGC 3713

RESULT 30  
CR382127\_03

WPCOMMENT

Sequence split into 23 fragments LOCUS CR382127 Accession CR382127

Fragment Name	Begin	End
CR382127_00	1	110000
CR382127_01	100001	210000
CR382127_02	200001	310000
CR382127_03	300001	410000
CR382127_04	400001	510000
CR382127_05	500001	610000
CR382127_06	600001	710000
CR382127_07	700001	810000
CR382127_08	800001	910000
CR382127_09	900001	1010000
CR382127_10	1000001	1110000
CR382127_11	1100001	1210000
CR382127_12	1200001	1310000
CR382127_13	1300001	1410000
CR382127_14	1400001	1510000
CR382127_15	1500001	1610000
CR382127_16	1600001	1710000
CR382127_17	1700001	1810000
CR382127_18	1800001	1910000
CR382127_19	1900001	2010000
CR382127_20	2000001	2110000
CR382127_21	2100001	2210000
CR382127_22	2200001	2303261

Continuation (4 of 23) of CR382127 from base 300001 (CR382127 Yarrowia lipolytica chromo

Query Match 3.6%; Score 20; DB 15; Length 110000;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 453 TGCATGCTGCTTGAAGCG 472  
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DB 79667 TGCATGCTGCTTGAAGCG 79686

RESULT 31  
AP008212\_289

WPCOMMENT

Sequence split into 308 fragments LOCUS AP008212 Accession AP008212

Fragment Name	Begin	End
AP008212_000	1	110000
AP008212_001	100001	210000
AP008212_002	200001	310000
AP008212_003	300001	410000
AP008212_004	400001	510000
AP008212_005	500001	610000
AP008212_006	600001	710000
AP008212_007	700001	810000
AP008212_008	800001	910000
AP008212_009	900001	1010000
AP008212_010	1000001	1110000
AP008212_011	1100001	1210000
AP008212_012	1200001	1310000
AP008212_013	1300001	1410000
AP008212_014	1400001	1510000
AP008212_015	1500001	1610000
AP008212_016	1600001	1710000

AP008212_017	1700001	1810000
AP008212_018	1800001	1910000
AP008212_019	1900001	2010000
AP008212_020	2000001	2110000
AP008212_021	2100001	2210000
AP008212_022	2200001	2310000
AP008212_023	2300001	2410000
AP008212_024	2400001	2510000
AP008212_025	2500001	2610000
AP008212_026	2600001	2710000
AP008212_027	2700001	2810000
AP008212_028	2800001	2910000
AP008212_029	2900001	3010000
AP008212_030	3000001	3110000
AP008212_031	3100001	3210000
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AP008212_065	6500001	6610000
AP008212_066	6600001	6710000
AP008212_067	6700001	6810000
AP008212_068	6800001	6910000
AP008212_069	6900001	7010000
AP008212_070	7000001	7110000
AP008212_071	7100001	7210000
AP008212_072	7200001	7310000
AP008212_073	7300001	7410000
AP008212_074	7400001	7510000
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AP008212_084	8400001	8510000
AP008212_085	8500001	8610000
AP008212_086	8600001	8710000
AP008212_087	8700001	8810000
AP008212_088	8800001	8910000
AP008212_089	8900001	9010000



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AP008212_090 9000001 9110000
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AP008212_196 19600001 1971000

Query Match 3.6%; Score 20; DB 15; Length 110000;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 396 TTCTGAAATTTCAGAGAGAT 415
Db 66030 TTCTGAAATTTCAGAGAGAT 66049

RESULT 32
AC069294 123778 bp DNA linear PRI 09-MAY-2001
LOCUS Homo sapiens BAC clone RP11-757A13 from 7, complete sequence.
DEFINITION AC069294
ACCESSION AC069294.5 GI:13112210
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
REFERENCE
AUTHORS Bielicki, L. and Cotton, M.
TITLE The sequence of Homo sapiens BAC clone RP11-757A13
JOURNAL Unpublished
PUBMED 3 (bases 1 to 123778)
REFERENCE
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (24-MAY-2000) Genome Sequencing Center, Washington
MO 63108, USA
REFERENCE
AUTHORS Waterston, R.H.
TITLE 4 (bases 1 to 123778)

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TITLE Direct Submission  
JOURNAL Submitted (23-FEB-2001) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis, MO 63108, USA  
REFERENCE 5 (bases 1 to 123778)  
AUTHORS Waterston,R.  
TITLE Direct Submission  
JOURNAL Submitted (09-MAY-2001) Department of Genetics, Washington University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA  
COMMENT On Feb 23, 2001 this sequence version replaced gi:9858450.  
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Genome Center  
Center: Washington University Genome Sequencing Center  
Center code: MUGSC  
Web site: <http://genome.wustl.edu/gsc>  
Contact: [sapiens@wustl.wustl.edu](mailto:sapiens@wustl.wustl.edu)  
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Summary Statistics  
Center project name: H\_NH0757A13  
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NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.  
  
This sequence was finished as follows unless otherwise noted:  
all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.  
  
MAPPING INFORMATION:  
The sequence of this clone was established as part of a mapping and sequencing collaboration between the NHGRI Chromosome 7 Mapping Project (Eric D. Green, Director), John D. McPherson in the Department of Genetics (Washington University), and the Washington University Genome Sequencing Center. For additional information about the map position of this sequence, see <http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send <mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>  
  
SOURCE INFORMATION:  
The RPCT-11 human BAC library was made from the blood of one male donor, as described by Osoegawa,K., Moon,P.Y., Zhao,B., Frengen,B., Tatemio,M., Catanese,J.J. and de Jong,P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (<http://bacpac.med.buffalo.edu>)  
VECTOR: pBAC3.6  
NEIGHBORING SEQUENCE INFORMATION:  
The clone sequenced to the right is GSI-259H13, 200 bp overlap; the clone sequenced to the left is CTD-324A018, 200 bp overlap. Actual start of this clone is at base position 59660 of CTD-324A018; actual end is at base position 25744 of GSI-259H13.  
  
The sequence from base position 113692 to 114784 is derived from a single plasmid subclone. Assembly in this region is supported by HindIII digest information.

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rpt\_family="L2" 1684..1900  
repeat\_region /rpt\_family="Alu" 2040..2334  
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rpt\_family="Alu" 3874..4033  
repeat\_region /rpt\_family="MER1\_type" 10188..10513  
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repeat\_region /note="similar to" 10569..10682  
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rpt\_family="Alu" 10936..11009  
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misc\_feature /note="similar to" 12025..12094  
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repeat\_region /rpt\_family="L1" 22194..23073  
rpt\_family="L1" 23074..23663  
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EST AA811274 (NID:g2880885) cb68e03.s1  
EST AA858281 (NID:g2946583) cb13a02.s1  
EST AA935054 (NID:g3091761) oo6dd11.s1  
EST BE682487 (NID:g10068399) \*







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 predicted by Genemark.hmm  
 this category is not included in IRGSP standard"  
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 /translation="MDRDHAGSPSPVHETDGPDRPTTIGRAAIAAAGLSASRPTGR  
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 GGVLTGGDGVRRGATGEGRHADGDRDLKNEKVEERERHRRRRCRPPAADM  
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 /gene="P0468G03.7"  
 /codon\_start=1  
 /product="putative 10-deacetyl baccatin III-10-O-acetyl  
 transferase"  
 /protein\_id="BAD53994.1"  
 /db\_xref="GI:53791872"  
 /translation="MKDIYVSRKSGPPVLTVPSSSEPTPAATRTLSADSKRLGSLFTA  
 FLVFERRRSRVRPAETVRSALVHYPLAGHVAADDDNVVLSCTGREGGL  
 PVAAVATCTLDVDDGDDGLPLADIAVYGGSCMSPLDMQVTEECGFGVGV  
 TNNHVVADTVGLAQLRAYGELACGLPSPSVPIKHYDFAYCDIMPMSEVGNVKALEF  
 SRNGGGGRRRCSTPVYTAITWQCTRTAIIHRCRSDAPALILAVNARPHIGAKDG  
 YVNCITRQLVASTADAVAGIIVDVVKLVNAKERIPBELRLNKLKRGQCGDGGG  
 GLFVGPMLRLVYSWAGLGDIDFGGPARVITPMEVTPMSCLPCPSRSNSGD  
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 complement (17698..19950)  
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 19482..19632,19771..>19950))  
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 /note="start and end point are not identified"  
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 19482..19632,19771..19950))  
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 /protein\_id="BAD53995.1"  
 /db\_xref="GI:53791873"  
 /translation="WGSSTSTSLVSLILPCLLSLLIRLSTHNPPTAARPRKRTPT

Query Match 3.6%; Score 20; DB 15; Length 143918;  
 Best Local Similarity 100.0%; Pred. No. 21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy 396 TTCTGAAATTCAGAGAAAT 415  
 Db 116074 TTCTGAAATTCAGAGAAAT 116093

RESULT 34  
 AL929530 152963 bp DNA linear VRT 11-FEB-2003  
 LOCUS Zebrafish DNA sequence from clone CH211-190H2, complete sequence.  
 DEFINITION  
 ACCESSION AL929530  
 VERSION AL929530.9 GI:28300590  
 KEYWORDS HTG.  
 SOURCE Dario reio (zebrafish)  
 ORGANISM Dario reio  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Actinopterygii; Neopterygii; Teleostei; Ostariophysi;  
 Cypriniformes; Cyprinidae; Danio.  
 1 (bases 1 to 152963)  
 Wallis, J.  
 Direct Submission  
 Submitted (11-FEB-2003) Wellcome Trust Sanger Institute, Hinxton,  
 Cambridgeshire, CB10 1SA, UK. E-mail enquiries:  
 zfish-help@sanger.ac.uk Clone requests: clonequests@sanger.ac.uk  
 On Feb 10, 2003 this sequence version replaced gi:27652803.  
 ----- Genome Center  
 Center: Wellcome Trust Sanger Institute  
 Center code: SC  
 Web site: http://www.sanger.ac.uk  
 Contact: zfish-help@sanger.ac.uk

During sequence assembly data is compared from overlapping clones.  
 Where differences are found these are annotated as variations  
 together with a note of the overlapping clone name. Note that the  
 variation annotation may not be found in the sequence submission  
 corresponding to the overlapping clone, as we submit sequences with  
 only a small overlap as described above.  
 This sequence was finished as follows unless otherwise noted: all  
 regions were either double-stranded or sequenced with an alternate  
 chemistry or covered by high quality data (i.e., phred quality >=  
 30); an attempt was made to resolve all sequencing problems, such  
 as compressions and repeats; all regions were covered by at least  
 one plasmid subclone or more than one M13 subclone; and the  
 assembly was confirmed by restriction digest, except on the rare  
 occasion of the clone being a YAC.  
 The following abbreviations are used to associate primary accession  
 numbers given in the feature table with their source databases:  
 Em:, EMBL; Sw:, SWISSPROT; Tr:, TrEMBL; Wp:, WormPep; Information  
 on the WormPep database can be found at



[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see [http://www.Projects/D\\_rexio/fishmask.shtml](http://www.Projects/D_rexio/fishmask.shtml) CH211-190H2 is from a CHOR1-211 BAC library

VECTOR: PTARBAC2.1.

Location/Qualifiers

1. 152963

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="CH211-190H2"

/clone\_lib="CHOR1-211"

# ORIGIN

Query Match 3.6%; Score 20; DB 5; Length 152963;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 TGATTGTAATGTTTAGAA 234

Db 9339 TGATTGTAATGTTTAGAA 9358

## RESULT 35

CR848759

LOCUS

zebrafish DNA sequence from clone CH211-229D2 in linkage group 15,

complete sequence.

ACCESSION

CR848759

VERSION

CR848759.4 GI:62867796

KEYWORDS

HTG.

SOURCE

Danio rerio

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes; Cyprinidae; Danio.  
1 (bases 1 to 167536)  
Mashreghi-Mohammadi, M.  
Direct Submission  
Submitted (22-APR-2005) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: zfish-help@sanger.ac.uk  
On Apr 23, 2005 this sequence version replaced gi:62318113.  
----- Genome Center  
Center: Wellcome Trust Sanger Institute  
Center code: SC  
Web site: <http://www.sanger.ac.uk>  
Contact: zfish-help@sanger.ac.uk  
-----

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.

The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em., EMBL; Sw., SWISSPROT; Tr., TREMBL; Wp., WORMPEP; Information on the WORMPEP database can be found at

[http://www.sanger.ac.uk/Projects/C\\_elegans/wormpep](http://www.sanger.ac.uk/Projects/C_elegans/wormpep) Clone-derived zebrafish pUC subclones occasionally display inconsistency over the length of mononucleotide A/T runs and conserved TA repeats. Where this is found the longest good quality representation will be

submitted.

Repeat names beginning 'Dr' were identified by the Recon repeat discovery system (Zhirong Bao and Sean Eddy, submitted), and those beginning 'drr' were identified by Rick Waterman (Stephen Johnson lab, WashU). For further information see

[http://www.sanger.ac.uk/Projects/D\\_rexio/fishmask.shtml](http://www.sanger.ac.uk/Projects/D_rexio/fishmask.shtml) CH211-229D2 is from a CHOR1-211 BAC library

VECTOR: PTARBAC2.1.

Location/Qualifiers

1. 167536

/organism="Danio rerio"

/mol\_type="genomic DNA"

/db\_xref="taxon:7955"

/clone="CH211-229D2"

/clone\_lib="CHOR1-211"

# ORIGIN

Query Match 3.6%; Score 20; DB 5; Length 167536;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 215 TGATTGTAATGTTTAGAA 234

Db 2754 TGATTGTAATGTTTAGAA 2773

## RESULT 36

AC044907/c

LOCUS

Homo sapiens chromosome 15, clone RP11-127P21, complete sequence.

AC044907

VERSION

AC044907.16 GI:17223375

KEYWORDS

HTG.

SOURCE

Homo sapiens

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

REFERENCE

AUTHORS

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae; Homo.  
1 (bases 1 to 170793)  
Birren, B., Linton, L., Nussbaum, C. and Lander, E.  
Homo sapiens chromosome 15, clone RP11-127P21  
Unpublished  
2 (bases 1 to 170793)  
Birren, B., Linton, L., Nussbaum, C., Lander, E., Abraham, H., Allen, N., Anderson, S., Baldwin, D., Barna, N., Bastien, V., Beda, F., Boguslavsky, L., Boukhalter, B., Brown, A., Burkett, G., Campoliano, A., Castle, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Domino, M., Doyle, M., Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Halford, A., Horton, L., Howland, J. C., Iliev, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., Labroque, K., Lamazares, R., Landers, T., Lechoczny, J., Levine, R., Lieu, C., Liu, G., Locke, K., Macdonald, P., Marcini, N., McCarthy, M., McEwan, P., McGurk, A., McKernan, K., McPheters, R., McDermid, J., Menais, L., Milnova, T., Miranda, C., Mlenga, V., Morrow, J., Murphy, T., Naylor, J., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neil, D., Oliver, T. M., Oliver, J., Peterson, K., Pierre, N., Pisanic, C., Pollara, V., Raymond, C., Riley, R., Rogov, P., Rothman, D., Roy, A., Santos, R., Schauer, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Tajamas, J., Teefaye, S., Theodore, D., Tittell, A., Travers, M., Triggillo, D., Vassiliev, H., Vael, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W. J., Young, G., Zainoun, J., Zimmer, A. and Zody, W.

Direct Submission

Submitted (12-APR-2000) Whitehead Institute/MIT Center for Genome

Research, 320 Charles Street, Cambridge, MA 02141, USA

3 (bases 1 to 170793)

Birren, B., Linton, L., Nussbaum, C., Lander, E., Ali, A., Allen, N.,

Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhalter, B.,

Brown, A., Camarata, J., Campoliano, A., Chang, J., Chazaro, B.,

Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cook, A.,

Cooke, P., Dearellano, K., Dewar, K., Diaz, J. S., Dodge, S., Fato, S.,



Ferreira, P., Fitzhugh, W., Gage, D., Galagan, J., Gardyna, S., Ginde, S., Gord, S., Goyette, M., Graham, L., Grand-Pierre, N., Hagos, B., Heatford, A., Horton, L., Hulme, W., Iliev, I., Johnson, R., Jones, C., Kamat, A., Karatas, A., Kells, C., Iakocque, K., Iamazares, R., Landers, T., Lehoczy, J., Levine, R., Liu, G., Maclean, C., Macdonald, P., Major, J., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McKernan, K., McSheehy, R., Meldrum, J., Menais, L., Mihova, T., Mlenga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C. H., O'Connor, T., O'Donnell, P., O'Neill, D., Oliver, J., Peterson, K., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R., Rieback, M., Riley, R., Rhee, C., Rogov, P., Roman, J., Rosetti, M., Roy, A., Santos, R., Schauer, S., Schupbach, R., Seaman, S., Severy, P., Spencer, B., Strange-Thomann, N., Stojanovic, N., Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J., Topham, K., Travers, M., Travis, N., Triggillo, J., Vassiliev, H., Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W., Young, G., Zainoun, J., Zembek, L., Zimmer, A. and Zody, W.

# TITLE JOURNAL

## COMMENT

Submitted (01-DEC-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA  
On Dec 1, 2001 this sequence version replaced gi:17149778.  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

## Genome Center

Center: Whitehead Institute/ MIT Center for Genome Research

Center code: WIBC

Web site: <http://www-seq.wi.mit.edu>

Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)

## Project Information

Center project name: 19680

Center clone name: 127\_F\_21

## Location/Qualifiers

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/chromosome="15"  
/map="15"  
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/clone\_lib="RP11-127F21 Human Male BAC"  
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complement(361..657)  
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complement(671..968)  
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1158..1204  
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1251..1278  
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1322..1340  
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complement(1970..2260)

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8602..8911  
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9484..9583  
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10522..10758  
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/rpt\_family="AluY"  
16206..16514  
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                    /rpt family="MIR"
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Query Match      3.6%; Score 20; DB 8; Length 170793;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      170 ATCAATTAATCTCCAAAT 189
Db      33487 ATCAATTAATCTCCAAAT 33468

RESULT 37
AC108733
LOCUS      Homo sapiens 3 BAC RP11-789F5 (Roswell Park Cancer Institute Human
DEFINITION      BAC library) complete sequence.
ACCESSION      AC108733
VERSION      AC108733.4 GI:19774328
KEYWORDS      HTG.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Hominidae; Homo.
1 (bases 1 to 171184)
Muzny,D.M., Adams,C., Adio-Odoola,B., Ali-osman,F.R., Allen,C.,
Aisbrooke,S.L., Amarantunga,H.C., Are,J.R., Ayale,M., Banks,T.,
Barbataia,J., Benton,J., Bimaga,K., Blankenburg,K., Bonnin,D.,
Bouch,J., Bowie,S., Brieva,M., Brown,B., Brown,M., Bryant,N.P.,
Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
Carroll,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
Chen,G., Chen,R., Chen,Z., Chowdhury,I., Christopoulos,C.,
Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
Deunhaey,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.,
Donthaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
Gabisel,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
Gorell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
Hernandez,J., Hernandez,O., Hodgson,A., Hognes,M., Holloway,C.,
Hollins,B., Homai,F., Howard,S., Huber,J., Huiyk,S., Hune,J.,
Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
Joudan,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korah,J.,
Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
Lewis,L., Li,J., Li,Z., Licharge,O., Lieu,C., Liu,J., Liu,W.,
Loulleged,H., Lozada,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
Me,J., Maheswari,M., Mapa,P., Martin,R., Matindale,A.,
Martinez,B., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,N., Neal,D.,
Nelson,D., Newton,J., Moorish,T., Morris,S., Moser,N., Neal,D.,
Nickerson,E., Nwokenko,S., Ogun,M., Okunnu,G., Oregunye,N.,
Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Peters,L.,
Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Saverly,G., Scherer,S.,
Scott,G., Shen,H., Shooshbari,N., Sisson,I., Sodergren,E.,
Sonakke,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Sytek,A.,
Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Taney,J., Taylor,C.,
Taylor,T., Telifrod,B., Thomas,N., Thomas,S., Usmani,K., Vaequez,L.,
Vera,V., Villalón,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
Warren,R., Washington,C., Wallington,S., Williams,G.,
Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstein,G. and

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TITLE      Gibbs,R.
JOURNAL    Direct Submission
REFERENCE  Unpublished
AUTHORS    2 (bases 1 to 171184)
TITLE      Worley,K.C.
JOURNAL    Direct Submission
AUTHORS    Submitted (31-JAN-2002) Human Genome Sequencing Center, Department
TITLE      of Molecular and Human Genetics, Baylor College of Medicine, One
JOURNAL    Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 171184)
AUTHORS    Worley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (28-FEB-2002) Human Genome Sequencing Center, Department
AUTHORS    of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE      Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 171184)
AUTHORS    Worley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (28-MAR-2002) Human Genome Sequencing Center, Department
AUTHORS    of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE      Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 171184)
AUTHORS    Worley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (28-JUN-2002) Human Genome Sequencing Center, Department
AUTHORS    of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE      Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 171184)
AUTHORS    Worley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (29-AUG-2002) Human Genome Sequencing Center, Department
AUTHORS    of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE      Baylor Plaza, Houston, TX 77030, USA
7 (bases 1 to 171184)
AUTHORS    Worley,K.C.
TITLE      Direct Submission
JOURNAL    Submitted (01-MAR-2003) Human Genome Sequencing Center, Department
AUTHORS    of Molecular and Human Genetics, Baylor College of Medicine, One
TITLE      Baylor Plaza, Houston, TX 77030, USA
On Mar 28, 2002 this sequence version replaced gi:18860637.
COMMENT    INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
          gc-help@bcm.tmc.edu

```

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

#### ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base







from more than one subclone; and the assembly was confirmed by restriction digest.

**MAPPING INFORMATION:**

Mapping information for this clone was provided by Dr. Wes Warren, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu>

**SOURCE INFORMATION:**

The RPT-24 BAC Library has been constructed by Pieter de Jong and coworkers (<http://www.chori.org>) from male C57BL/6J mouse spleen and/or brain genomic DNA. The clone and detailed information can be obtained from Pieter de Jong and coworkers at <http://www.chori.org>

**NEIGHBORING SEQUENCE INFORMATION:**

This sequence is the entire insert of the clone.

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1801..1918
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Query Match 3.6%; Score 20; DB 9; Length 171403;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 39
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LOCUS ALJ59853 173031 bp DNA linear PRI 18-MAY-2005
DEFINITION Human DNA sequence from clone Rpl1-12M5 on chromosome 1. Contains
five novel genes and a CpG island, complete sequence.
ACCESSION ALJ59853 AC026028
VERSION ALJ59853.18 GI:12331075
KEYWORDS HTG; CpG island.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
Homnidae; Homo
1 (bases 1 to 173031)
REFERENCE 1
AUTHORS Coville,G.
TITLE Direct Submission
JOURNAL Submitted (13-MAY-2005) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries: vegas@sanger.ac.uk
COMMENT Clone requests: clonerequest@sanger.ac.uk
On or before May 15, 2001 this sequence version replaced
GI:10989878, GI:12191378.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sw: SWISSPROT; Tr: TREMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C_elegans/wormpep
This sequence
was generated from part of bacterial clone configs of human
chromosome 1, constructed by the Sanger Centre Chromosome 1 Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/Chr1
Rpl1-12M5 is from the library RPCT-11.1 constructed by the group of
Pleier de Jong. For further details see
http://www.chori.org/bacpac/home.htm
VECTOR: pBACe3.6
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: vegas@sanger.ac.uk
-----
Draft Sequence Produced by Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
http://genome.wustl.edu/gsc/index.shtml
This sequence was finished as follows unless otherwise noted: all
regions were either double-stranded or sequenced with an alternate
chemistry or covered by high quality data (i.e., phred quality >=
30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by at least
one subclone; and the assembly was confirmed by restriction digest
except on the rare occasion of the clone being a YAC.
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1. 173031
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/clone_1fb="RPCT-11.1"
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/note="Clone_left_end: Rpl1-12M5"
7154. 7191
/note="Sequence confirmed by AC026028. Sequenced by
WJGSC."
7192. 7251
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WJGSC."
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/locus_tag="RP11-12M5.1-001"
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Em:A1954798.1 Em:A1954834.1 Em:AW291932.1 Em:BG723880.1
Em:BX094624.1
match: CDNA5: Em:BC033359.1"
join(35315..35399,35661..36003)
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/locus_tag="RP11-12M5.1-002"
/product="novel transcript"
/note="match: ESTs: Em:A1041258.1"
35975..35980
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/locus_tag="RP11-12M5.1-002"
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join(36469..36729,101104..101194,105416..105437,
106382..106496,107085..109504)
/gene="RP11-12M5.2"
/locus_tag="RP11-12M5.2-001"
join(36469..36729,101104..101194,105416..105437,
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SPFYRTADAPVWNGSGGERLSPAFYYKEGPPSLKLAPOSYPVTWPGSGREAFVME
RAISTDV"
109478..109483
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               /complement(109506..109511)
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gene          /complement(join(122915..123137,129301..129430))
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gene          /complement(join(133273..140134,140841..140942,
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               Em:BF992387.1 Em:BQ183378.1 Em:BQ447883.1
               match: CDNA: Em:AF464140.1"
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               /locus_tag="RP11-12M5.5-001"
polyA_signal  /complement(133288..133293)
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polyA_signal  /complement(133295..133300)
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polyA_signal  /complement(134221)
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polyA_site    /complement(134225)
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               /locus_tag="RP11-12M5.5-001"
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Query Match 3.6%; Score 20; DB 8; Length 173031;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 270 AGTAGCTGAGCTTCTACTG 289
Db 160751 AGTAGCTGAGCTTCTACTG 160732

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RESULT 40
AC090226

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LOCUS AC090226 173602 bp DNA linear PRI 28-NOV-2001
DEFINITION Homo sapiens chromosome 18, clone RP11-723020, complete sequence.
ACCESSION AC090226
VERSION AC090226.3 GI:17047144
KEYWORDS HTS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
  Bkaryote: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
  Hominiidae; Homo.
  1 (bases 1 to 173602)
  Homo sapiens chromosome 18, clone RP11-723020
  Unpublished
  2 (bases 1 to 173602)
  Birren,B., Linton,L., Nusbaum,C., Lander,E., Allen,N., Anderson,S.,
  Camarata,N., Bastien,V., Boguslavsky,L., Boukhalter,B., Brown,A.,
  Camarata,J., Campopiano,A., Choepel,Y., Colangelo,M., Collins,S.,
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  Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (17-FEB-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 173602)
  Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
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  Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G.,
  Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (28-NOV-2001) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Nov 22, 2001 this sequence version replaced gi:13940676.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu

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Contact: sequence\_submissions@genome.wi.mit.edu  
 -----Project Information  
 Center project name: LI2268  
 Center clone name: 723\_D\_20  
 -----Location/Qualifiers

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 repeat\_region complement(28988..29392)  
 /rpt\_family="L1"  
 29672..29799  
 /rpt\_family="MIR"  
 repeat\_region 31253..31575  
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 repeat\_region complement(31590..31897)  
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 repeat\_region 31900..31942  
 /rpt\_family="MLT1A1"  
 31943..32116  
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 complement(32520..33064)  
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 repeat\_region 33894..35193  
 /rpt\_family="HERVL"  
 complement(36003..36109)  
 /rpt\_family="LTR33"  
 repeat\_region 36500..36864  
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 repeat\_region 37146..37367  
 /rpt\_family="LTR33"  
 repeat\_region complement(37368..37653)

Query Match 3.6% Score 20; DB 8; Length 173602;  
 Best Local Similarity 100.0%; Pred.No.21;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 392 ATAAATTCAGAAATTCAGAA 411  
 |||  
 DB 113547 ATAAATTCAGAAATTCAGAA 113566

Search completed: April 11, 2006, 18:07:41  
 Job time : 3515.08 secs



GenCore version 5.1.7  
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OM nucleic - nucleic search, using sw model

Run on: April 11, 2006, 14:24:17 ; Search time 780.231 Seconds  
(without alignments)  
4783.489 Million cell updates/sec

Title: US-10-712-654-34

Perfect score: 560

Sequence: 1 acaactggtacatctgcgcg.....ggagcaatgagattacacg 560

Scoring table: OLIGO\_NUC

Gapop 60.0 , Gapext 60.0

Searched: 4996997 seqs, 3332346308 residues

Word size: 1

Total number of hits satisfying chosen parameters: 9993364

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :

N Geneseq\_21:\*

1: geneseqn1980s:\*  
2: geneseqn1990s:\*  
3: geneseqn2000s:\*  
4: geneseqn2001as:\*  
5: geneseqn2001bs:\*  
6: geneseqn2002as:\*  
7: geneseqn2002bs:\*  
8: geneseqn2003as:\*  
9: geneseqn2003bs:\*  
10: geneseqn2003cs:\*  
11: geneseqn2003ds:\*  
12: geneseqn2004as:\*  
13: geneseqn2004bs:\*  
14: geneseqn2005s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	560	100.0	560	13 ADR48536	Adt48536 capB targ
2	112	20.0	112	13 ADR48527	Adt48527 capB targ
3	56	10.0	56	13 ADR48528	Adt48528 capB targ
4	32	5.7	32	8 ADR48513	Adt48513 capB prob
5	30	5.4	30	8 ACC71903	Acc71903 B. anthra
6	29	5.2	29	10 ADF44860	Adf44860 Internal
7	29	5.2	29	13 ADR48515	Adt48515 capB prob
8	29	5.2	29	13 ADR48512	Adt48512 capB prob
9	29	5.2	29	13 ADR48513	Adt48513 capB prob
10	27	4.8	27	13 ADR48514	Adt48514 capB prob
11	27	4.8	27	13 ADR48511	Adt48511 capB prob
12	27	4.8	27	13 ADR48516	Adt48516 capB prob
13	26	4.6	26	8 ACC71914	Acc71914 B. anthra
14	25	4.5	25	8 ACC71913	Acc71913 B. anthra
15	24	4.3	24	10 ADF44858	Adf44858 Internal
16	23	4.1	23	10 ADF44859	Adf44859 Internal
17	20	3.6	33226	13 ADM03357	Adm03357 CYP 3A7 g
18	20	3.6	123785	10 ABX77171	Abx77171 DNA seque
19	19	3.4	555	8 ACA24403	ACA24403 Prokaryot

20	19	3.4	1004	13 ADX36536	Adx36536 Plant ful
21	19	3.4	1092	13 ADX28662	Adx28662 Plant ful
22	19	3.4	1776	4 AAK94697	AAK94697 Human ful
23	19	3.4	1776	12 ADL31687	ADL31687 Full leng
24	19	3.4	1863	10 ADH84577	Adh84577 Enterococ
25	19	3.4	1914	10 ADF83696	Adf83696 1914bp hu
26	19	3.4	2301	13 ADS48807	Ads48807 Bacterial
27	19	3.4	3028	12 ADG67450	Adg67450 Novel hum
28	19	3.4	4661	13 ADR24156	Adr24156 Breast ca
29	19	3.4	4661	14 ADZ22652	Adz22652 Neoblasto
30	19	3.4	4748	4 ABA07182	AbA07182 Human pan
31	19	3.4	4748	4 AAK89814	AAK89814 Human dig
32	19	3.4	4748	12 ADJ87640	Adj87640 Nervous s
33	19	3.4	4959	10 ADF83694	Adf83694 4959bp hu
34	19	3.4	10093	4 AAS3890	Aas3890 Human car
35	19	3.4	10093	4 ABA07184	AbA07184 Human pan
36	19	3.4	10093	4 AAK89816	AAK89816 Human dig
37	19	3.4	10093	10 ADE46584	Ade46584 Human car
38	19	3.4	10093	13 ADJ08002	Adj08002 Human car
39	19	3.4	10872	6 ABK31389	AbK31389 Signal tr
40	19	3.4	10872	6 ABL70336	AbL70336 Chemicali
41	19	3.4	10872	6 AAS61289	Aas61289 Human gen
42	19	3.4	32768	2 AAX13336	Aax13336 Enterococ
43	19	3.4	32768	6 ABS99131	Abs99131 Enterococ
44	18	3.2	18	8 ACC71902	Acc71902 B. anthra
45	18	3.2	433	4 AAI91808	Aai91808 Human pol
46	18	3.2	687	4 AAD38768	Aad38768 Murine ep
47	18	3.2	687	6 AAD38769	Aad38769 Human eph
48	18	3.2	697	6 ABQ44024	Abq44024 Oligonuc1
49	18	3.2	697	6 ABQ44025	Abq44025 Oligonuc1
50	18	3.2	849	6 ABQ38270	Abq38270 Oligonuc1
51	18	3.2	849	6 ABQ38271	Abq38271 Oligonuc1
52	18	3.2	866	6 ABQ39566	Abq39566 Oligonuc1
53	18	3.2	866	6 ABQ39567	Abq39567 Oligonuc1
54	18	3.2	1002	2 AAQ99288	Aaq99288 Human LER
55	18	3.2	1002	6 ABV78142	Abv78142 Human DNA
56	18	3.2	1002	6 ABZ35718	Abz35718 Human pol
57	18	3.2	1002	6 ABX09961	Abx09961 Human DNA
58	18	3.2	1002	6 ABX16833	Abx16833 Human pol
59	18	3.2	1002	8 ABX12670	Abx12670 CDNA enco
60	18	3.2	1024	8 ABZ34652	Abz34652 Coding se
61	18	3.2	1042	12 ADJ42339	Adj42339 Plant CDN
62	18	3.2	1051	2 AAT18395	Aat18395 Receptor
63	18	3.2	1051	2 AAT42594	Aat42594 Coding se
64	18	3.2	1051	2 AAT51236	Aat51236 Receptor
65	18	3.2	1188	8 ACA50619	Aca50619 Prokaryot
66	18	3.2	1240	2 AAT40230	Aat40230 Mouse Bph
67	18	3.2	1306	13 ADX36486	Adx36486 Plant ful
68	18	3.2	1823	10 ADP89043	Adp89043 Encoding
69	18	3.2	1953	2 AAT16471	Aat16471 Human hep
70	18	3.2	1953	14 ADV73183	Adv73183 Human col
71	18	3.2	1977	3 AAA51346	Aaa51346 Ephrin-B2
72	18	3.2	2000	6 ABZ17087	Abz17087 Arabidops
73	18	3.2	2337	6 ABN85768	Abn85768 Arabidops
74	18	3.2	2407	6 AAD20952	Aad20952 Rice isop
75	18	3.2	2407	6 ABQ78638	Abq78638 Nucleotid
76	18	3.2	2611	8 ABX12545	Abx12545 CDNA enco
77	18	3.2	2857	4 AAH18005	Aah18005 Human CDN
78	18	3.2	2898	8 ABX12544	Abx12544 CDNA enco
79	18	3.2	2902	6 AAD27895	Aad27895 Human eph
80	18	3.2	2902	8 ABZ34866	Abz34866 Coding se
81	18	3.2	2902	8 ABZ34727	Abz34727 Coding se
82	18	3.2	2902	12 ADN03885	Adn03885 Antipsoxi
83	18	3.2	2902	12 ADP26755	Adp26755 Human Eph
84	18	3.2	2902	13 ADR67183	Adr67183 Human bla
85	18	3.2	3550	4 ABL05222	AbL05222 Drosophi1
86	18	3.2	4335	13 ADR86704	Adr86704 Human Eph
87	18	3.2	4335	13 ADR82651	Adr82651 Human Eph
88	18	3.2	4342	2 AAT16470	Aat16470 Murine he
89	18	3.2	4380	12 ADN03883	Adn03883 Antipsoxi
90	18	3.2	4440	5 ABV25160	Abv25160 Human pro
91	18	3.2	4484	12 ADQ25375	Adq25375 Human sof
92	18	3.2	10515	6 ABK10772	Abk10772 Human sma



c	93	18	3.2	11964	6	ABQ67026	AbQ67026 Human ang	166	17	3.0	741	4	AAD06206	Aad06206 S. aureus
c	94	18	3.2	25003	5	ABA19679	AbA19679 Human nei	167	17	3.0	741	8	ACA19895	AcA19895 Prokaryot
c	95	18	3.2	32205	4	AAS29831	AaA29831 Human cyt	168	17	3.0	741	14	ADW94350	AdW94350 Prolifera
c	96	18	3.2	32205	4	AAS33426	AaA33426 DNA encod	169	17	3.0	750	4	AAK58052	AaK58052 Human imm
c	97	18	3.2	39969	4	AAK85853	AaA85853 Human imm	c	170	3.0	751	8	ABZ18371	AbZ18371 Group III
c	98	18	3.2	40681	6	ABA92787	Continuation (7 of	c	171	3.0	803	3	AAH07988	AaH07988 Human CDN
c	99	18	3.2	43948	13	ADR86703	AdR86703 Human Eph	c	172	3.0	829	12	ACH87263	AcH87263 Human gen
c	100	18	3.2	43948	13	ADR86703	AdR86703 Human Eph	c	173	3.0	829	5	AAI58750	AaI58750 Human poi
c	101	18	3.2	47513	4	AAK74979	AaK74979 Human imm	c	174	3.0	829	5	ADO98970	AdO98970 DNA encod
c	102	18	3.2	49000	12	ADP26762	AdP26762 Human Eph	c	175	3.0	829	5	ADB48730	AbD48730 Novel hum
c	103	18	3.2	94000	12	ADP08387	AdP08387 Human gly	c	176	3.0	855	13	ADX09767	AdX09767 Plant ful
c	104	18	3.2	110000	6	ABA92787	Continuation (6 of	c	177	3.0	858	5	AAH67237	AaH67237 C. glutami
c	105	18	3.2	110000	12	ADN46845	Continuation (3 of	c	178	3.0	858	8	ACA00707	AcA00707 C. glutam
c	106	18	3.2	110000	12	ADN47591	Continuation (19 o	c	179	3.0	886	12	ADL12541	AdL12541 Human ste
c	107	18	3.2	110000	12	ADN46123	Continuation (3 of	c	180	3.0	929	8	ADL12541	AdL12541 Human ste
c	108	18	3.2	110000	12	ADN47209	Continuation (19 o	c	181	3.0	929	4	AAH52933	AaH52933 Enterococ
c	109	18	3.2	110000	12	ADN46464	Continuation (19 o	c	182	3.0	951	10	ADH84308	AdH84308 Enterococ
c	110	18	3.2	110000	12	ADN47960	Continuation (19 o	c	183	3.0	973	13	ADX30084	AdX30084 Plant ful
c	111	18	3.2	117829	12	ADO97319	AdO97319 Human can	c	184	3.0	974	13	ADX46261	AdX46261 Plant ful
c	112	18	3.2	321491	11	ACN44202	AdC44202 Human gen	c	185	3.0	1006	5	AAH71459	AaH71459 DNA encod
c	113	17	3.0	20	12	ADL58099	AdL58099 Human ESM	c	186	3.0	1008	5	AAH65563	AaH65563 DNA encod
c	114	17	3.0	20	12	ADL58193	AdL58193 Human ESM	c	187	3.0	1047	4	AAH41117	AaH41117 CDNA encod
c	115	17	3.0	20	12	ADL58555	AdL58555 Human ESM	c	188	3.0	1074	6	AAH67345	AaH67345 C. glutami
c	116	17	3.0	20	12	ADL58250	AdL58250 Human ESM	c	189	3.0	1113	5	AAH67866	AaH67866 Corynebact
c	117	17	3.0	100	10	ABX61314	AbX61314 Arabidops	c	190	3.0	1170	4	AAH67866	AaH67866 Corynebact
c	118	17	3.0	123	4	AAH51099	AaH51099 Staphyloc	c	191	3.0	1181	6	ABZ11370	AbZ11370 Human poi
c	119	17	3.0	123	4	AAH51071	AaH51071 Staphyloc	c	192	3.0	1181	12	ADM43888	AdM43888 Novel hum
c	120	17	3.0	123	4	AAH51100	AaH51100 Staphyloc	c	193	3.0	1236	2	AAZ31091	AdZ31091 Nucleotid
c	121	17	3.0	123	4	AAH51102	AaH51102 Staphyloc	c	194	3.0	1243	11	ADL65586	AdL65586 C. glutam
c	122	17	3.0	123	8	ACA18306	AcA18306 Prokaryot	c	195	3.0	1248	8	ACF73745	AcF73745 Staphyloc
c	123	17	3.0	123	8	ACA18290	AcA18290 Prokaryot	c	196	3.0	1271	2	AAH34991	AaH34991 Vasculat
c	124	17	3.0	123	8	ACA18264	AcA18264 Prokaryot	c	197	3.0	1271	14	ADY91216	AdY91216 Human Vas
c	125	17	3.0	123	8	ACA18302	AcA18302 Prokaryot	c	198	3.0	1320	6	ACF72839	AcF72839 Staphyloc
c	126	17	3.0	125	10	ADG25938	AdG25938 Human gen	c	199	3.0	1335	6	ABA00639	AbA00639 Human pro
c	127	17	3.0	133	2	AAH23659	AaH23659 Human gen	c	200	3.0	1364	8	AEQ82906	AdE82906 Human lun
c	128	17	3.0	193	2	AAV76646	AdV76646 Staphyloc	c	201	3.0	1366	12	ADN05244	AdN05244 Antiporot
c	129	17	3.0	201	6	ABZ12232	AbZ12232 Arabidops	c	202	3.0	1366	12	ADN05949	AdN05949 Novel bro
c	130	17	3.0	248	12	ACH82332	AcH82332 Human gen	c	203	3.0	1467	14	ADY18455	AdY18455 DNA encod
c	131	17	3.0	263	4	AAH49743	AaH49743 Staphyloc	c	204	3.0	1467	11	ACN23889	AcN23889 Breast ca
c	132	17	3.0	263	4	AAH49713	AaH49713 Staphyloc	c	205	3.0	1469	11	ACN23889	AcN23889 Breast ca
c	133	17	3.0	263	8	ACA16981	AcA16981 Prokaryot	c	206	3.0	1506	10	ADB69813	AdB69813 C. neofo
c	134	17	3.0	263	8	ACA16989	AcA16989 Prokaryot	c	207	3.0	1551	6	AAH51081	AaH51081 Arabidops
c	135	17	3.0	286	3	ABO31666	AbO31666 Plant mic	c	208	3.0	1551	6	ABA95252	AbA95252 C. glutam
c	136	17	3.0	318	6	ABO98735	AbO98735 Human ORF	c	209	3.0	1553	6	ABR34638	AbR34638 Human CDN
c	137	17	3.0	340	2	AAH27973	AaH27973 Hepatitis	c	210	3.0	1555	3	AAH40208	AaH40208 Arabidops
c	138	17	3.0	368	9	AAH96240	AaH96240 Human bon	c	211	3.0	1577	13	ADT15195	AdT15195 Plant CDN
c	139	17	3.0	384	9	ACH21321	AcH21321 Human adu	c	212	3.0	1743	12	ADH61844	AdH61844 Transcrip
c	140	17	3.0	390	5	AAH71456	AaH71456 DNA encod	c	213	3.0	1816	10	ADB69452	AdB69452 C. neofo
c	141	17	3.0	422	4	AAH49886	AaH49886 Staphyloc	c	214	3.0	1854	13	ADT05337	AdT05337 Haemophil
c	142	17	3.0	422	8	ACA17140	AcA17140 Prokaryot	c	215	3.0	1916	12	ADQ24056	AdQ24056 Human bof
c	143	17	3.0	468	9	ACCT3002	AcC3002 Cat. filea	c	216	3.0	1937	2	AAH34869	AaH34869 DNA encod
c	144	17	3.0	468	12	ADL09645	AdL09645 Cat. filea	c	217	3.0	1937	9	ACD28104	AdC28104 Ubiquitin
c	145	17	3.0	474	6	AAH28245	AaH28245 Human pan	c	218	3.0	1939	9	ACD27731	AdC27731 Human CDN
c	146	17	3.0	500	6	ABH71886	AbH71886 Human pan	c	219	3.0	1944	4	AAI60536	AaI60536 Human poi
c	147	17	3.0	502	8	ACA04688	AcA04688 CDNA encod	c	220	3.0	1953	10	ADB47506	AdB47506 Human CDN
c	148	17	3.0	552	4	AAH80552	AaH80552 Receptor	c	221	3.0	1978	9	ACD28101	AdC28101 Ubiquitin
c	149	17	3.0	558	2	AAH78769	AaH78769 Human NCE	c	222	3.0	1980	10	ADP00291	AdP00291 Bacteriat
c	150	17	3.0	562	5	AAH65120	AaH65120 DNA encod	c	223	3.0	2000	8	ADH74129	AdH74129 Rice gene
c	151	17	3.0	590	12	AAH99138	AaH99138 Human gen	c	224	3.0	2000	10	ADH74129	AdH74129 Rice gene
c	152	17	3.0	595	10	ACH68632	AcH68632 Human gen	c	225	3.0	2001	14	ADZ45141	AdZ45141 Human cho
c	153	17	3.0	595	12	ACH68632	AcH68632 Human gen	c	226	3.0	2001	14	ADZ45143	AdZ45143 Human cho
c	154	17	3.0	631	6	ABH62995	AbH62995 Rat sequ	c	227	3.0	2001	14	ADZ45143	AdZ45143 Human cho
c	155	17	3.0	631	10	ADH57073	AdH57073 Toxicity	c	228	3.0	2001	14	ADZ45143	AdZ45143 Human cho
c	156	17	3.0	631	10	ADH57073	AdH57073 Toxicity	c	229	3.0	2006	6	ABH57941	AbH57941 Human end
c	157	17	3.0	631	10	ADH57073	AdH57073 Toxicity	c	230	3.0	2006	6	ABH57941	AbH57941 Human end
c	158	17	3.0	693	13	AAH46336	AaH46336 Arabidops	c	231	3.0	2006	11	ADH08781	AdH08781 Angiogene
c	159	17	3.0	693	13	AAH46336	AaH46336 Arabidops	c	232	3.0	2006	11	ADH08781	AdH08781 Angiogene
c	160	17	3.0	738	4	AAH51824	AaH51824 Human sec	c	233	3.0	2006	11	ADH08781	AdH08781 Angiogene
c	161	17	3.0	738	4	AAH51824	AaH51824 Human sec	c	234	3.0	2006	11	ADH08781	AdH08781 Angiogene
c	162	17	3.0	741	4	AAH4685	AaH4685 Staphyloc	c	235	3.0	2017	12	ADM24879	AdM24879 Human end
c	163	17	3.0	741	4	AAH4685	AaH4685 Staphyloc	c	236	3.0	2019	12	ADL59759	AdL59759 Human end
c	164	17	3.0	741	4	AAH55365	AaH55365 Staphyloc	c	237	3.0	2019	14	ADY61838	AdY61838 Breast ca
c	165	17	3.0	741	4	AAH55365	AaH55365 Staphyloc	c	238	3.0	2040	7	ADW41959	AdW41959 Human xlev



239	17	3.0	2276	3	AAc60011	Human	sec	312	17	3.0	55875	12	ADQ59503	Adg59503	Human	can
240	17	3.0	2276	8	ADa98026	Human	sec	313	17	3.0	62713	14	ADZ13880	Adz13880	Murine	ca
241	17	3.0	2276	8	ADa39233	Human	sec	314	17	3.0	69611	11	ACN45102	Acn45102	Human	gen
242	17	3.0	2276	10	ADC20183	Human	sec	315	17	3.0	94672	11	ACN44560	Acn44560	Mouse	gen
243	17	3.0	2276	10	ADP10613	Human	sec	316	17	3.0	96593	11	ADL27166	Adl27166	Human	gen
244	17	3.0	2319	8	ABZ35851	Human	sec	317	17	3.0	96595	9	ADA03068	Ada03068	Human	ppp
245	17	3.0	2347	10	ADC30575	Human	sec	317	17	3.0	96595	10	ADB72806	Adb72806	Human	ppp
246	17	3.0	2615	2	AAZ42217	Human	nov	318	17	3.0	96596	9	ADA02864	Ada02864	Human	itp
247	17	3.0	2796	4	ABL02516	Drosophill	nor	319	17	3.0	96596	9	ADAB6352	Ada66352	Human	ppp
248	17	3.0	2856	9	ADA28754	Drosophill	encod	320	17	3.0	96596	10	ADB72602	Adb72602	Human	ppp
249	17	3.0	2971	4	AAH15091	Human	cdN	321	17	3.0	96596	10	ADGC5343	Adc5343	Mouse	itp
250	17	3.0	2985	6	ABN59981	Human	nov	322	17	3.0	96596	10	ADM74459	Adm74459	Human	cat
251	17	3.0	3156	10	ADB69091	Novel	hum	323	17	3.0	96596	12	ADQ79403	Adq79403	KJRA0783	cat
252	17	3.0	3159	5	AA593543	DNA	encod	324	17	3.0	98300	12	AAT42063	Aat42063	12	o
253	17	3.0	3195	14	ADW94120	Staphyloc		325	17	3.0	110000	2	AA199682	AA199682	17	o
254	17	3.0	3231	10	ADC08228	Rice	DNA	326	17	3.0	110000	4	AA199682	AA199682	13	o
255	17	3.0	3234	4	AA159851	Human	pol	327	17	3.0	110000	4	AA199682	AA199682	13	o
256	17	3.0	3234	4	AA159852	Human	pol	328	17	3.0	110000	4	AA199682	AA199682	28	o
257	17	3.0	3247	2	AAAX20656	Polynucle		329	17	3.0	110000	4	AA199682	AA199682	12	o
258	17	3.0	3342	10	ADC08140	Rice	DNA	330	17	3.0	110000	4	AA199682	AA199682	13	o
259	17	3.0	3405	6	ADG688132	Adg688132	A. thalia	331	17	3.0	110000	4	AA199682	AA199682	13	o
260	17	3.0	3918	10	ADG25966	INP1NCH0		332	17	3.0	110000	5	AAFA84800	Aafa84800	28	o
261	17	3.0	4001	8	ADNA20411	Prostate		333	17	3.0	110000	6	ABR42787	ABR42787	1	o
262	17	3.0	4001	8	ADNA4218	Human	ren	334	17	3.0	110000	11	ACNA45090	ACNA45090	2	o
263	17	3.0	4183	12	ADJ57462	Breast	ca	335	17	3.0	110000	12	ADQ34927	ADQ34927	1	o
264	17	3.0	4260	13	AA592663	Bacterial		336	17	3.0	110000	14	ADZ45062	ADZ45062	04	o
265	17	3.0	4280	2	AAV74392	Staphyloc		337	17	3.0	110000	14	ADZ46976	ADZ46976	1	o
266	17	3.0	4371	5	AA593544	DNA	encod	338	17	3.0	110000	14	ABE39175	ABE39175	21	o
267	17	3.0	4371	12	ADJ57488	Human	pol	339	17	3.0	110000	14	ABR42787	ABR42787	07	o
268	17	3.0	4410	4	ABL22703	Drosophill		340	17	3.0	112418	13	ABD32927	ABD32927	8	o
269	17	3.0	4782	13	ADU47046	Mouse	can	341	17	3.0	121129	13	ABD33446	ABD33446	Murine	ca
270	17	3.0	5051	13	ABD32826	Mouse	can	342	17	3.0	134442	13	ABD32824	ABD32824	Mouse	can
271	17	3.0	5066	12	ADL82030	Human	ER+	343	17	3.0	134465	14	ABE35713	ABE35713	L. pneumo	
272	17	3.0	5109	13	ADU47050	Human	ER+	344	17	3.0	177556	14	ABE71426	ABE71426	Human	sgc
273	17	3.0	5473	14	ADW94119	Staphyloc		345	17	3.0	177563	9	ACD828257	ACD828257	Mouse	sol
274	17	3.0	5893	13	ABD32825	Chemical	can	346	17	3.0	263853	14	ABE39171	ABE39171	L. pneumo	
275	17	3.0	6033	6	AA563337	Staphyloc		347	17	3.0	301477	11	ABD33362	ABD33362	Human	can
276	17	3.0	6251	2	AAV74336	DNA	encod	348	17	3.0	321491	13	ACNA44202	ACNA44202	Human	gen
277	17	3.0	6450	5	AA593545	DNA	encod	349	17	3.0	325791	5	AA543104	AA543104	Human	Oes
278	17	3.0	6450	12	ADJ57487	Human	pol	350	17	3.0	349980	13	AA66531	AA66531	C. glutrami	
279	17	3.0	6577	4	ABL22702	Drosophill		351	17	3.0	349980	13	ADT05649	ADT05649	Haemophil	
280	17	3.0	6577	4	ABL17410	Drosophill		352	17	2.9	20	12	ADL58030	ADL58030	Human	ESM
281	17	3.0	7598	14	ADW94118	Staphyloc		353	17	2.9	20	12	ADL58037	ADL58037	Human	ESM
282	17	3.0	7749	6	ABL70435	Chemical		354	17	2.9	26	12	ADQ31362	ADQ31362	Human	tra
283	17	3.0	8033	2	AA113058	Enterococ		355	17	2.9	30	8	ABZ70624	ABZ70624	Plasmid	p
284	17	3.0	8033	6	AB598853	Enterococ		356	17	2.9	33	6	AB557048	AB557048	Human	nat
285	17	3.0	9096	2	AA1788015	Human	int	357	17	2.9	40	8	ABT17495	ABT17495	Human	sel
286	17	3.0	9253	5	ABAI15922	Human	ner	358	17	2.9	60	6	ABN47471	ABN47471	Human	spl
287	17	3.0	9253	5	ABAI15922	Human	ner	359	17	2.9	151	12	ACH85864	ACH85864	Human	gen
288	17	3.0	10663	5	ABAI18961	Human	ner	360	17	2.9	152	12	ACH88828	ACH88828	Human	gen
289	17	3.0	10663	5	ABAI18961	Human	ner	361	17	2.9	158	3	AAO05090	AAO05090	Human	sec
290	17	3.0	10899	4	AA103656	Drosophill		362	17	2.9	195	6	ABN90940	ABN90940	Staphyloc	
291	17	3.0	12810	3	AA195272	Zmetsa	me	363	17	2.9	202	2	ABT69648	ABT69648	Amplifica	
292	17	3.0	13480	4	ABL03944	Drosophill		364	17	2.9	211	2	AAZ52988	AAZ52988	Human	pro
293	17	3.0	13521	4	ABL19270	Drosophill		365	17	2.9	219	2	AAQ37002	AAQ37002	CAT	1-73
294	17	3.0	15505	4	ABL19268	Drosophill		366	17	2.9	225	2	AAK10983	AAK10983	Human	bia
295	17	3.0	15505	4	ABL19268	Drosophill		367	17	2.9	226	2	AAO03560	AAO03560	Restricti	
296	17	3.0	15649	6	ABL70543	Chemical		368	17	2.9	227	6	ABK16025	ABK16025	Human	lum
297	17	3.0	17213	6	ABJ33483	Human	imm	369	17	2.9	227	10	ADB95288	ADB95288	Human	lum
298	17	3.0	18512	6	ABJ32976	Human	imm	370	17	2.9	227	10	ADB95288	ADB95288	Human	lum
299	17	3.0	23695	6	ABG66982	Human	ang	371	17	2.9	238	6	ABZ15108	ABZ15108	Arabidops	
300	17	3.0	28118	10	ADBA3798	Polymorph		372	17	2.9	249	2	AAK13801	AAK13801	Human	col
301	17	3.0	28118	10	ADBA3798	Polymorph		373	17	2.9	249	2	AAK13801	AAK13801	Human	col
302	17	3.0	28118	12	ADH54276	Human	TNF	374	17	2.9	257	2	AAK11906	AAK11906	Enterococ	
303	17	3.0	28118	12	ADH54276	Human	TNF	375	17	2.9	257	2	AAK11906	AAK11906	Enterococ	
304	17	3.0	31680	9	ACD19229	E. coli	0	376	17	2.9	294	6	ABN90897	ABN90897	Staphyloc	
305	17	3.0	34148	10	ADC00969	Enterohaie		377	17	2.9	294	10	ABX87658	ABX87658	Corn ear-	
306	17	3.0	36976	13	ABD32930	Human	can	378	17	2.9	300	3	AAAO1009	AAAO1009	Human	col
307	17	3.0	43672	11	ACN44452	Mouse	gen	379	17	2.9	302	4	AAAO1009	AAAO1009	Human	col
308	17	3.0	45121	10	ADAO2744	Human	TNF	380	17	2.9	302	11	ADJ09565	ADJ09565	DNA	encod
309	17	3.0	45121	10	ADAO2744	Human	TNF	381	17	2.9	307	5	AAAO1009	AAAO1009	Human	pro
310	17	3.0	45121	12	ADM74339	Human	cat	382	17	2.9	307	11	ADJ09565	ADJ09565	DNA	encod
311	17	3.0	45154	14	ADZ12594	Human	can	383	17	2.9	307	11	ADJ09565	ADJ09565	DNA	encod
312	17	3.0	46107	4	AAK711730	Human	imm	384	17	2.9	315	6	ABN67546	ABN67546	Streptoco	



385	16	2.9	316	5	ABAI1535	Abai1535 Human ner	458	16	2.9	531	13	ACN59829	ACN59829 Cotton gy
386	16	2.9	324	5	AAS67496	Aae67496 DNA encod	C 459	16	2.9	538	4	AAK89773	AAK89773 Human dig
387	16	2.9	329	6	ABV86873	ABv86873 Human col	C 460	16	2.9	538	4	AAK89774	AAK89774 Human dig
C 388	16	2.9	330	6	ABV88851	ABv88851 Human col	C 461	16	2.9	538	4	AAS25077	AAS25077 Human ova
389	16	2.9	341	10	ADJ37827	Adj37827 Rat etrok	C 462	16	2.9	538	5	AAH83722	AAH83722 Human ova
C 390	16	2.9	341	12	ADJ30615	Adj30615 Rat etrok	C 463	16	2.9	543	12	ACH72108	ACH72108 Human gen
C 391	16	2.9	349	2	AAO60980	Aae60980 Human bra	C 464	16	2.9	543	13	ADT90536	ADT90536 Human gen
C 392	16	2.9	350	4	AAI84591	AAi84591 Human pol	C 465	16	2.9	548	6	AAK65636	AAK65636 Human imm
393	16	2.9	351	10	ADH82796	ADh82796 Enterococ	C 466	16	2.9	548	6	ABZ82572	ABZ82572 Human sec
C 394	16	2.9	361	5	ABAI1515	ABai1515 Human ner	C 467	16	2.9	550	6	AAK88106	AAK88106 Human dig
C 395	16	2.9	361	14	ADY61261	ADy61261 Gene trap	C 468	16	2.9	561	6	ABK30710	ABK30710 Plant dwa
396	16	2.9	373	5	ABVI0856	ABvi0856 Human pro	C 469	16	2.9	564	4	AAK92673	AAK92673 Human CDN
C 397	16	2.9	375	14	ABE90063	ABe90063 Isolated	C 470	16	2.9	564	12	ADL29100	ADL29100 3' end of
C 398	16	2.9	378	4	AAK86508	AAk86508 Human imm	C 471	16	2.9	564	13	ADU12685	ADu12685 Solid tum
C 399	16	2.9	378	8	ABX40744	ABx40744 Bovine ES	C 472	16	2.9	564	14	ADX16743	ADx16743 Human can
C 400	16	2.9	385	6	ABK63228	ABk63228 Rat seque	C 473	16	2.9	567	12	ACH87252	ACH87252 Human gen
C 401	16	2.9	385	11	ADW22076	ADw22076 Rat hepat	C 474	16	2.9	569	12	ACH80220	ACH80220 Human gen
C 402	16	2.9	388	5	ABV23117	ABv23117 Human pro	C 475	16	2.9	573	4	AAK92711	AAK92711 Human CDN
C 403	16	2.9	388	5	AAK95540	AAk95540 Human neu	C 476	16	2.9	573	12	ADL29138	ADL29138 3' end of
C 404	16	2.9	390	4	AAK64071	AAk64071 Human imm	C 477	16	2.9	584	13	ADR64790	ADR64790 Cotton cd
C 405	16	2.9	395	6	ABJ37831	ABj37831 Human col	C 478	16	2.9	584	13	ACH75128	ACH75128 Human gen
C 406	16	2.9	396	2	AAQ03563	AAq03563 Sequence	C 479	16	2.9	587	12	ACH75128	ACH75128 Human gen
C 407	16	2.9	400	5	ABV14087	ABv14087 Human pro	C 480	16	2.9	590	12	ACH76435	ACH76435 Human gen
C 408	16	2.9	400	5	ABV32012	ABv32012 Human pro	C 481	16	2.9	593	4	AAK94013	AAK94013 Human CDN
C 409	16	2.9	401	4	AAK95540	AAk95540 Human neu	C 482	16	2.9	593	12	ADL30440	ADL30440 3' end of
C 410	16	2.9	401	4	AAK97033	AAk97033 Human neu	C 483	16	2.9	595	4	AAK80553	AAK80553 Receptor
C 411	16	2.9	401	6	ABT00310	ABt00310 Human neu	C 484	16	2.9	596	13	ACN54889	ACN54889 Cotton an
C 412	16	2.9	401	6	ABT01803	ABt01803 Human neu	C 485	16	2.9	601	14	ABE33753	ABE33753 Human DNA
C 413	16	2.9	402	11	ADW70629	ADw70629 Human neu	C 486	16	2.9	601	14	ABE33956	ABE33956 Human DNA
C 414	16	2.9	402	4	AAAD13497	AAad13497 Human par	C 487	16	2.9	608	13	ACN60627	ACN60627 Cotton gy
C 415	16	2.9	405	5	AAS71671	AAs71671 DNA encod	C 488	16	2.9	614	3	AAAC08827	AAc08827 Human sec
C 416	16	2.9	405	14	ADW06112	ADw06112 Human gen	C 489	16	2.9	615	13	ADOS1693	ADos1693 Novel can
C 417	16	2.9	407	5	ABY04918	ABy04918 Human pro	C 490	16	2.9	618	4	AAH53395	AAH53395 S. epider
C 418	16	2.9	414	2	AAAT61810	AAa61810 TV RNA se	C 491	16	2.9	631	13	ADQ79266	ADq79266 Novel can
C 419	16	2.9	415	4	AAAS30345	AAa30345 DNA encod	C 492	16	2.9	635	8	ABQ82876	ABQ82876 Human lun
C 420	16	2.9	415	4	AAAL02133	AAa102133 Human rep	C 493	16	2.9	642	11	ABD16936	ABD16936 Pseudomon
C 421	16	2.9	418	14	ADV74926	ADv74926 Human col	C 494	16	2.9	645	13	ADSO0960	ADs00960 Stephyloc
C 422	16	2.9	422	6	AAI87211	AAi87211 Human pol	C 495	16	2.9	654	3	AAAC0245	AAa0245 Arabidops
C 423	16	2.9	427	6	ABN78948	ABn78948 Human nuc	C 496	16	2.9	657	2	AAO15266	AAo15266 SP-C from
C 424	16	2.9	434	6	ABO80502	ABo80502 Human leu	C 497	16	2.9	657	2	AAO49262	AAo49262 Vector de
C 425	16	2.9	435	8	ACP72366	ACP72366 Stephyloc	C 498	16	2.9	658	10	ABL61148	ABl61148 CAT repor
C 426	16	2.9	444	11	ADT97115	ADt97115 Colton can	C 499	16	2.9	658	10	ADP79371	ADp79371 Chloromph
C 427	16	2.9	444	11	ADX43597	ADx43597 Human CDN	C 500	16	2.9	660	13	ADY03530	ADy03530 Histidine
C 428	16	2.9	446	5	ABY44030	ABy44030 Human pro	C 501	16	2.9	660	12	AAH02154	AAH02154 Escherich
C 429	16	2.9	446	5	ABY35189	ABy35189 Human pro	C 502	16	2.9	660	12	ADQ36313	ADq36313 Intreacell
C 430	16	2.9	453	4	AAK54064	AAK54064 Murine tr	C 503	16	2.9	660	14	ADZ39850	ADz39850 Chloromph
C 431	16	2.9	453	6	ABQ58127	ABq58127 Human col	C 504	16	2.9	662	11	AAAN90107	AAa90107 Sequence
C 432	16	2.9	458	4	AAK88848	AAk88848 Human dig	C 505	16	2.9	662	11	ACN83326	ACN83326 Breast ca
C 433	16	2.9	460	5	ABV45852	ABv45852 Human pro	C 506	16	2.9	663	11	ACN83326	ACN83326 Breast ca
C 434	16	2.9	460	5	ABY09637	ABy09637 Human pro	C 507	16	2.9	666	5	AAAS75826	AAa575826 DNA encod
C 435	16	2.9	461	5	ABY39780	ABv39780 Human pro	C 508	16	2.9	666	5	AAAS6578	AAa65578 DNA encod
C 436	16	2.9	461	5	ABV30812	ABv30812 Human pro	C 509	16	2.9	666	6	ABO65866	ABo65866 Arabidops
C 437	16	2.9	463	4	AAI92079	AAi92079 Human pol	C 510	16	2.9	672	2	AAQ72700	AAq72700 pGm/B.9 t
C 438	16	2.9	465	8	ABO82875	ABo82875 Human lun	C 511	16	2.9	679	2	AAQ62055	AAq62055 Chloromph
C 439	16	2.9	468	8	ACF74042	ACf74042 Stephyloc	C 512	16	2.9	679	2	AAQ62056	AAq62056 Chloromph
C 440	16	2.9	471	4	AAK02082	AAk02082 Human bra	C 513	16	2.9	690	5	AAAS71500	AAa71500 DNA encod
C 441	16	2.9	471	4	ABS27104	ABs27104 Human liv	C 514	16	2.9	695	13	ADSO9908	ADs09908 Human the
C 442	16	2.9	480	8	ACA28407	ACa28407 Prokaryot	C 515	16	2.9	702	13	ADR92288	ADR92288 Novel S.
C 443	16	2.9	481	10	ADBS5967	ADb55967 Toxicity-	C 516	16	2.9	702	14	ABAS6158	ABa6158 streptoco
C 444	16	2.9	481	13	ADV40679	ADv40679 Rat cardl	C 517	16	2.9	703	13	ADDB82670	ADd82670 Human CDN
C 445	16	2.9	482	6	ABZ08466	ABz08466 Human leu	C 518	16	2.9	703	12	ADQ02103	ADq02103 Human sof
C 446	16	2.9	491	5	ACH48340	ACH48340 Human lun	C 519	16	2.9	703	13	ADR25925	ADR25925 Breast ca
C 447	16	2.9	495	5	ABV57245	ABv57245 Human pro	C 520	16	2.9	703	14	ADY61876	ADy61876 Human gen
C 448	16	2.9	496	5	AAST7936	AAst7936 DNA encod	C 521	16	2.9	720	2	ADR02097	ADR02097 A. gossyp
C 449	16	2.9	497	2	AAQ72699	AAq72699 pGm/B.14	C 522	16	2.9	722	13	ADR64791	ADR64791 Cotton CD
C 450	16	2.9	501	13	ACF88829	ACf88829 Human SIR	C 523	16	2.9	723	2	AAAN90100	AAa90100 as sequen
C 451	16	2.9	503	12	ABK43697	ABk43697 DNA encod	C 524	16	2.9	723	2	AAQ03557	AAq03557 Sequence
C 452	16	2.9	503	12	ADIS4084	ADi54084 CDNA enco	C 525	16	2.9	725	4	AAAS27288	AAa27288 CDNA enco
C 453	16	2.9	511	9	ACH36869	ACH36869 Human end	C 526	16	2.9	735	10	ADB93466	ADB93466 Human CDN
C 454	16	2.9	526	2	AAV27228	AAv27228 Hela gene	C 527	16	2.9	736	11	AAAC43928	AAc43928 Arabidops
C 455	16	2.9	526	2	AAH43146	AAh43146 seqLPD#60	C 528	16	2.9	745	11	ADJ31197	ADj31197 Human CDN
C 456	16	2.9	526	11	ACN88034	ACn88034 Breast ca	C 529	16	2.9	745	13	ADSB3264	ADsB3264 Human lym
C 457	16	2.9	526	13	ACN55647	ACn55647 Cotton an	C 530	16	2.9	746	2	AAK77360	AAK77360 Polynucle



531	16	2.9	746	3	AAAG0392	AAAG0392	Chloramph
532	16	2.9	747	10	ADH83043	ADH83043	Enterococ
533	16	2.9	754	4	AAD13499	Aad13499	Human CUB
534	16	2.9	754	4	AAD13498	Aad13498	Human CUB
535	16	2.9	754	13	ADS09909	Ads09909	Human the
536	16	2.9	755	2	AAZ31078	Aaz31078	Nucleotid
537	16	2.9	755	4	AAH07325	Aah07325	Human CDN
538	16	2.9	759	8	ACA47297	Ac447297	Prokaryot
539	16	2.9	760	10	ADF55570	Adf55570	Cell-free
540	16	2.9	760	10	ADU66013	Adj66013	CAT prote
541	16	2.9	762	13	ADU41912	Adt41912	Bacterial
542	16	2.9	763	2	AAZ34458	Aaz34458	DNA encod
543	16	2.9	763	2	AAZ31408	Aaz31408	N-termina
544	16	2.9	763	10	AAD62887	Aad62887	Streptococ
545	16	2.9	763	12	ADRI0812	Adr10812	CdPa sero
546	16	2.9	768	11	ACH96281	Ach96281	Klebslell
547	16	2.9	772	6	ABL90355	Ab190355	Human pol
548	16	2.9	772	10	ADH28918	Adh28918	Human chr
549	16	2.9	781	2	AAV13116	Aav13116	Transposo
550	16	2.9	781	3	AAZ33902	Aaz33902	Chloramph
551	16	2.9	781	4	AAH26981	Aah26981	Chloramph
552	16	2.9	781	6	ABO89730	Ab089730	Human pro
553	16	2.9	782	2	AAQ92253	Aaq92253	Donor vec
554	16	2.9	789	9	ADA29069	Ada29069	DNA encod
555	16	2.9	800	1	AAAN90101	Aan90101	ss DNA in
556	16	2.9	801	5	AAAS79598	Aas79598	DNA encod
557	16	2.9	803	2	AAQ15265	Aaq15265	SP-C from
558	16	2.9	814	10	ADG32998	Adg32998	Human DNA
559	16	2.9	818	2	AAV75053	Aav75053	Staphyloc
560	16	2.9	825	2	ADRO1833	Adr01833	A. gossyp
561	16	2.9	828	13	ADK45171	Adk45171	Streptococ
562	16	2.9	829	10	ADF74847	Adf74847	Murine NO
563	16	2.9	829	10	ADF74833	Adf74833	Murine NO
564	16	2.9	833	4	AAH07421	Aah07421	Human CDN
565	16	2.9	848	2	AAQ03565	Aaq03565	SP-C expr
566	16	2.9	855	5	AAAS88738	Aas88738	DNA encod
567	16	2.9	863	4	AAI17359	Aai17359	Human bre
568	16	2.9	865	4	AAH08536	Aah08536	Human CDN
569	16	2.9	882	8	ADA69701	Ada69701	Rice gene
570	16	2.9	882	11	ABDI6885	Abdi6885	Pseudomon
571	16	2.9	882	11	ACT26716	Act26716	Rice abio
572	16	2.9	900	10	ADC92700	Adc92700	E. faeciu
573	16	2.9	930	10	ACF67751	Acf67751	Phototrab
574	16	2.9	945	14	ADY30142	Ady30142	DNA seque
575	16	2.9	948	4	AAAS26182	Aas26182	Human CDN
576	16	2.9	948	8	ABX73523	Abx73523	Human nov
577	16	2.9	961	4	AAAS77442	Aas77442	DNA encod
578	16	2.9	962	4	AAH51000	Aah51000	Human ngr
579	16	2.9	962	6	ABS70233	Ab570233	DNA encod
580	16	2.9	963	8	ABX05453	Abx05453	Human nov
581	16	2.9	974	2	AAQ03564	Aaq03564	SP-B expr
582	16	2.9	981	4	AAI93357	Aai93357	Human pol
583	16	2.9	986	5	ABV26156	Abv26156	Human pro
584	16	2.9	986	5	ABV20324	Abv20324	Human pro
585	16	2.9	1002	5	AAAS82394	Aas82394	DNA encod
586	16	2.9	1002	10	ADCS91488	Adc91488	E. faeciu
587	16	2.9	1041	12	ADK16074	Adk16074	Nanoarcha
588	16	2.9	1044	5	AAAS91786	Aas91786	Arabidops
589	16	2.9	1055	12	ADO80244	Ado80244	Arabidops
590	16	2.9	1056	5	AAAS90840	Aas90840	DNA encod
591	16	2.9	1086	5	AAAS88715	Aas88715	DNA encod
592	16	2.9	1086	5	AAAS85860	Aas85860	DNA encod
593	16	2.9	1086	5	AAAS77622	Aas77622	Prokaryot
594	16	2.9	1098	8	ACA47381	Ac447381	Prokaryot
595	16	2.9	1106	6	AAAS62554	Aas62554	DNA seque
596	16	2.9	1108	6	AAAD33708	Aad33708	Human sec
597	16	2.9	1113	1	AAAN80481	Aan80481	XhoI/XbaI
598	16	2.9	1118	6	AAAS92020	Aas92020	DNA encod
599	16	2.9	1118	6	ABZ70799	Abz70799	Human gon
600	16	2.9	1118	13	ADW21238	Adw21238	Human gon
601	16	2.9	1125	3	AAAS97356	Aas97356	Human col
602	16	2.9	1125	4	AAH53084	Aah53084	S. epider
603	16	2.9	1125	5	AAAS68472	Aas68472	DNA encod
604	16	2.9	1125	10	ADFA8039	Adfa8039	DNA encod
605	16	2.9	1129	2	AAZ34456	Aaz34456	DNA encod
606	16	2.9	1129	2	AAZ31406	Aaz31406	N-termina
607	16	2.9	1129	10	AAD62885	Aad62885	Streptococ
608	16	2.9	1139	12	ADRI0810	Adr10810	CdPa sero
609	16	2.9	1137	12	ADN59026	Adn59026	Novel B c
610	16	2.9	1138	4	AAH51012	Aah51012	Human ngr
611	16	2.9	1138	6	ABH70245	Abh70245	DNA encod
612	16	2.9	1162	14	ADM88785	Adm88785	PA2 promo
613	16	2.9	1162	14	ADW97839	Adw97839	Plasmid p
614	16	2.9	1163	5	ABAI2188	Abai2188	Human ner
615	16	2.9	1170	3	AAAG6504	Aag6504	DNA encod
616	16	2.9	1172	5	AAAS77423	Aas77423	DNA encod
617	16	2.9	1179	8	ACRA29175	Acra29175	Prokaryot
618	16	2.9	1188	13	ADT77871	Adt77871	Regulator
619	16	2.9	1191	12	ADN02068	Adn02068	mlc mutan
620	16	2.9	1194	6	ABN91804	Abn91804	Staphyloc
621	16	2.9	1194	13	ADSO2106	Adso2106	Staphyloc
622	16	2.9	1221	1	AAAN8153	Aan81153	XhoI/XbaI
623	16	2.9	1221	5	AAAS76539	Aas76539	DNA encod
624	16	2.9	1233	5	AAAS88288	Aas88288	DNA encod
625	16	2.9	1242	2	AAZ31084	Aaz31084	Nucleotid
626	16	2.9	1245	5	AAAS92782	Aas92782	DNA encod
627	16	2.9	1247	5	AAAF28561	Aaf28561	DNA fragm
628	16	2.9	1254	10	ACPF58169	Acf58169	Modified
629	16	2.9	1270	12	ADN59036	Adn59036	Novel B c
630	16	2.9	1275	8	AAZ31085	Aaz31085	Nucleotid
631	16	2.9	1275	8	ACF74154	Acf74154	Staphyloc
632	16	2.9	1278	13	ADU80746	Adu80746	Staphyloc
633	16	2.9	1278	13	ADU80744	Adu80744	Staphyloc
634	16	2.9	1284	2	AAZ31081	Aaz31081	Nucleotid
635	16	2.9	1284	5	AAAS89838	Aas89838	DNA encod
636	16	2.9	1295	2	AAZ31077	Aaz31077	Nucleotid
637	16	2.9	1297	4	AAAS27292	Aas27292	DNA encod
638	16	2.9	1297	10	ADB93470	Adb93470	Human CDN
639	16	2.9	1314	5	AAAS74865	Aas74865	DNA encod
640	16	2.9	1317	11	ABDI6744	Abdi6744	Pseudomon
641	16	2.9	1320	12	ADN59031	Adn59031	Novel B c
642	16	2.9	1323	8	ACA38843	Ac38843	Prokaryot
643	16	2.9	1323	12	ADNO4941	Adno4941	Antipior
644	16	2.9	1323	13	ACN39792	Acn39792	Tumour-as
645	16	2.9	1323	14	ADY17691	Ady17691	DNA encod
646	16	2.9	1343	4	AAI04320	Aai04320	Human rep
647	16	2.9	1349	6	AAAI7063	Aai17063	Transposo
648	16	2.9	1350	5	AAAS91602	Aas91602	DNA encod
649	16	2.9	1350	12	ADM76970	Adm76970	GalP-Ptcrc
650	16	2.9	1352	10	ADM76972	Adm76972	GLK-tric D
651	16	2.9	1362	12	ADCS1775	Adcs1775	Cm-resist
652	16	2.9	1371	2	AAAT84188	Aat84188	DNA encod
653	16	2.9	1377	3	AAAC48363	Aac48363	Arabidops
654	16	2.9	1379	3	AAAC35373	Aac35373	Arabidops
655	16	2.9	1381	5	AAAS91492	Aas91492	DNA encod
656	16	2.9	1391	6	ABL89657	Ab189657	Human pol
657	16	2.9	1392	10	ADP74831	Adp74831	Murine NO
658	16	2.9	1392	10	ADP74839	Adp74839	Murine NO
659	16	2.9	1398	4	AAH62717	Aah62717	Shrimp wh
660	16	2.9	1399	10	ADP74835	Adp74835	Murine NO
661	16	2.9	1428	5	AAAS92815	Aas92815	DNA encod
662	16	2.9	1428	5	AAAS92815	Aas92815	DNA encod
663	16	2.9	1413	5	AAAS77551	Aas77551	DNA encod
664	16	2.9	1419	10	ADCS3705	Adcs3705	E. faeciu
665	16	2.9	1428	5	AAAS88734	Aas88734	DNA encod
666	16	2.9	1470	5	AAAS86009	Aas86009	DNA encod
667	16	2.9	1470	5	AAAS77632	Aas77632	DNA encod
668	16	2.9	1476	5	AAAS88739	Aas88739	DNA encod
669	16	2.9	1494	10	ADP74827	Adp74827	Murine NO
670	16	2.9	1494	5	AAAS77624	Aas77624	DNA encod



677	16	2.9	1494	5	AA886001	AA886001 DNA encod	750	16	2.9	1992	5	AA885142	AA885142 DNA encod
678	16	2.9	1494	5	AA888716	AA888716 DNA encod	751	16	2.9	1992	10	ADP44788	ADP44788 De novo s
679	16	2.9	1500	12	AA873346	AA873346 Thale cre	752	16	2.9	1992	10	ADP62886	ADP62886 Streptoco
680	16	2.9	1501	8	ABX34601	ABX34601 Human mod	753	16	2.9	1992	12	ADR10811	ADR10811 CpA sero
681	16	2.9	1503	8	ACA46218	ACA46218 Prokaryot	754	16	2.9	2000	11	ADL37062	ADL37062 Rice stre
682	16	2.9	1529	8	AB270622	AB270622 Plasmid p	755	16	2.9	2000	11	ACL34918	ACL34918 Rice stre
683	16	2.9	1529	8	AB270621	AB270621 Plasmid p	756	16	2.9	2000	12	ADJ41001	ADJ41001 Plant cdn
684	16	2.9	1535	1	AA660260	AA660260 Plasmid p	757	16	2.9	2004	2	AAT51538	AAT51538 Mycobacte
685	16	2.9	1542	1	AA660258	AA660258 Plasmid p	758	16	2.9	2008	6	AAH16499	AAH16499 Human CDN
686	16	2.9	1542	4	AAH16949	AAH16949 Human CDN	759	16	2.9	2010	6	ABA02283	ABA02283 Human DNA
687	16	2.9	1551	4	AA165566	AA165566 Nucleotid	760	16	2.9	2016	5	AA872434	AA872434 DNA encod
688	16	2.9	1551	4	AA165566	AA165566 Nucleotid	761	16	2.9	2017	3	AAA97355	AAA97355 Human col
689	16	2.9	1576	13	ADX14643	ADX14643 Plant ful	762	16	2.9	2017	10	AD848038	AD848038 CA2 DNA
690	16	2.9	1585	13	ADRS9376	ADRS9376 Cotton cu	763	16	2.9	2022	5	AA874778	AA874778 DNA encod
691	16	2.9	1590	5	AA880619	AA880619 DNA encod	764	16	2.9	2073	10	AAU52179	AAU52179 Radish cy
692	16	2.9	1596	10	ACR68564	ACR68564 Phototrab	765	16	2.9	2082	8	ABX63595	ABX63595 Human dia
693	16	2.9	1599	5	AA874854	AA874854 DNA encod	766	16	2.9	2082	13	ACN42317	ACN42317 Drosophili
694	16	2.9	1599	5	AA868220	AA868220 DNA encod	767	16	2.9	2084	4	ABL10239	ABL10239 Thale cre
695	16	2.9	1599	10	ADP50272	ADP50272 Dog flavl	768	16	2.9	2096	13	ADR73377	ADR73377 Yeast sel
696	16	2.9	1606	12	ADQ24563	ADQ24563 Dog wild-	769	16	2.9	2101	13	ADT77978	ADT77978 Yeast sel
697	16	2.9	1620	2	AAZ31964	AAZ31964 S. pneumo	770	16	2.9	2101	13	ADT77978	ADT77978 Yeast sel
698	16	2.9	1626	6	AA877404	AA877404 DNA encod	771	16	2.9	2101	14	ABE16998	ABE16998 Yeast sel
699	16	2.9	1626	6	ABK30789	ABK30789 Plant dwa	772	16	2.9	2103	5	AA889976	AA889976 DNA encod
700	16	2.9	1635	4	ABK30756	ABK30756 Plant dwa	773	16	2.9	2103	5	AA881425	AA881425 DNA encod
701	16	2.9	1635	4	AAH62728	AAH62728 Shrimp wh	774	16	2.9	2106	5	AA889965	AA889965 DNA encod
702	16	2.9	1653	5	AA877420	AA877420 DNA encod	775	16	2.9	2106	6	ABK10700	ABK10700 DNA encod
703	16	2.9	1665	5	ADL45295	ADL45295 Human ova	776	16	2.9	2106	8	ACA50174	ACA50174 Prokaryot
704	16	2.9	1680	5	AA891711	AA891711 DNA encod	777	16	2.9	2106	13	ADT50218	ADT50218 S. pneumo
705	16	2.9	1684	10	ADL24803	ADL24803 Intestina	778	16	2.9	2106	14	ABE91904	ABE91904 DNA encod
706	16	2.9	1686	14	ADV42555	ADV42555 Human psy	779	16	2.9	2109	6	ABK35075	ABK35075 Human CDN
707	16	2.9	1707	12	ADO07867	ADO07867 Human pol	780	16	2.9	2110	8	ACC50155	ACC50155 Breast ca
708	16	2.9	1712	5	AA871512	AA871512 DNA encod	781	16	2.9	2154	5	AA869421	AA869421 DNA encod
709	16	2.9	1719	5	AA890558	AA890558 DNA encod	782	16	2.9	2159	4	AA160601	AA160601 Human pol
710	16	2.9	1722	11	ABD16824	ABD16824 Pseudomon	783	16	2.9	2163	6	ABN67518	ABN67518 Streptoco
711	16	2.9	1745	3	AA873686	AA873686 Arabidops	784	16	2.9	2165	12	ADQ86444	ADQ86444 Human tum
712	16	2.9	1746	2	AAZ31965	AAZ31965 S. pneumo	785	16	2.9	2165	12	ADQ83364	ADQ83364 Human tum
713	16	2.9	1750	6	ABQ75092	ABQ75092 Plasmid p	786	16	2.9	2166	8	ACA50621	ACA50621 Prokaryot
714	16	2.9	1762	13	ADT18357	ADT18357 Plant cdn	787	16	2.9	2167	14	ABE91926	ABE91926 DNA encod
715	16	2.9	1763	3	AA869518	AA869518 Human sec	788	16	2.9	2175	6	ABL64405	ABL64405 Stomach c
716	16	2.9	1763	8	ADN40419	ADN40419 Human sec	789	16	2.9	2175	14	ABE53850	ABE53850 Plasmid p
717	16	2.9	1763	8	ACC50787	ACC50787 Human sec	790	16	2.9	2175	14	ABE53847	ABE53847 Plasmid p
718	16	2.9	1763	8	ABZ71432	ABZ71432 Secreted	791	16	2.9	2177	2	AAZ77489	AAZ77489 Human ova
719	16	2.9	1763	9	ADB91389	ADB91389 Human sec	792	16	2.9	2181	14	ADZ48812	ADZ48812 Insulin s
720	16	2.9	1763	10	ADC73889	ADC73889 Human sec	793	16	2.9	2181	14	ABE53851	ABE53851 Plasmid p
721	16	2.9	1763	10	ADP56585	ADP56585 Gene encod	794	16	2.9	2191	10	ADP44787	ADP44787 De novo s
722	16	2.9	1767	5	AA887797	AA887797 DNA encod	795	16	2.9	2197	4	AAH16465	AAH16465 Human CDN
723	16	2.9	1767	5	AA888753	AA888753 DNA encod	796	16	2.9	2208	11	ADN95564	ADN95564 Human BEC
724	16	2.9	1781	4	ABL22744	ABL22744 Drosophili	797	16	2.9	2208	13	ADR14176	ADR14176 Human NF-
725	16	2.9	1782	13	AD860981	AD860981 Bacterial	798	16	2.9	2208	13	ADP23153	ADP23153 PRO polyp
726	16	2.9	1797	5	AA877665	AA877665 DNA encod	799	16	2.9	2208	14	ADY14445	ADY14445 DNA encod
727	16	2.9	1825	2	AAV54825	AAV54825 TMV repli	800	16	2.9	2208	14	ADY14445	ADY14445 DNA encod
728	16	2.9	1825	2	AAV54825	AAV54825 Replicon	801	16	2.9	2253	12	ADQ86505	ADQ86505 Human tum
729	16	2.9	1833	13	ADX54751	ADX54751 Plant ful	802	16	2.9	2253	12	ADQ84540	ADQ84540 Human tum
730	16	2.9	1846	6	AD44626	AD44626 Gateway t	803	16	2.9	2256	13	ADDS0980	ADDS0980 Bacterial
731	16	2.9	1853	2	AAQ13156	AAQ13156 Self-clea	804	16	2.9	2268	12	ADP07318	ADP07318 Human LOC
732	16	2.9	1864	6	AAQ35079	AAQ35079 GeneHunte	805	16	2.9	2268	13	ADR25777	ADR25777 Breast ca
733	16	2.9	1866	1	AA880482	AA880482 Xhol/XbaI	806	16	2.9	2268	13	ACN93791	ACN93791 Tumour-as
734	16	2.9	1866	1	AA881356	AA881356 Sequence	807	16	2.9	2268	13	ADU46821	ADU46821 Nucleolar
735	16	2.9	1866	1	AA881152	AA881152 XhoI/XbaI	808	16	2.9	2268	13	ADU46821	ADU46821 Nucleolar
736	16	2.9	1866	1	AA880955	AA880955 XhoI/XbaI	809	16	2.9	2268	14	ADY17343	ADY17343 DNA encod
737	16	2.9	1866	1	AA880713	AA880713 Natural r	810	16	2.9	2268	14	ADY61862	ADY61862 Human gen
738	16	2.9	1874	2	AAO87169	AAO87169 Natural r	811	16	2.9	2281	6	ACA03950	ACA03950 CDNA down
739	16	2.9	1883	13	ADT43296	ADT43296 Plant tra	812	16	2.9	2295	4	AAH27573	AAH27573 Human CDN
740	16	2.9	1883	13	ADU77687	ADU77687 Novel DNA	813	16	2.9	2307	12	ADU40194	ADU40194 Plant CDN
741	16	2.9	1906	10	ADP44789	ADP44789 De novo s	814	16	2.9	2319	4	AAH17325	AAH17325 Human ATP
742	16	2.9	1935	5	AA877440	AA877440 DNA encod	815	16	2.9	2319	4	AAH17325	AAH17325 Human ATP
743	16	2.9	1935	5	AA882161	AA882161 DNA encod	816	16	2.9	2346	5	AA877547	AA877547 DNA encod
744	16	2.9	1966	12	ADQ62084	ADQ62084 Transcrip	817	16	2.9	2352	4	AAH19122	AAH19122 Angiogene
745	16	2.9	1986	4	AAH28460	AAH28460 Nucleotid	818	16	2.9	2367	5	ABV28550	ABV28550 Human pro
746	16	2.9	1988	6	AAH24491	AAH24491 Fruit fly	819	16	2.9	2367	5	ABV28713	ABV28713 Human pro
747	16	2.9	1992	2	AAZ34457	AAZ34457 DNA encod	820	16	2.9	2367	5	ABV22725	ABV22725 Human pro
748	16	2.9	1992	2	AAZ31407	AAZ31407 DNA encod	821	16	2.9	2367	5	ABV22882	ABV22882 Human pro
749	16	2.9	1992	3	AA606655	AA606655 Human H81	822	16	2.9	2367	5	ADL62287	ADL62287 Human ova



823	16	2.9	2386	4	AAK74279	Aak74279 Human imm	c 896	16	2.9	3064	14	ADV09403	Adv09403 Plasmid p
824	16	2.9	2388	4	AAK74278	Aak74278 Human imm	c 897	16	2.9	3088	4	ABL19849	Ab119849 Drosophill
825	16	2.9	2394	8	ACC43127	Acc43127 Nucleotid	c 898	16	2.9	3098	3	AAC63962	Aac63962 Methyloph
826	16	2.9	2428	11	ADM03390	Adm03390 Human cDN	c 899	16	2.9	3134	10	ADBS6806	Adbs6806 Human gen
827	16	2.9	2436	5	AAV91158	AAv91158 DNA encod	c 900	16	2.9	3146	11	ADM64637	Adm64637 CDNA sequ
828	16	2.9	2462	2	AAV05102	AAv05102 CDNA of c	c 901	16	2.9	3170	4	AAH15757	Aah15757 Human cDN
829	16	2.9	2480	2	AAZ31966	AAz31966 S. pneumo	c 902	16	2.9	3170	10	ADD18919	Add18919 Human dis
830	16	2.9	2499	5	AA568213	AA568213 DNA encod	c 903	16	2.9	3178	14	ADU92114	Adu92114 Becherich
831	16	2.9	2499	5	AA589952	AA589952 DNA encod	c 904	16	2.9	3181	14	ADU92115	Adu92115 Becherich
832	16	2.9	2501	10	ADB54235	ADB54235 Pretreate	c 905	16	2.9	3187	5	AA572112	Aa572112 DNA encod
833	16	2.9	2501	10	ADB54107	ADB54107 Pretreate	c 906	16	2.9	3198	4	AAH17881	Aah17881 Human cDN
834	16	2.9	2501	10	ADBE84097	Adbe84097 Human lym	c 907	16	2.9	3216	5	AA591100	AA591100 DNA encod
835	16	2.9	2501	10	ADBE84173	Adbe84173 Human lym	c 908	16	2.9	3216	5	AA577626	Aa577626 DNA encod
836	16	2.9	2504	1	AA588792	AA588792 DNA encod	c 909	16	2.9	3216	5	AA571304	Aa571304 DNA encod
837	16	2.9	2504	1	AA560261	AA560261 Plasmid p	c 910	16	2.9	3216	5	AA588722	Aa588722 DNA encod
838	16	2.9	2517	11	ACN91623	Acn91623 Breast ca	c 911	16	2.9	3216	5	AA577389	Aa577389 DNA encod
839	16	2.9	2519	10	ADD22468	Add22468 HLA-B*6 T	c 912	16	2.9	3221	4	AAK94775	Aak94775 Human ful
840	16	2.9	2519	10	AD115984	Ad115984 Human col	c 913	16	2.9	3221	12	ADL11839	Adl11839 Full leng
841	16	2.9	2520	4	AAH34235	AAh34235 Human dit	c 914	16	2.9	3221	14	ADY17920	Ady17920 DNA encod
842	16	2.9	2527	8	ACC46205	Acc46205 Human col	c 915	16	2.9	3225	4	AA572847	Aa572847 EcORI -Hi
843	16	2.9	2528	6	ABK63696	ABk63696 Rat beque	c 916	16	2.9	3225	10	ADB88975	Adb88975 E. coli p
844	16	2.9	2528	10	ADBS8197	Adbs8197 Toxicity-	c 917	16	2.9	3225	12	ADJ33432	Adj33432 EcOR I-Hi
845	16	2.9	2528	10	ADBS8197	Adbs8197 Toxicity-	c 918	16	2.9	3225	5	AA577439	Aa577439 DNA encod
846	16	2.9	2528	10	ABT41904	Abt41904 Toxicity	c 919	16	2.9	3249	2	AAQ71367	Aaq71367 E.coli/S.
847	16	2.9	2528	12	ADP72746	Adp72746 Renal tox	c 920	16	2.9	3253	4	AAH54523	Aah54523 S. epider
848	16	2.9	2528	13	ADVA1005	Adv41005 Rat cardit	c 921	16	2.9	3267	13	ADU49869	Adu49869 Plasmid p
849	16	2.9	2538	5	AA586039	AA586039 DNA encod	c 922	16	2.9	3273	5	AA590355	Aa590355 DNA encod
850	16	2.9	2544	5	AA568223	AA568223 DNA encod	c 923	16	2.9	3288	5	AA585789	Aa585789 DNA encod
851	16	2.9	2559	10	ADCI10039	Adci10039 Human NOV	c 924	16	2.9	3288	5	AA587346	Aa587346 DNA encod
852	16	2.9	2568	12	ADOC3405	Adoc3405 Novel hum	c 925	16	2.9	3288	5	AA577395	Aa577395 DNA encod
853	16	2.9	2571	3	AAAC49894	Aac49894 Arbidops	c 926	16	2.9	3288	5	AA588746	Aa588746 DNA encod
854	16	2.9	2577	2	AAO68672	Aao68672 Partial p	c 927	16	2.9	3288	5	AA586010	Aa586010 DNA encod
855	16	2.9	2589	14	ABBS3852	Abbs3852 Plasmid p	c 928	16	2.9	3295	14	ABBS5419	Abbs5419 Nucleotid
856	16	2.9	2594	4	AAK94300	Aak94300 Human ful	c 929	16	2.9	3317	6	ABZ11660	Abz11660 Human pol
857	16	2.9	2594	6	ABK30920	Abk30920 Plant dwt	c 930	16	2.9	3347	12	ADOC67449	Adoc67449 Human nov
858	16	2.9	2594	6	ABK90887	ABk90887 CDNA enc	c 931	16	2.9	3384	5	AA577630	Aa577630 DNA encod
859	16	2.9	2594	11	ADMS6265	Adms6265 Human ATP	c 932	16	2.9	3384	5	AA577630	Aa577630 DNA encod
860	16	2.9	2594	12	AD130925	Ad130925 Full leng	c 933	16	2.9	3384	5	AA588731	Aa588731 DNA encod
861	16	2.9	2594	14	ADV85872	Adv85872 Human pro	c 934	16	2.9	3390	8	ABX97633	Abx97633 CDNA enc
862	16	2.9	2601	5	AA571636	Aa571636 DNA encod	c 935	16	2.9	3400	7	ADL18593	Adl18593 Plasmid p
863	16	2.9	2615	12	ADQ24157	Adq24157 Human sof	c 936	16	2.9	3414	2	AA580956	Aa580956 Plasmid p
864	16	2.9	2628	5	AA585488	AA585488 DNA encod	c 937	16	2.9	3414	2	AAQ12785	Aaq12785 PD56/RBS
865	16	2.9	2689	4	AAK94740	Aak94740 Human ful	c 938	16	2.9	3414	2	AAQ34609	Aaq34609 Expressio
866	16	2.9	2689	12	AD131770	Ad131770 Full leng	c 939	16	2.9	3415	2	AAQ12784	Aaq12784 PD56/RBS
867	16	2.9	2694	5	AA588785	AA588785 DNA encod	c 940	16	2.9	3415	2	AAQ34608	Aaq34608 Expressio
868	16	2.9	2714	10	ADFA4786	Adfa4786 De novo s	c 941	16	2.9	3416	1	AA580958	Aa580958 Plasmid p
869	16	2.9	2732	8	AAAD5610	AAad5610 Staphyloc	c 942	16	2.9	3416	2	AAQ06302	Aaq06302 Sequence
870	16	2.9	2732	8	ABX95894	ABx95894 Complemen	c 943	16	2.9	3416	2	AAQ12783	Aaq12783 PD56/RBS
871	16	2.9	2732	8	ABX95892	ABx95892 DNA encod	c 944	16	2.9	3416	2	AAQ34607	Aaq34607 Expressio
872	16	2.9	2753	8	ABT42874	ABt42874 Human neu	c 945	16	2.9	3416	13	ADS73676	Ads73676 Vector pb
873	16	2.9	2757	5	AA569873	AA569873 DNA encod	c 946	16	2.9	3420	4	AAH20728	Aah20728 Expressio
874	16	2.9	2758	4	ABL05869	ABl05869 Drosophill	c 947	16	2.9	3420	4	AA563718	Aaf63718 Expressio
875	16	2.9	2774	2	AAZ31959	AAz31959 S. pneumo	c 948	16	2.9	3427	2	AAQ06304	Aaq06304 Sequence
876	16	2.9	2802	4	AAH16052	Aah16052 Human cDN	c 949	16	2.9	3431	10	AD515907	Ad515907 Plasmid p
877	16	2.9	2823	5	AA590026	AA590026 DNA encod	c 950	16	2.9	3433	14	ADM44135	Adm44135 Plasmid p
878	16	2.9	2837	4	AAH43515	AAh43515 CDNA enc	c 951	16	2.9	3440	2	AAQ06303	Aaq06303 Sequence
879	16	2.9	2840	5	AAH41283	Aah41283 Human ATP	c 952	16	2.9	3440	2	AAQ13728	Aaq13728 PD56/RBS
880	16	2.9	2840	6	ABQ54203	ABq54203 Human ova	c 953	16	2.9	3462	4	AAH49175	Aah49175 Human pro
881	16	2.9	2843	5	ADL62269	Adl62269 Human cya	c 954	16	2.9	3462	6	ABA97908	AbA97908 Plasmid p
882	16	2.9	2862	4	ABL17554	ABl17554 Drosophill	c 955	16	2.9	3480	4	AA596011	Aa596011 Expressio
883	16	2.9	2941	8	ACC50156	ACC50156 Breast ca	c 956	16	2.9	3501	4	AAH26920	Aah26920 Human G p
884	16	2.9	2987	8	ABK63590	ABk63590 Human cDN	c 957	16	2.9	3501	5	AA588943	Aa588943 DNA encod
885	16	2.9	2988	12	ADOC67306	Adoc67306 Novel hum	c 958	16	2.9	3519	3	AAA98035	Aaa98035 Expressio
886	16	2.9	2989	12	ADOC63919	Adoc63919 Novel hum	c 959	16	2.9	3529	6	AAAD40165	Aaad40165 pPZHIV1 p
887	16	2.9	2995	3	AAAF16046	AAf16046 Human pro	c 960	16	2.9	3542	5	AAH54388	Aah54388 S. epider
888	16	2.9	3000	8	ACC50319	ACC50319 Breast ca	c 961	16	2.9	3542	5	AA585900	Aa585900 DNA encod
889	16	2.9	3006	6	ABBS7044	ABbs7044 CDNA enc	c 962	16	2.9	3545	4	AAH54785	Aah54785 S. epider
890	16	2.9	3015	13	ADTA7147	Adt47147 Bacterial	c 963	16	2.9	3545	4	ABL06360	Ab106360 Drosophill
891	16	2.9	3023	2	AAV38817	Aav38817 C3 Bindin	c 964	16	2.9	3551	11	ADM01925	Adm01925 Human cDN
892	16	2.9	3026	10	ADBS6296	Adbs6296 Human gen	c 965	16	2.9	3552	4	AA551592	Aa551592 Staphyloc
893	16	2.9	3026	10	ADBS6289	Adbs6289 Human gen	c 966	16	2.9	3555	4	AA527737	Aaf27737 Human tra
894	16	2.9	3031	6	ABK12683	ABk12683 CDNA enc	c 967	16	2.9	3558	3	AAA75006	Aa575006 Nucleotid
895	16	2.9	3053	4	AAH54150	Aah54150 S. epider	c 968	16	2.9	3567	4	AA554390	Aa554390 Staphyloc



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969 16 2.9 3567 8 ACA19944 Acal19944 Prokaryot
970 16 2.9 3567 14 ADW94353 Adw94353 Prolifera
971 16 2.9 3575 4 ABL09719 ABL09719 Drosophill
972 16 2.9 3576 10 ADE53776 ADE53776 Human pro
973 16 2.9 3587 4 ABL04840 ABL04840 Drosophill
974 16 2.9 3643 12 ADP46476 ADP46476 Human col
975 16 2.9 3668 12 ADL61199 ADL61199 Human tyr
976 16 2.9 3668 14 ADY20154 ADY20154 DNA encod
977 16 2.9 3668 14 ADY16262 ADY16262 DNA encod
978 16 2.9 3681 4 ABL06346 ABL06346 Drosophill
979 16 2.9 3693 10 ADE54645 ADE54645 Human gen
980 16 2.9 3693 10 ADD45723 ADD45723 Human gen
981 16 2.9 3693 10 ADE54649 ADE54649 Human gen
982 16 2.9 3717 13 ADRO7007 ADRO7007 Full leng
983 16 2.9 3741 4 ABL05203 ABL05203 Drosophill
984 16 2.9 3770 13 ADR08362 ADR08362 Full leng
985 16 2.9 3792 3 AAC88443 AAC88443 Thiamine
986 16 2.9 3801 12 ADL72227 ADL72227 DNA seque
987 16 2.9 3803 2 AAQ03155 AAQ03155 Phage dis
988 16 2.9 3817 10 ADD14893 ADD14893 Phage dis
989 16 2.9 3818 12 ADM44178 ADM44178 Novel hum
990 16 2.9 3822 2 AAV13171 AAV13171 Complete
991 16 2.9 3833 1 AAN91060 AAN91060 Sequence
992 16 2.9 3840 4 AAH53897 AAH53897 S. epider
993 16 2.9 3861 2 AAV13174 AAV13174 Complete
994 16 2.9 3869 4 AAK79858 AAK79858 Human imm
995 16 2.9 3873 5 ADL63500 ADL63500 Human ova
996 16 2.9 3876 3 AA98037 AA98037 Expressio
997 16 2.9 3876 3 AA98038 AA98038 Expressio
998 16 2.9 3879 3 AA98031 AA98031 Expressio
999 16 2.9 3879 3 AA98016 AA98016 Expressio
1000 16 2.9 3879 3 AAA98036 AAA98036 Expressio

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## ALIGNMENTS

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RESULT 1
ID ADR48536 standard; DNA; 560 BP.
XX
AC ADR48536;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB target sequence #3.
XX
KM Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
XX px01; px02; target sequence; de.
XX
OS Bacillus anthracis.
XX
PN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX PR 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WC;
XX
DR WPI; 2004-604428/58.
XX
XX
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
PS Claim 1; SEQ ID NO 34; 61bp; English.
XX

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The present invention relates to an oligonucleotide of 20-40 nucleotides that specifically hybridizes to a sequence contained in a *Bacillus anthracis* target sequence. The methods and compositions of the present invention are useful for detecting the presence of *Bacillus anthracis* nucleic acid in a sample, in particular for detecting cutaneous and respiratory anthrax infections. Two synthetic genetic target sequences, derived from pagA and capB gene sequences, were synthesized to provide known standards for testing oligonucleotides for detection of the genes carried by the plasmids px01 and px02, without requiring handling of virulent *Bacillus anthracis*. The present sequence represents a capB target sequence.

Sequence 560 BP; 181 A; 89 C; 131 G; 159 T; 0 U; 0 Other;

Query Match 100.0%; Score 560; DB 13; Length 560;

Best Local Similarity 100.0%; Pred. No. 3.7e-270;

Matches 560; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 ACAACTGGTACATCTGCGGATGATATATTTGGTTTACTGACGAGGACCAACGATTAG 60
DB 1 ACAACTGGTACATCTGCGGATGATATATTTGGTTTACTGACGAGGACCAACGATTAG 60
QY 61 CGCCGTAAAGAGGTCTTAATATCGTGAGCAACGCGGTATGTTAAAGAGCTGCTGAT 120
DB 61 CGCCGTAAAGAGGTCTTAATATCGTGAGCAACGCGGTATGTTAAAGAGCTGCTGAT 120
QY 121 TTAGAGCAGAGCACTTATTTGTAATGTATGACGTTCAACCCGATTCAATTAATTC 180
DB 121 TTAGAGCAGAGCACTTATTTGTAATGTATGACGTTCAACCCGATTCAATTAATTC 180
QY 181 TTCCAAATATAATATGATTCAGCAAAATGTTGAGATGTTGTAATGTTTGAAGATCAT 240
DB 181 TTCCAAATATAATATGATTCAGCAAAATGTTGAGATGTTGTAATGTTTGAAGATCAT 240
QY 241 ATGATGTTATGGAACCTCACTTGAAGATGAGTACTGAAGCTTTCACCTGCTACATTCGA 300
DB 241 ATGATGTTATGGAACCTCACTTGAAGATGAGTACTGAAGCTTTCACCTGCTACATTCGA 300
QY 301 TATATGAGCATTTAGTACTATTGAAGATGAATTAATTGATTAAGAGGTTGCA 360
DB 301 TATATGAGCATTTAGTACTATTGAAGATGAATTAATTGATTAAGAGGTTGCA 360
QY 361 GAAGAGAAATATACAAAGATGATTTGGTCCGATTAATTCTAGAAATTCAGAAATTTCTTA 420
DB 361 GAAGAGAAATATACAAAGATGATTTGGTCCGATTAATTCTAGAAATTCAGAAATTTCTTA 420
QY 421 CGAAATTTGATTTACATGCTCTCCAGATTAATGATGCTTGTAGCGGTAGCAAG 480
DB 421 CGAAATTTGATTTACATGCTCTCCAGATTAATGATGCTTGTAGCGGTAGCAAG 480
QY 481 GCTCTGGGATTTGATGAGAAACAGCATTCGCTGGTATGTTGAATGCTCATCCGATCCA 540
DB 481 GCTCTGGGATTTGATGAGAAACAGCATTCGCTGGTATGTTGAATGCTCATCCGATCCA 540
QY 541 GGAGCAATGAGATTACAG 560
DB 541 GGAGCAATGAGATTACAG 560

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RESULT 2
ID ADR48527 standard; DNA; 112 BP.
XX
AC ADR48527;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB target sequence #1.
XX
KM Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
XX px01; px02; target sequence; de.
XX
OS Bacillus anthracis.

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XX	WO2004070001-A2.
PN	
PD	19-AUG-2004.
XX	
PF	12-NOV-2003; 2003WO-US036240.
XX	
PR	15-NOV-2002; 2002US-0426552P.
PR	16-MAY-2003; 2003US-0471082P.
XX	
PA	(GENP-) GEN-PROBE INC.
XX	
PI	Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX	
DR	WPI; 2004-604428/58.
PT	
PT	New oligonucleotides that hybridize specifically to a <i>Bacillus anthracis</i>
PT	sequence, useful for detecting cutaneous and respiratory <i>Bacillus anthracis</i>
PT	infections.
XX	
PS	Claim 1; SEQ ID NO 25; 61pp; English.
XX	
CC	The present invention relates to an oligonucleotide of 20-40 nucleotides
CC	that specifically hybridizes to a sequence contained in a <i>Bacillus</i>
CC	<i>anthracis</i> target sequence. The methods and compositions of the present
CC	invention are useful for detecting the presence of <i>Bacillus anthracis</i>
CC	nucleic acid in a sample, in particular for detecting cutaneous and
CC	respiratory anthrax infections. Two synthetic genetic target sequences,
CC	derived from <i>paga</i> and <i>capB</i> gene sequences, were synthesized to provide
CC	known standards for testing oligonucleotides for detection of the genes
CC	carried by the plasmids <i>pX01</i> and <i>pX02</i> , without requiring handling of
CC	virulent <i>Bacillus anthracis</i> . The present sequence represents a <i>capB</i>
XX	target sequence.
SQ	
SQ	Sequence 112 BP; 33 A; 20 C; 34 G; 25 T; 0 U; 0 Other;
	Query Match 20.0%; Score 112; DB 13; Length 112;
	Best Local Similarity 100.0%; Pred.No. 1.5e-45;
	Matches 112; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	
QY	7 GGTAAATCTGCCCGAATGATATATTGGTTTACTGACGAGACACCGATTAAAGCGCGCT 66
DB	1 GGTAAATCTGCCCGAATGATATATTGGTTTACTGACGAGACACCGATTAAAGCGCGCT 60
QY	67 AAAGAAGGCTCTATATATCGGTGAGCAACGACGAGTAAAGAGGCTGCTG 118
DB	61 AAAGAAGGCTCTATATATCGGTGAGCAACGACGAGTAAAGAGGCTGCTG 112
	RESULT 3
	ADR48528
ID	ADR48528 standard; DNA; 56 BP.
XX	
AC	ADR48528;
XX	
DT	04-NOV-2004 (first entry)
XX	
DE	capB target sequence #2.
XX	
XX	<i>Bacillus anthracis</i> ; cutaneous; respiratory anthrax infection; <i>paga</i> ; <i>capB</i> ;
KW	<i>pX01</i> ; <i>pX02</i> ; target sequence; ds.
XX	
OS	<i>Bacillus anthracis</i> .
XX	
PN	WO2004070001-A2.
XX	
PD	19-AUG-2004.
XX	
PF	12-NOV-2003; 2003WO-US036240.
XX	
PR	15-NOV-2002; 2002US-0426552P.
PR	16-MAY-2003; 2003US-0471082P.
XX	

PA	(GENP-) GEN-PROBE INC.
XX	
PI	Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX	
DR	WPI; 2004-604428/58.
XX	
PT	New oligonucleotides that hybridize specifically to a <i>Bacillus anthracis</i>
PT	sequence, useful for detecting cutaneous and respiratory <i>Bacillus anthracis</i>
PT	infections.
XX	
PS	Claim 1; SEQ ID NO 26; 61pp; English.
XX	
CC	The present invention relates to an oligonucleotide of 20-40 nucleotides
CC	that specifically hybridizes to a sequence contained in a <i>Bacillus</i>
CC	<i>anthracis</i> target sequence. The methods and compositions of the present
CC	invention are useful for detecting the presence of <i>Bacillus anthracis</i>
CC	nucleic acid in a sample, in particular for detecting cutaneous and
CC	respiratory anthrax infections. Two synthetic genetic target sequences,
CC	derived from <i>pagA</i> and <i>capB</i> gene sequences, were synthesized to provide
CC	known standards for testing oligonucleotides for detection of the genes
CC	carried by the plasmids pXOI and pXO2, without requiring handling of
CC	virulent <i>Bacillus anthracis</i> . The present sequence represents a <i>capB</i>
CC	target sequence.
XX	
SO	Sequence 56 BP; 15 A; 12 C; 15 G; 14 T; 0 U; 0 Other;
XX	
Query Match	10.0%; Score 56; DB 13; Length 56;
Best Local Similarity	100.0%; Pred. No. 1.8e-17;
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
OY	505 GCATTCGGTGTATGTAATGCTCATCCGATCCAGATCAGACAAATGAGATTACG 560
DB	1 GCATTCGGTGTATGTAATGCTCATCCGATCCAGATCAGACAAATGAGATTACG 56
XX	
RESULT 4	
ID	ACC71903 standard; DNA; 32 BP.
AC	ACC71903;
XX	
DT	04-AUG-2003 (first entry)
XX	
DE	B. anthracis capB specific probe 1.
XX	
KM	Encapsulation protein B; capB; protective antigen; pagA; lethal factor;
KM	lef; fluorescence resonance energy transfer; FRET; probe; ss.
XX	
OS	<i>Bacillus anthracis</i> .
XX	
PN	EP1304387-A1.
PD	23-APR-2003.
XX	
PF	10-OCT-2002; 2002EP-00022398.
XX	
PR	15-OCT-2001; 2001US-0329826P.
BR	05-FEB-2002; 2002US-00068238.
XX	
PA	(HOFF) ROCHE DIAGNOSTICS GMBH.
PA	(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
PI	Bell CA, Uni JR, Cockerill FR;
XX	
XX	WPI; 2003-450920/43.
XX	
PT	Detecting <i>Bacillus anthracis</i> in a sample by amplifying B. <i>anthracis</i> capB,
PT	pagA and lef nucleic acids followed by hybridization with labeled capB,
PT	pagA and lef probes, and detection by fluorescence resonance energy
PT	transfer.
XX	
XX	Disclosure; Page 3; 31pp; English.
XX	



CC The invention relates to detecting Bacillus anthracis in a biological or  
CC non-biological sample. The method involves (a) amplifying a portion of B.  
CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA)  
CC and/or lethal factor (lef) nucleic acids using specific primers; (b)  
CC contacting the sample with a pair of capB and/or pagA and/or lef probes  
CC labelled with fluorescent moieties; and (c) detecting the presence or  
CC absence of fluorescence resonance energy transfer (FRET) between the  
CC probes. The method is useful for identifying B. anthracis DNA from  
CC specimens for diagnosis of B. anthracis infection and to identifying hoax  
CC cases of B. anthracis. The method can also be used for B. anthracis  
CC efficacy studies or epidemiology studies. The method is rapid, and allows  
CC real-time detection of B. anthracis in a biological sample or in a non-  
CC biological sample. The method is more sensitive and specific than  
CC existing assays. Sequences ACC71903-904 represent B. anthracis capB  
CC specific probes  
CC  
XX  
SQ Sequence 32 BP; 11 A; 7 C; 7 G; 7 T; 0 U; 0 Other;  
Query Match 5.7%; Score 32; DB 8; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 53 CGATTAGCGCGGTAAAGAGGCTCTTAATATC 84  
Db 1 CGATTAGCGCGGTAAAGAGGCTCTTAATATC 32  
RESULT 5  
ACC71904  
ID ACC71904 standard; DNA; 30 BP.  
XX  
AC ACC71904;  
XX  
DT 04-AUG-2003 (first entry)  
XX  
DE B. anthracis capB specific probe 2.  
XX  
KM Encapsulation protein B; capB; protective antigen; pagA; lethal factor;  
KM lef; fluorescence resonance energy transfer; FRET; probe; ss.  
XX  
OS Bacillus anthracis.  
XX  
PN EP1304387-A1.  
XX  
PD 23-APR-2003.  
XX  
PF 10-OCT-2002; 2002EP-00022398.  
XX  
PR 15-OCT-2001; 2001US-0329826P.  
PR 05-FEB-2002; 2002US-00068238.  
XX  
PA (HOPF) ROCHE DIAGNOSTICS GMBH.  
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.  
XX  
PI Bell CA, Uhl JR, Cockerill FR;  
XX  
DR WPI; 2003-450920/43.  
XX  
PT Detecting Bacillus anthracis in a sample by amplifying B. anthracis capB,  
PT pagA and lef nucleic acids followed by hybridization with labelled capB,  
PT pagA and lef probes, and detection by fluorescence resonance energy  
PT transfer.  
XX  
PS Disclosure; Page 3; 31pp; English.  
XX  
CC The invention relates to detecting Bacillus anthracis in a biological or  
CC non-biological sample. The method involves (a) amplifying a portion of B.  
CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA)  
CC and/or lethal factor (lef) nucleic acids using specific primers; (b)  
CC contacting the sample with a pair of capB and/or pagA and/or lef probes  
CC labelled with fluorescent moieties; and (c) detecting the presence or  
CC absence of fluorescence resonance energy transfer (FRET) between the  
CC probes. The method is useful for identifying B. anthracis DNA from

CC specimens for diagnosis of B. anthracis infection and to identifying hoax  
CC cases of B. anthracis. The method can also be used for B. anthracis  
CC efficacy studies or epidemiology studies. The method is rapid, and allows  
CC real-time detection of B. anthracis in a biological sample or in a non-  
CC biological sample. The method is more sensitive and specific than  
CC existing assays. Sequences ACC71903-904 represent B. anthracis capB  
CC specific probes  
CC  
XX  
SQ Sequence 30 BP; 9 A; 4 C; 12 G; 5 T; 0 U; 0 Other;  
Query Match 5.4%; Score 30; DB 8; Length 30;  
Best Local Similarity 100.0%; Pred. No. 0.0002;  
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 86 GTGAGCAACGCGGTAGTTAAAGAGGCTG 115  
Db 1 GTGAGCAACGCGGTAGTTAAAGAGGCTG 30  
RESULT 6  
ADF44860  
ID ADF44860 standard; DNA; 29 BP.  
XX  
AC ADF44860;  
XX  
DT 12-FEB-2004 (first entry)  
XX  
DE Internal positive control related probe BACAPBPIS SEQ ID NO:67.  
XX  
KM Internal positive control; IPC; probe; probe-based nucleic acid; probe;  
KM ss.  
XX  
OS Synthetic.  
XX  
PN WO2003075837-A2.  
XX  
PD 18-SEP-2003.  
XX  
PF 03-MAR-2003; 2003WO-US006347.  
XX  
PR 04-MAR-2002; 2002US-0361455P.  
XX  
PA (USGA) US ARMY MEDICAL RES & MATERIAL COMMAND.  
XX  
PI Hartman LJ, Norwood DA;  
XX  
DR WPI; 2003-756781/71.  
XX  
PT New nucleic acid molecule, useful as internal positive control in probe-  
PT based nucleic acid assay such as TaqMan based assay.  
XX  
PS Example 3; SEQ ID NO 67; 56pp; English.  
XX  
CC The present invention describes an isolated nucleic acid molecule (I)  
CC comprising the 548 base pair (bp) sequence of ADF44842, which is an  
CC internal positive control (IPC) nucleic acid molecule. Also described:  
CC (1) a probe comprising (I) and a label; (2) an assay using the probe; (3)  
CC a kit for a probe-based nucleic acid assay comprising the isolated  
CC nucleic acid molecule (I) packaged with instructions for use; and (4)  
CC making an IPC nucleic acid molecule for a probe-based nucleic acid  
CC molecule assay. The nucleic acid molecule (I) is useful as an IPC in  
CC probe-based nucleic acid assay such as TaqMan (RTM) based assay. The  
CC present sequence is used in the exemplification of the present invention.  
XX  
SQ Sequence 29 BP; 9 A; 4 C; 10 G; 6 T; 0 U; 0 Other;  
Query Match 5.2%; Score 29; DB 10; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.00064;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Gy 476 CAGAGCTCTTGGGATGTGATGAGAAACA 504  
Db 1 CAGAGCTCTTGGGATGTGATGAGAAACA 29



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RESULT 7
ID ADR48515/c
XX ADR48515 standard; DNA; 29 BP.
AC
XX ADR48515;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #5.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
XX pXO1; pXO2; probe; ss.
XX
OS Unidentified.
XX
FN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX WPI; 2004-604428/58.
XX
DR WPI; 2004-604428/58.
XX
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
PS Claim 9; SEQ ID NO 13; 61pp; English.
XX
CC The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXO1 and pXO2, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pXO1 and pXO2 detection kits.
XX
SQ Sequence 29 BP; 10 A; 7 C; 7 G; 5 T; 0 U; 0 Other;
XX
Query Match 5.2%; Score 29; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 505 GCATTCGCGTGTGATGTAATGCTCATCC 533
Db 29 GCATTCGCGTGTGATGTAATGCTCATCC 1
XX
RESULT 8
ID ADR48512/c
XX ADR48512 standard; DNA; 29 BP.
AC ADR48512;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #2.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
XX pXO1; pXO2; probe; ss.
XX

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XX
OS Unidentified.
XX
FN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX
PI Norman SA, Bungo JJ, Hogan JJ, Weisburg WG;
XX WPI; 2004-604428/58.
XX
DR WPI; 2004-604428/58.
XX
PT New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthrax
PT infections.
XX
PS Claim 8; SEQ ID NO 10; 61pp; English.
XX
CC The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXO1 and pXO2, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pXO1 and pXO2 detection kits.
XX
SQ Sequence 29 BP; 6 A; 8 C; 6 G; 9 T; 0 U; 0 Other;
XX
Query Match 5.2%; Score 29; DB 13; Length 29;
Best Local Similarity 100.0%; Pred. No. 0.00064;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 34 TTACTGACGAGGAGCAACCGATTAAAGCG 62
Db 29 TTACTGACGAGGAGCAACCGATTAAAGCG 1
XX
RESULT 9
ID ADR48513 standard; DNA; 29 BP.
XX
AC ADR48513;
XX
DT 04-NOV-2004 (first entry)
XX
DE capB probe #3.
XX
KW Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
XX pXO1; pXO2; probe; ss.
XX
OS Unidentified.
XX
FN WO2004070001-A2.
XX
PD 19-AUG-2004.
XX
PF 12-NOV-2003; 2003WO-US036240.
XX
PR 15-NOV-2002; 2002US-0426552P.
XX 16-MAY-2003; 2003US-0471082P.
XX
PA (GENP-) GEN-PROBE INC.
XX

```



PI Norman SA, Bungo JU, Hogan JU, Weisburg WG;  
XX WPI; 2004-604428/58.  
XX New oligonucleotides that hybridize specifically to a *Bacillus anthracis*  
PT sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis*  
XX infections.  
XX Claim 8; SEQ ID NO 11; 61pp; English.  
XX  
XX The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pX01 and pX02, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a capB  
CC probe, used in the pX01 and pX02 detection kits.  
XX  
XX Sequence 29 BP; 6 A; 8 C; 6 G; 9 T; 0 U; 0 Other;  
SQ  
Query Match 5.2%; Score 29; DB 13; Length 29;  
Best Local Similarity 100.0%; Pred. No. 0.00064;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 63 CCGTAAAGAGGCTCTTAATATCGTGAGC 91  
DB 29 CCGTAAAGAGGCTCTTAATATCGTGAGC 1  
RESULT 10  
ADR48514/C  
ID ADR48514 standard; DNA; 27 BP.  
XX  
XX ADR48514;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX capB probe #4.  
XX  
XX *Bacillus anthracis*; cutaneous; respiratory anthrax infection; pagA; capB;  
XX pX01; pX02; probe; ss.  
XX  
XX Unidentified.  
XX  
XX WO2004070001-A2.  
XX  
XX 19-AUG-2004.  
XX  
XX 12-NOV-2003; 2003WO-US036240.  
XX  
XX 15-NOV-2002; 2002US-0426552P.  
XX  
XX 16-MAY-2003; 2003US-0471082P.  
XX  
XX (GENP-) GEN-PROBE INC.  
XX  
XX Norman SA, Bungo JU, Hogan JU, Weisburg WG;  
XX WPI; 2004-604428/58.  
XX  
XX New oligonucleotides that hybridize specifically to a *Bacillus anthracis*  
PT sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis*  
XX infections.  
XX Claim 8; SEQ ID NO 12; 61pp; English.  
XX  
XX The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*

CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pX01 and pX02, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a capB  
CC probe, used in the pX01 and pX02 detection kits.  
XX  
XX Sequence 27 BP; 5 A; 10 C; 4 G; 8 T; 0 U; 0 Other;  
SQ  
Query Match 4.8%; Score 27; DB 13; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 92 AACGAGGCTGTATTAAGAGGCTGCTG 118  
DB 27 AACGAGGCTGTATTAAGAGGCTGCTG 1  
RESULT 11  
ADR48511/C  
ID ADR48511 standard; DNA; 27 BP.  
XX  
XX ADR48511;  
XX  
XX 04-NOV-2004 (first entry)  
XX  
XX capB probe #1.  
XX  
XX *Bacillus anthracis*; cutaneous; respiratory anthrax infection; pagA; capB;  
XX pX01; pX02; probe; ss.  
XX  
XX Unidentified.  
XX  
XX WO2004070001-A2.  
XX  
XX 19-AUG-2004.  
XX  
XX 12-NOV-2003; 2003WO-US036240.  
XX  
XX 15-NOV-2002; 2002US-0426552P.  
XX  
XX 16-MAY-2003; 2003US-0471082P.  
XX  
XX (GENP-) GEN-PROBE INC.  
XX  
XX Norman SA, Bungo JU, Hogan JU, Weisburg WG;  
XX WPI; 2004-604428/58.  
XX  
XX New oligonucleotides that hybridize specifically to a *Bacillus anthracis*  
PT sequence, useful for detecting cutaneous and respiratory *Bacillus anthracis*  
XX infections.  
XX Claim 8; SEQ ID NO 9; 61pp; English.  
XX  
XX The present invention relates to an oligonucleotide of 20-40 nucleotides  
CC that specifically hybridizes to a sequence contained in a *Bacillus*  
CC anthracis target sequence. The methods and compositions of the present  
CC invention are useful for detecting the presence of *Bacillus anthracis*  
CC nucleic acid in a sample, in particular for detecting cutaneous and  
CC respiratory anthrax infections. Two synthetic genetic target sequences,  
CC derived from pagA and capB gene sequences, were synthesized to provide  
CC known standards for testing oligonucleotides for detection of the genes  
CC carried by the plasmids pX01 and pX02, without requiring handling of  
CC virulent *Bacillus anthracis*. The present sequence represents a capB  
CC probe, used in the pX01 and pX02 detection kits.  
XX  
XX Sequence 27 BP; 8 A; 8 C; 4 G; 7 T; 0 U; 0 Other;  
SQ  
Query Match 4.8%; Score 27; DB 13; Length 27;  
Best Local Similarity 100.0%; Pred. No. 0.0064;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



```
Oy 7 GGATACATCTGCGGAGATGATATATTTGG 33
XX |||||
KM |||||
KW |||||
Db 27 GGATACATCTGCGGAGATGATATATTTGG 1
XX |||||

RESULT 12
ADRA48516/C
ID ADRA48516 standard; DNA; 27 BP.
XX
XX ADRA48516;
AC
XX
XX 04-NOV-2004 (first entry)
DT
XX
XX capB probe #6.
DE
XX
XX Bacillus anthracis; cutaneous; respiratory anthrax infection; pagA; capB;
KM pXOI; pXOI; probe; ss.
XX
XX Unidentified.
XX
XX MO2004070001-A2.
PN
XX
XX 19-AUG-2004.
PD
XX
XX 12-NOV-2003; 2003WO-US036240.
PF
XX
XX 15-NOV-2002; 2002US-0426552P.
PR
XX 16-MAY-2003; 2003US-0471082P.
PR
XX
XX (GENP-) GEN-PROBE INC.
PA
XX
XX Nozman SA, Bungo JJ, Hogan JJ, Weisburg WG;
PI
XX
XX WPI; 2004-604428/58.
DR
XX
XX New oligonucleotides that hybridize specifically to a Bacillus anthracis
PT sequence, useful for detecting cutaneous and respiratory Bacillus anthracis
PT infections.
XX
XX Claim 9; SEQ ID NO 14; 61pp; English.
PS
XX
XX The present invention relates to an oligonucleotide of 20-40 nucleotides
CC that specifically hybridizes to a sequence contained in a Bacillus
CC anthracis target sequence. The methods and compositions of the present
CC invention are useful for detecting the presence of Bacillus anthracis
CC nucleic acid in a sample, in particular for detecting cutaneous and
CC respiratory anthrax infections. Two synthetic genetic target sequences,
CC derived from pagA and capB gene sequences, were synthesized to provide
CC known standards for testing oligonucleotides for detection of the genes
CC carried by the plasmids pXOI and pXOI, without requiring handling of
CC virulent Bacillus anthracis. The present sequence represents a capB
CC probe, used in the pXOI and pXOI detection kits.
CC
XX
XX Sequence 27 BP; 4 A; 8 C; 5 G; 10 T; 0 U; 0 Other;
SQ

Query Match 4.8%; Score 27; DB 13; Length 27;
Best Local Similarity 100.0%; Pred. No. 0.0064;
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 534 GGATCCAGAGCAATGAGATTACACG 560
XX |||||
KM |||||
KW |||||
Db 27 GGATCCAGAGCAATGAGATTACACG 1
XX |||||

RESULT 13
ACCT71914
ID ACCT71914 standard; DNA; 26 BP.
XX
XX ACCT71914;
AC
XX
XX 04-AUG-2003 (first entry)
DT
XX
XX Bacillus anthracis capB specific probe 4.
XX
```

```
XX
XX Encapsulation protein B; capB; protective antigen; pagA; lethal factor;
KM left; fluorescence resonance energy transfer; FRIT; probe; ss.
XX
XX Bacillus anthracis.
OS
XX
XX EP1304387-A1.
PN
XX
XX 23-APR-2003.
PD
XX
XX 10-OCT-2002; 2002EP-00022398.
PF
XX
XX 15-OCT-2001; 2001US-0329826P.
PR
XX 05-FEB-2002; 2002US-00068228.
PR
XX
XX (HOPF) ROCHE DIAGNOSTICS GMBH.
PA (MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX
XX Bell CA, Uhl JR, Cockerill FR;
PI
XX
XX WPI; 2003-450920/43.
DR
XX
XX Detecting Bacillus anthracis in a sample by amplifying B. anthracis capB,
PT pagA and left nucleic acids followed by hybridization with labelled capB,
PT pagA and left probes, and detection by fluorescence resonance energy
PT transfer.
XX
XX Disclosure; Page 3; 31pp; English.
PS
XX
XX The invention relates to detecting Bacillus anthracis in a biological or
CC non-biological sample. The method involves (a) amplifying a portion of B.
CC anthracis encapsulation protein B (capB) and/or protective antigen (pagA)
CC and/or lethal factor (left) nucleic acids using specific primers; (b)
CC contacting the sample with a pair of capB and/or pagA and/or left probes
CC labelled with fluorescent moieties; and (c) detecting the presence or
CC absence of fluorescence resonance energy transfer (FRET) between the
CC probes. The method is useful for identifying B. anthracis DNA from
CC specimens for diagnosis of B. anthracis infection and to identifying hoax
CC cases of B. anthracis. The methods can also be used for B. anthracis
CC efficacy studies or epidemiology studies. The method is rapid, and allows
CC real-time detection of B. anthracis in a biological sample or in a non-
CC biological sample. The method is more sensitive and specific than
CC existing assays. Sequences ACC71913-914 represent B. anthracis capB
CC specific probes
XX
XX
XX Sequence 26 BP; 9 A; 3 C; 10 G; 4 T; 0 U; 0 Other;
SQ

Query Match 4.6%; Score 26; DB 8; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.02;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 87 TGAGCAAGCGAGGTAAGAGG 112
XX |||||
KM |||||
KW |||||
Db 1 TGAGCAAGCGAGGTAAGAGG 26
XX |||||

RESULT 14
ACCT71913
ID ACCT71913 standard; DNA; 25 BP.
XX
XX ACCT71913;
AC
XX
XX 04-AUG-2003 (first entry)
DT
XX
XX Bacillus anthracis capB specific probe 3.
DE
XX
XX Encapsulation protein B; capB; protective antigen; pagA; lethal factor;
KM left; fluorescence resonance energy transfer; FRIT; probe; ss.
XX
XX Bacillus anthracis.
OS
XX
XX EP1304387-A1.
PN
XX
```



PD	23-APR-2003.
XX	
PF	10-OCT-2002; 2002EP-00022398.
XX	
FR	15-OCT-2001; 2001US-0329826P.
XX	
PR	05-FEB-2002; 2002US-00068238.
XX	
PA	(HOFF ) ROCHE DIAGNOSTICS GMBH.
XX	
PA	(MAYO-) MAYO FOUND MEDICAL EDUCATION & RES.
XX	
PI	Bell CA, Uhl JR, Cockerill FR;
XX	
DR	WPI; 2003-450920/43.
XX	
PT	Detecting Bacillus anthracis in a sample by amplifying B.anthraxis capB,
XX	
PT	pagA and left nucleic acids followed by hybridization with labelled capB,
XX	
PT	pagA and left probes, and detection by fluorescence resonance energy
XX	
PT	transfer.
XX	
PS	Disclosure; Page 3; 31pp; English.
XX	
CC	The invention relates to detecting Bacillus anthracis in a biological or
XX	
CC	non-biological sample. The method involves (a) amplifying a portion of B.
XX	
CC	anthracis encapsulation protein B (capB) and/or protective antigen (pagA)
XX	
CC	and/or lethal factor (left) nucleic acids using specific primers; (b)
XX	
CC	contracting the sample with a pair of capB and/or pagA and/or left probes
XX	
CC	labelled with fluorescent moieties; and (c) detecting the presence or
XX	
CC	absence of fluorescence resonance energy transfer (FRET) between the
XX	
CC	probes. The method is useful for identifying B. anthracis DNA from
XX	
CC	specimens for diagnosis of B. anthracis infection and to identifying hoax
XX	
CC	cases of B. anthracis. The methods can also used for B. anthracis
XX	
CC	efficacy studies or epidemiology studies. The method is rapid, and allows
XX	
CC	real-time detection of B. anthracis in a biological sample or in a non-
XX	
CC	biological sample. The method is more sensitive and specific than
XX	
CC	existing assays. Sequences ACC71913-914 represent B. anthracis capB
XX	
CC	specific probes
XX	
SQ	Sequence 25 BP; 8 A; 6 C; 6 G; 5 T; 0 U; 0 Other;
XX	
Query Match	4.5%; Score 25; DB 8; Length 25;
Best Local Similarity	100.0%; Pred.No. 0.065;
Matches	25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	61 CGCCGTAAGAGGTCCTAATTCG 85
DB	1 CGCCGTAAGAGGTCCTAATTCG 25
XXXXXX	
RESULT 15	
ADP44858	
ID1	ADP44858 standard; DNA; 24 BP.
XX	
AC	ADP44858;
XX	
DT	12-FEB-2004 (first entry)
XX	
DE	Internal positive control related PCR primer BACAPB4U SEQ ID NO:65.
XX	
KW	internal positive control; IPC; probe; probe-based nucleic acid;
XX	
KW	PCR primer; ss.
XX	
OS	Synthetic.
XX	
PN	WO2003075837-A2.
XX	
PD	18-SEP-2003.
XX	
PF	03-MAR-2003; 2003WO-US006347.
XX	
PR	04-MAR-2002; 2002US-0361455P.
XX	
PA	(USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.
XX	

PI Hartman LJ, Norwood DA;  
 DR WPI, 2003-756781/71.  
 XX  
 PT New nucleic acid molecule, useful as internal positive control in probe-based nucleic acid assay such as Taqman based assay.  
 XX  
 PS Example 3; SEQ ID NO 65; 56pp; English.  
 XX  
 CC The present invention describes an isolated nucleic acid molecule (1) comprising the 548 base pair (bp) sequence of ADF44859, which is an internal positive control (IPC) nucleic acid molecule. Also described:  
 CC (1) a probe comprising (1) and a label; (2) an assay using the probe; (3) a kit for a probe-based nucleic acid assay comprising the isolated nucleic acid molecule (1) packaged with instructions for use; and (4) making an IPC nucleic acid molecule for a probe-based nucleic acid molecule assay. The nucleic acid molecule (1) is useful as an IPC in probe-based nucleic acid assay such as Taqman (RTM) based assay. The present sequence is used in the exemplification of the present invention.  
 CC  
 CC Sequence 24 BP; 6 A; 5 C; 5 G; 8 T; 0 U; 0 Other;  
 XX  
 SO  
 QY Query Match 4.3%; Score 24; DB 10; Length 24;  
 ID Best Local Similarity 100.0%; Pred. No. 0.21;  
 ID ADF44859 standard; DNA; 23 BP.  
 XX  
 AC ADF44859;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Internal positive control related PCR primer BACAPB4L SEQ ID NO:66.  
 XX  
 XX Internal positive control; IPC; probe; probe-based nucleic acid;  
 XX PCR primer; ss.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX WO2003075837-A2.  
 PN  
 XX  
 PD 18-SEP-2003.  
 XX  
 XX 03-MAR-2003; 2003WO-US006347.  
 PF  
 XX 04-MAR-2002; 2002US-0361455P.  
 PR  
 XX (USSA ) US ARMY MEDICAL RES & MATERIAL COMMAND.  
 PA  
 PI Hartman LJ, Norwood DA;  
 XX  
 DR WPI, 2003-756781/71.  
 XX  
 PT New nucleic acid molecule, useful as internal positive control in probe-based nucleic acid assay such as Taqman based assay.  
 XX  
 PS Example 3; SEQ ID NO 66; 56pp; English.  
 XX  
 CC The present invention describes an isolated nucleic acid molecule (1) comprising the 548 base pair (bp) sequence of ADF44842, which is an internal positive control (IPC) nucleic acid molecule. Also described:  
 CC (1) a probe comprising (1) and a label; (2) an assay using the probe; (3) a kit for a probe-based nucleic acid assay comprising the isolated nucleic acid molecule (1) packaged with instructions for use; and (4) making an IPC nucleic acid molecule for a probe-based nucleic acid molecule assay. The nucleic acid molecule (1) is useful as an IPC in



CC probe-based nucleic acid assay such as TaqMan (RTM) based assay. The  
 CC present sequence is used in the exemplification of the present invention.  
 XX  
 SQ Sequence 23 BP; 8 A; 6 C; 5 G; 4 T; 0 U; 0 Other;

Query Match 4.1%; Score 23; DB 10; Length 23;  
 Best Local Similarity 100.0%; Pred. No. 0.66;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 511 CGTGTATGTTGATGCTCATCC 533  
 |||  
 Db 23 CGTGTATGTTGAATGCTCATCC 1

RESULT 17  
 ADM03357  
 ID ADM03357 standard; DNA; 33226 BP.  
 XX  
 AC ADM03357;  
 XX  
 DT 24-FEB-2005 (first entry)  
 XX  
 DE CYP 3A7 genomic DNA.  
 XX  
 KM ds; cytochrome P450 3A7; CYP 3A7; mutation; DNA detection; diagnosis.  
 XX  
 OS Unidentified.

## Location/Qualifiers

FT Key 3016..3192  
 FT exon /tag= a  
 FT /number= 1  
 FT 3193..7062  
 FT /tag= b  
 FT /number= 1  
 FT 7063..7155  
 FT /tag= c  
 FT /number= 2  
 FT 7156..15866  
 FT /tag= d  
 FT /number= 2  
 FT 15867..15920  
 FT /tag= e  
 FT /number= 3  
 FT 15921..17803  
 FT /tag= f  
 FT /number= 3  
 FT 17804..17902  
 FT /tag= g  
 FT /number= 4  
 FT 17903..20575  
 FT /tag= h  
 FT /number= 4  
 FT 20576..20689  
 FT /tag= i  
 FT /number= 5  
 FT 20690..20949  
 FT /tag= j  
 FT /number= 5  
 FT 20950..21039  
 FT /tag= k  
 FT /number= 6  
 FT 21040..22309  
 FT /tag= l  
 FT /number= 6  
 FT 22310..22456  
 FT /tag= m  
 FT /number= 7  
 FT 22457..23532  
 FT /tag= n  
 FT /number= 7  
 FT 23533..23660  
 FT /tag= o

FT /number= 8  
 FT 23661..24679  
 FT /tag= p  
 FT /number= 8  
 FT 24680..24745  
 FT /tag= q  
 FT /number= 9  
 FT 24746..27321  
 FT /tag= r  
 FT /number= 9  
 FT 27322..27483  
 FT /tag= s  
 FT /number= 10  
 FT 27484..28953  
 FT /tag= t  
 FT /number= 10  
 FT 28954..29181  
 FT /tag= u  
 FT /number= 11  
 FT 29182..30241  
 FT /tag= v  
 FT /number= 11  
 FT 30242..30403  
 FT /tag= w  
 FT /number= 12  
 FT 30404..32619  
 FT /tag= x  
 FT /number= 12  
 FT 32620..33178  
 FT /tag= y  
 FT /number= 13

KR2004032838-A.

17-APR-2004.

29-MAR-2004; 2004KR-00021068.

29-MAR-2004; 2004KR-00021068.

(UYIN-) UNIV INJE.

Cha IU, Jung HJ, Lee SS, Shin JG;

WPI; 2004-568813/55.

Genetic marker for decreased activity of cytochrome p450 3a7(cyp 3a7)  
 protein and method for detection.

Example 2; SBQ ID NO 24; 36pp; Korean.

This invention describes a novel genetic marker for decreased activity of  
 cytochrome P450 3A7(CYP 3A7) protein. A method for detecting decreased  
 activity of cytochrome P450 3A7(CYP 3A7) is also provided, which is used  
 to anticipate drug response difference between individuals to a drug  
 metabolized by CYP 2D2. The genetic marker comprises a T nucleotide  
 insertion at between a C nucleotide at position 134 and T nucleotide at  
 position 135 of ADM03353 resulting in a termination codon at residue 55  
 of the CYP 3A7 protein represented in ADM03354. The marker can be  
 detected by amplifying the cytochrome P450 3A7 from a blood sample with  
 PCR primers ADM03350 and ADM03351 then pyrosequencing the PCR product  
 with a primer (ADM03352) to confirm the mutation of the CYP 3A7 gene.  
 This sequence represents CYP 3A7 genomic DNA.

SQ Sequence 33226 BP; 9482 A; 6371 C; 7528 G; 9845 T; 0 U; 0 Other;

Query Match 3.6%; Score 20; DB 13; Length 33226;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTGGAGTGATTTGTAATG 226  
 |||  
 Db 19301 TGTGGAGTGATTTGTAATG 19320



RESULT 18  
 ABX77171 ID ABX77171 standard; DNA; 123785 BP.  
 XX  
 AC ABX77171;  
 XX  
 DT 25-APR-2003 (first entry)  
 XX  
 DE DNA sequence of human BAC clone RP11-757A13.  
 XX  
 KW Human; ss; transgenic; drug metabolism; behaviour; gene; mouse;  
 KW pharmacokinetic assay; pharmacodynamic assay; toxicology; serum albumin;  
 KW alpha-acidic glycoprotein; CYP; multidrug resistance protein; MRP;  
 KW uridine diphosphoglucuronosyl transferase; UGT; cytochrome P450.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200283897-A1.  
 XX  
 PD 24-OCT-2002.  
 XX  
 PF 18-APR-2002; 2002WO-AU000485.  
 XX  
 PR 18-APR-2001; 2001AU-00004467.  
 XX  
 PA (GENE-) GENE STREAM PTY LTD.  
 XX  
 PI Daily JM;  
 XX  
 DR WPI; 2003-093021/08.  
 XX  
 PT New transgenic non-human animal expressing a foreign polypeptide  
 PT associated with drug behavior and/or metabolism, useful for studying the  
 PT behavior and/or metabolism of a drug in other animals.  
 XX  
 PS Example 2A; Page 229-295; 408pp; English.  
 XX  
 CC This invention relates to a transgenic non-human animal which may be used  
 CC for assessing the behaviour and/or metabolism of a drug in another animal  
 CC and which expresses a foreign polypeptide associated with drug behaviour  
 CC and/or metabolism. The invention also comprises a nucleic acid construct  
 CC for use in producing the above transgenic non-human animal and a method  
 CC of assessing the metabolism and/or behavior of a drug in an animal of  
 CC interest, comprising administering a test agent to the transgenic animal  
 CC and conducting analytical tests to determine drug metabolism and/or  
 CC behaviour. The transgenic animal is useful in studying drug metabolism  
 CC and/or behaviour in other animals. The nucleic acid construct is useful  
 CC in producing the above transgenic animal and the methods are used for  
 CC producing, breeding and using transgenic animals for pharmacological  
 CC (e.g. pharmacokinetic or pharmacodynamic assays) and/or toxicological  
 CC studies. Nucleic acid sequences used within the invention are serum  
 CC albumin; alpha-acidic glycoprotein; cytochrome P450 (CYP); uridine  
 CC diphosphoglucuronosyl transferase (UGT); multidrug resistance proteins  
 CC and (MRP's). The present sequence represents a DNA sequence used to  
 CC create a transgenic animal within the scope of the invention  
 XX  
 SQ Sequence 123785 BP; 34793 A; 24793 C; 26537 G; 37655 T; 0 U; 7 Other;  
 Query Match 3.6%; Score 20; DB 10; Length 123785;  
 Best Local Similarity 100.0%; Pred. No. 13;  
 Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 207 TGTGGAGTGATTTGTAATG 226  
 |||||  
 DB 100480 TGTGGAGTGATTTGTAATG 100499  
 |||||  
 RESULT 19  
 ACA24403 ID ACA24403 standard; DNA; 555 BP.  
 XX

AC ACA24403;  
 XX  
 DT 19-JUN-2003 (first entry)  
 XX  
 DE Prokaryotic essential gene #6060.  
 XX  
 KW Antisense; ds; prokaryotic essential gene; cell proliferation;  
 KW drug design; gene.  
 XX  
 OS Bacteroides fragilis.  
 XX  
 PN WO200277183-A2.  
 XX  
 PD 03-OCT-2002.  
 XX  
 PF 21-MAR-2002; 2002WO-US009107.  
 XX  
 PR 21-MAR-2001; 2001US-00815242.  
 PR 06-SEP-2001; 2001US-00948993.  
 PR 25-OCT-2001; 2001US-0342923P.  
 PR 08-FEB-2002; 2002US-00072851.  
 PR 06-MAR-2002; 2002US-0362699P.  
 XX  
 PA (ELIT-) ELITRA PHARM INC.  
 XX  
 PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zykkind JM;  
 PI Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH;  
 XX  
 DR WPI; 2003-029926/02.  
 XX  
 PT New antisense nucleic acids, useful for identifying proteins or screening  
 PT for homologous nucleic acids required for cellular proliferation to  
 PT isolate candidate molecules for rational drug discovery programs.  
 XX  
 PS Claim 14; SEQ ID NO 12273; 1766pp; English.  
 XX  
 CC The invention relates to an isolated nucleic acid comprising any one of  
 CC the 6213 antisense sequences given in the specification where expression  
 CC of the nucleic acid inhibits proliferation of a cell. Also included are:  
 CC (1) a vector comprising a promoter operably linked to the nucleic acid  
 CC encoding a polypeptide whose expression is inhibited by the antisense  
 CC nucleic acid; (2) a host cell containing the vector; (3) an isolated  
 CC polypeptide or its fragment whose expression is inhibited by the  
 CC antisense nucleic acid; (4) an antibody capable of specifically binding  
 CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular  
 CC proliferation; (7) identifying a gene in an operon required for  
 CC proliferation; (8) identifying a compound that influences the activity of  
 CC the gene product or that has an activity against a biological pathway  
 CC required for proliferation, or that inhibits cellular proliferation; (8)  
 CC identifying a gene required for cellular proliferation or the biological  
 CC pathway in which a proliferation-required gene or its gene product lies  
 CC or a gene on which the test compound that inhibits proliferation of an  
 CC organism acts; (9) manufacturing an antibiotic; (10) profiling a  
 CC compound's activity; (11) a culture comprising strains in which the gene  
 CC product is overexpressed or underexpressed; (12) determining the extent  
 CC to which each of the strains is present in a culture or collection of  
 CC strains; or (13) identifying the target of a compound that inhibits the  
 CC proliferation of an organism. The antisense nucleic acids are useful for  
 CC identifying proteins or screening for homologous nucleic acids required  
 CC for cellular proliferation to isolate candidate molecules for rational  
 CC drug discovery programs, or for screening homologous nucleic acids  
 CC required for proliferation in cells other than S. aureus, S. typhimurium,  
 CC K. pneumoniae or P. aeruginosa. The present sequence is one of the target  
 CC prokaryotic essential genes. Note: The sequence data for this patent did  
 CC not form part of the printed specification, but was obtained in  
 CC electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences  
 XX  
 SQ Sequence 555 BP; 171 A; 93 C; 143 G; 148 T; 0 U; 0 Other;  
 Query Match 3.4%; Score 19; DB 8; Length 555;  
 Best Local Similarity 100.0%; Pred. No. 56;



Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 268 GAAGTAGCTGAAGCTTTCA 286  
|||  
Db 277 GAAGTAGCTGAAGCTTTCA 295

RESULT 20  
ADX36536  
ID ADX36536 standard; cDNA; 1004 BP.  
XX  
AC ADX36536;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 19356.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAOV/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 19356; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake  
CC or by providing improved plant growth and development under at least one  
CC stress condition or for modifying seed oil or protein yield and/or  
CC content. This sequence represents a plant full length insert  
CC polynucleotide that can be used in the recombinant DNA construct of the  
CC invention.

XX  
SQ Sequence 1004 BP; 275 A; 213 C; 213 G; 303 T; 0 U; 0 Other;  
Query Match 3.4%; Score 19; DB 13; Length 1004;  
Best Local Similarity 100.0%; Pred. No. 55;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 299 CATATAATGACATTAGT 317  
|||  
Db 932 CATATAATGACATTAGT 950

RESULT 21  
ADX28662  
ID ADX28662 standard; cDNA; 1092 BP.  
XX  
AC ADX28662;  
XX  
DT 21-APR-2005 (first entry)  
XX  
DE Plant full length insert polynucleotide seqid 11482.  
XX  
KW plant protectant; plant growth regulant; gene therapy; plant;  
KW recombinant DNA construct; physical array; plant breeding marker;  
KW cold tolerance; heat tolerance; drought tolerance; herbicide tolerance;  
KW extreme osmotic condition; pathogen tolerance; pest tolerance;  
KW growth rate; cell cycle pathway; disease resistance;  
KW galactomannan production; lignin production; plant growth regulator;  
KW yield; plant growth; plant development; seed oil; protein yield;  
KW protein content; gene; ss.  
XX  
OS Unidentified.  
XX  
PN US2004034888-A1.  
XX  
PD 19-FEB-2004.  
XX  
PF 28-APR-2003; 2003US-00425114.  
XX  
PR 06-MAY-1999; 99US-00304517.  
PR 05-NOV-2001; 2001US-00985678.  
XX  
PA (LITU/) LIU J.  
PA (ZHOU/) ZHOU Y.  
PA (KOVA/) KOVALIC D K.  
PA (SCRE/) SCREEN S E.  
PA (TABAS/) TABASKA J E.  
PA (CAOV/) CAO Y.  
XX  
PI Liu J, Zhou Y, Kovalic DK, Screen SE, Tabaska JE, Cao Y;  
XX  
DR WPI; 2004-180133/17.  
XX  
PT New recombinant DNA construct, useful for improving plant tolerance to  
PT cold, heat, drought, herbicides, extreme osmotic conditions, pathogens or  
PT pests, for conferring increased resistance to plant disease, or for  
PT improving yield.  
XX  
PS Claim 1; SEQ ID NO 11482; 15pp; English.  
XX  
CC The invention describes a recombinant DNA construct comprising a  
CC polynucleotide consisting of a sequence encoding an amino acid sequence  
CC available in electronic form from the US patent office at  
CC ftp.segdata.uspto.gov/sequence.html?docid:2004034888. The polynucleotide  
CC of the invention are also useful in physical arrays of molecules and as  
CC plant breeding markers. The recombinant DNA construct is useful for  
CC improving plant tolerance to cold, heat, drought, herbicides, extreme  
CC osmotic conditions, pathogens or pests, for manipulating growth rate in  
CC plant cells by modification of the cell cycle pathway, for conferring  
CC increased resistance to plant disease, for producing galactomannan,  
CC lignin or plant growth regulators, for increasing the rate of homologous  
CC recombination in plants, for improving yield by modification of  
CC photosynthesis or carbohydrate, nitrogen or phosphorus use and/or uptake



CC or by providing improved plant growth and development under at least one  
 CC stress condition or for modifying seed oil or protein yield and/or  
 CC content. This sequence represents a plant full length insert  
 CC polynucleotide that can be used in the recombinant DNA construct of the  
 CC invention.

SO Sequence 1092 BP; 287 A; 247 C; 218 G; 340 T; 0 U; 0 Other;

Query Match 3.4%; Score 19; DB 13; Length 1092;

Best Local Similarity 100.0%; Pred. No. 54;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 299 CATATATGACATTAGT 317

DB 1044 CATATATGACATTAGT 1062

RESULT 22

AAK94697 standard; cDNA; 1776 BP.

AC AAK94697;

DT 06-NOV-2001 (first entry)

DE Human full-length cDNA, SEQ ID NO: 3720.

KM Human; full length cDNA; cDNA synthesis; oligo-capping; ss.

OS Homo sapiens.

PN EP130094-A2.

PD 05-SEP-2001.

PF 07-JUL-2000; 2000EP-00114089.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183765.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2001-524255/58.

DR P-PSDB; AAM93745.

PT 830 Primers useful for synthesizing full length cDNA clones and their use

PT in genetic manipulation.

PS Claim 8; SEQ ID NO 3720; 1380bp + Sequence listing; English.

CC The invention relates to primers for synthesizing full length cDNA  
 CC clones. 830 cDNA molecules encoding a human protein have been isolated  
 CC and nucleotide sequences of 5' and 3' ends of the cDNA molecules have  
 CC been determined. Primers for synthesizing the full length cDNA are useful  
 CC for clarifying the function of the protein encoded by the cDNA. The full  
 CC length clones were obtained by construction of full length enriched cDNA  
 CC libraries that were synthesized by the oligo-capping method. The primers  
 CC enable the production of the full length cDNA easily without any special  
 CC methods. The present sequence is a full length human cDNA of the  
 CC invention. Note: The sequence data for this patent did not form part of  
 CC the printed specification, but was obtained in CD-ROM format directly  
 CC from EPO

SO Sequence 1776 BP; 482 A; 448 C; 547 G; 299 T; 0 U; 0 Other;

Query Match 3.4%; Score 19; DB 4; Length 1776;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 493 GATGAGAAACAGCATTC 511

DB 1206 GATGAGAAACAGCATTC 1224

RESULT 23

ADL31687 standard; cDNA; 1776 BP.

AC ADL31687;

DT 20-MAY-2004 (first entry)

DE Full length human cDNA clone Segid 3720.

KM human; medicine; signal transduction; glycoprotein; transcription;

KM oligo-capping method; ss; gene.

OS Homo sapiens.

PN EP1396543-A2.

PD 10-MAR-2004.

PF 07-JUL-2000; 2003EP-00025638.

PR 08-JUL-1999; 99JP-00194486.

PR 11-JAN-2000; 2000JP-00118774.

PR 02-MAY-2000; 2000JP-00183865.

PR 07-JUL-2000; 2000EP-00114089.

PA (REAS-) RES ASSOC BIOTECHNOLOGY.

PI Ota T, Nishikawa T, Isogai T, Hayashi K, Ishii S, Kawai Y;

PI Wakamatsu A, Sugiyama T, Nagai K, Kojima S, Otsuki T, Koga H;

DR WPI; 2004-204755/20.

DR P-PSDB; ADL31688.

PT New oligonucleotide primers (830 cDNAs) useful for synthesizing full

PT length human cDNAs.

PS Example 1; SEQ ID NO 3720; 1340bp; English.

CC This invention relates to a novel primers useful for synthesizing full  
 CC length cDNA molecules that encode human proteins. Specifically, it refers  
 CC to secretory or membrane proteins that are potential therapeutic agents/  
 CC target molecules in the field of medicine, and in particular genes  
 CC encoding proteins that are associated with signal transduction,  
 CC glycoproteins and transcription. The present invention describes a method  
 CC for efficiently cloning a full length human cDNA from both the 5' and 3'  
 CC ends using the oligo-capping method. This polynucleotide sequence is a  
 CC full length human cDNA clone of the invention.

SO Sequence 1776 BP; 482 A; 448 C; 547 G; 299 T; 0 U; 0 Other;

Query Match 3.4%; Score 19; DB 12; Length 1776;

Best Local Similarity 100.0%; Pred. No. 53;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 493 GATGAGAAACAGCATTC 511

DB 1206 GATGAGAAACAGCATTC 1224

RESULT 24

ADH84577 standard; DNA; 1863 BP.

AC ADH84577;

DT 22-APR-2004 (first entry)



```

DE Enterococcus faecalis polynucleotide #2462.
XX
XX Enterococcus faecalis infection; transcription regulatory element;
KM antibacterial; gene; ds.
XX
OS Enterococcus faecalis.
XX
XX US6617156-B1.
XX
XX 09-SEP-2003.
XX
XX 13-AUG-1998; 98US-00134000.
XX
XX 15-AUG-1997; 97US-0055778P.
XX
XX (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
PI Doucette-Stamm LA, Bush D;
XX
XX WPI; 2003-895394/82.
DR P-PSDB; ADH87982.
XX
XX New nucleic acid comprising a sequence encoding an Enterococcus faecalis
PT polypeptide, useful for preparing a composition for diagnosing or
PT treating E. faecalis infection.
PS Disclosure; SEQ ID NO 2462; 193bp; English.
XX
XX The invention relates to Enterococcus faecalis polynucleotides and
CC polypeptides. The invention also relates to a recombinant expression
CC vector comprising a polynucleotide operably linked to a transcription
CC regulatory element, a cell comprising a recombinant vector, a method for
CC producing an E. faecalis polypeptide, an isolated nucleic acid comprising
CC a sequence not given in the specification, a recombinant vector
CC comprising the nucleic acid and a cell comprising the recombinant vector.
CC The polynucleotides can be used to detect the presence of E. faecalis in
CC a sample. The sequences are useful for preparing a composition for
CC diagnosing or treating Enterococcus faecalis infection. This sequence
CC represents an E. faecalis polynucleotide of the invention.
XX
SQ Sequence 1863 BP; 626 A; 304 C; 381 G; 552 T; 0 U; 0 Other;
Query Match 3.4%; Score 19; DB 10; Length 1863;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 114 TGTGATTAGAGCAGAA 132
Db 1491 TGTGATTAGAGCAGAA 1509

RESULT 25
ADP83696
ID ADP83696 standard; DNA; 1914 BP.
XX
XX ADF83696;
AC
XX
XX 26-FEB-2004 (first entry)
DT
XX
XX 1914bp human 21163 nucleic acid.
DE
XX
XX 21163; prollyl oligopeptidase; cytosolic; neuroprotective; nootropic;
KM cerebroprotective; virucide; immunosuppressive; dermatological; cardiant;
KM cardiovascular; nephrotropic; osteopathic; hypotensive; gene therapy;
KM proliferative disorder; neurodegenerative disease; tissue; glial;
KM neuronal disorder; cerebrovascular disease; infection; T cell;
KM skin disease; heart disorder; blood vessel; red cell;
KM developmental disorder; kidney; breast; prostate; testis; thyroid;
KM pancreas; small intestine; ovary; skeletal muscle; antigen; immunogen;
KM chromosome mapping; tissue typing; forensic biology; surrogate marker;
KM human; gene; ds.
XX

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OS Homo sapiens.
XX
XX W0200251992-A2.
XX
XX 04-JUL-2002.
XX
XX 20-DEC-2001; 2001WO-US050317.
XX
XX 22-DEC-2000; 2000US-0257736P.
XX
XX 19-DEC-2001; 2001US-00025950.
XX
XX (MIL-) MILLENIUM PHARM INC.
PA
XX
XX Hunter JJ, Kapeller-Libermann R;
PI
XX
XX WPI; 2003-201195/19.
DR
XX
XX New prollyl oligopeptidase nucleic acids, designated 21163 nucleic acids,
PT useful for treating and/or diagnosing e.g. proliferative disorders,
PT neurodegenerative diseases, glial and neuronal disorders or
PT cerebrovascular disorders.
PS Claim 1; SEQ ID NO 3; 130pp; English.
XX
XX The invention relates to novel isolated nucleic acid molecules,
CC designated 21163 nucleic acid molecules, which encode novel prollyl
CC oligopeptidase family members. More specifically the invention relates to
CC 21163 nucleic acids comprising either a fully defined 4959 bp or 1914 bp
CC sequence given in the specification, which encode a prollyl oligopeptidase
CC having a sequence of 638 amino acids also fully defined in the
CC specification. The 21163 nucleic acid molecules have the following
CC activities: cytosolic, neuroprotective, nootropic, cerebroprotective,
CC virucide, immunosuppressive, dermatological, cardiant, cardiovascular,
CC nephrotropic, osteopathic, and hypotensive. The 21163 nucleic acid
CC molecules can be used in gene therapy to treat disorders. 21163 nucleic
CC acids and proteins are useful for treating and/or diagnosing
CC proliferative disorders (e.g. haematopoietic neoplastic disorders),
CC neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease
CC or Pick's disease), disorders that arise in the tissues in which it is
CC expressed (e.g. splenomegaly, or neoplasms), glial and neuronal disorders
CC (e.g. cerebral edema or hydrocephalus), cerebrovascular diseases (e.g.
CC hypoxia, ischaemia or infarction), infections (e.g. HIV or AIDS),
CC disorders involving T cells (e.g. transplant rejection), skin diseases
CC (e.g. vitiligo, melanoma, or lentigo), heart disorders (e.g. heart failure
CC or hypertensive heart disease), disorders involving blood vessels (e.g.
CC vascular cell wall injury) and red cells (e.g. anaemia), developmental
CC disorders (e.g. aplasia or thymic hypoplasia), and disorders of the
CC kidney, breast, prostate, testis, thyroid, pancreas, small intestine,
CC ovary, and skeletal muscle. The polypeptides are further useful as
CC antigens or immunogens to raise or test anti-21163 antibodies. The
CC polynucleotides may further be used in chromosome mapping, tissue typing,
CC forensic biology, and as surrogate markers. This polynucleotide sequence
CC represents a 21163 nucleic acid of the invention.
XX
SQ Sequence 1914 BP; 602 A; 370 C; 415 G; 527 T; 0 U; 0 Other;
Query Match 3.4%; Score 19; DB 10; Length 1914;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 365 AGAGAAATACAAAAGTGAT 383
Db 764 AGAGAAATACAAAAGTGAT 782

RESULT 26
ADS48807/c
ID ADS48807 standard; cDNA; 2301 BP.
XX
XX ADS48807;
AC
XX
XX 02-DEC-2004 (first entry)
DT
XX

```



DE Bacterial polynucleotide #3550.  
XX  
XX Recombinant DNA construct; transformed plant; improved plant property;  
XX cold tolerance; heat tolerance; drought tolerance; herbicide; osmotic;  
XX pathogen tolerance; pest tolerance; plant disease resistance;  
XX cell cycle pathway modification; plant growth regulator;  
XX homologous recombination; seed oil yield; protein yield; carbohydrate;  
XX nitrogen; phosphorus; photosynthesis; lignin; galactomannan;  
XX bacterial polynucleotide; gene; ss.  
XX  
XX Bacteria.  
XX  
XX US2003233675-A1.  
XX  
XX 18-DEC-2003.  
XX  
XX 20-FEB-2003; 2003US-00369493.  
XX  
XX 21-FEB-2002; 2002US-0360039P.  
XX  
XX (CAOY/) CAO Y.  
XX (HINK/) HINKLE G J.  
XX (SLAT/) SLATER S C.  
XX (CHEN/) CHEN X.  
XX (GOLD/) GOLDMAN B S.  
XX  
XX Cao Y, Hinkle GJ, Slater SC, Chen X, Goldman BS;  
XX  
XX WPI; 2004-061375/06.  
XX  
XX New recombinant DNA construct comprising a promoter positioned to provide  
XX PT for expression of a polynucleotide encoding a polypeptide from a  
XX PT microbial source, useful for producing plants with improved properties.  
XX  
XX Claim 1; SEQ ID NO 27237; 122pp; English.  
XX  
XX  
XX The invention relates to a recombinant DNA construct comprising a  
XX CC promoter functional in a plant cell, where the promoter is positioned to  
XX CC provide for expression of a polynucleotide encoding a polypeptide from a  
XX CC microbial source. The invention also relates to a transformed plant  
XX CC comprising the recombinant DNA construct and a method of producing a  
XX CC transformed plant having an improved property. The plant is a crop plant  
XX CC such as maize or soybean. The method of producing a transformed plant  
XX CC having an improved property comprises transforming a plant with the  
XX CC recombinant DNA construct and growing the transformed plant, where the  
XX CC polynucleotide or polypeptide is useful for improving plant properties.  
XX CC The recombinant DNA construct is useful for producing plants with  
XX CC improved plant properties, e.g. improved cold, heat or drought tolerance,  
XX CC tolerance to herbicides, extreme osmotic conditions, pathogens or pests,  
XX CC increased resistance to plant disease, better growth rate by modification  
XX CC of the cell cycle pathway with plant growth regulators, increased rate of  
XX CC homologous recombination, modified seed oil or protein yield and/or  
XX CC content, improved yield by modification of carbohydrate, nitrogen or  
XX CC phosphorus use and/or uptake, by modification of photosynthesis or by  
XX CC providing improved plant growth and development under at least one stress  
XX CC condition, improved lignin production or improved galactomannan  
XX CC production. This sequence represents a bacterial polynucleotide used in  
XX CC the scope of the invention. Note: The sequence data for this patent did  
XX CC not form part of the printed specification but was obtained in electronic  
XX CC format from USPTO at [seqdata.uspto.gov/sequence.html](http://seqdata.uspto.gov/sequence.html).  
XX  
XX Sequence 2301 BP; 621 A; 602 C; 613 G; 465 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 3.4%; Score 19; DB 13; Length 2301;  
XX Best Local Similarity 100.0%; Pred. No. 52;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 382 ATTGTTGGGATTAATCTA 400  
XX ||||||||||||||||||  
XX Db 1245 ATTGTTGGGATTAATCTA 1227  
XX  
XX  
XX RESULT 27

AD067450  
ID AD067450 standard; cDNA; 3028 BP.  
XX  
XX AD067450;  
XX  
XX 07-OCT-2004 (first entry)  
XX  
XX Novel human cDNA sequence #2423.  
XX  
XX DE  
XX BS; gene; osteopathic; neuroprotective; nootropic; antiparkinsonian;  
XX KW cytosolic; gene therapy; diagnostic marker; morbid state; osteoporosis;  
XX KW neurological disease; Alzheimer's disease; Parkinson's disease; dementia;  
XX KW cancer.  
XX  
XX OS Homo sapiens.  
XX  
XX EP1440981-A2.  
XX  
XX 28-JUL-2004.  
XX  
XX 21-JAN-2004; 2004EP-00001196.  
XX  
XX 21-JAN-2003; 2003JP-00102206.  
XX PR 09-MAY-2003; 2003JP-00131392.  
XX  
XX (REAS-) RES ASSOC BIOTECHNOLOGY.  
XX  
XX Isegaki T, Sugiyama T, Otsuki T, Wakamatsu A, Sato H, Ichii S;  
XX PI Yamamoto J, Isono Y, Nagai K, Irie R;  
XX  
XX WPI; 2004-535376/52.  
XX DR P-PSDB; AD067757.  
XX  
XX Novel 2495 cDNA, useful for treating osteoporosis, neurological diseases,  
XX PT Alzheimer's diseases, Parkinson's diseases, dementia and various cancers.  
XX  
XX Claim 1; SEQ ID NO 4611; 2449pp; English.  
XX  
XX  
XX The invention relates to 2495 novel polynucleotides (I) and their encoded  
XX CC polypeptides, sequences hybridizing to these nucleotides, sequences  
XX CC encoding partial polypeptides and sequences having 70% or 90% identity to  
XX CC the nucleotide and protein sequences. The nucleotides and polypeptides  
XX CC are useful as diagnostic markers or therapeutic target for the diseases  
XX CC or morbid states. They are also useful for treating osteoporosis,  
XX CC neurological diseases, Alzheimer's diseases, Parkinson's diseases,  
XX CC dementia and various cancers. This sequence corresponds to a nucleotide  
XX CC sequence of the invention.  
XX  
XX Sequence 3028 BP; 953 A; 600 C; 633 G; 842 T; 0 U; 0 Other;  
XX  
XX  
XX Query Match 3.4%; Score 19; DB 12; Length 3028;  
XX Best Local Similarity 100.0%; Pred. No. 52;  
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
XX  
XX 365 AGAGAAATACAAAGTGAT 383  
XX ||||||||||||||||||  
XX Db 1348 AGAGAAATACAAAGTGAT 1366  
XX  
XX  
XX RESULT 28  
XX ADR24156  
XX ID ADR24156 standard; DNA; 4661 BP.  
XX  
XX ADR24156;  
XX  
XX 21-OCT-2004 (first entry)  
XX  
XX Breast cancer prognosis marker #17.  
XX  
XX DE  
XX ds; breast cancer; prognosis; gene expression; diagnosis.  
XX  
XX OS Homo sapiens.  
XX  
XX



PN WO2004065545-A2.  
XX  
PD 05-AUG-2004.  
XX  
PF 15-JAN-2004; 2004WO-US001100.  
XX  
PR 15-JAN-2003; 2003US-00342887.  
XX  
PA (ROSE-) ROSETTA INPHARMATICS LLC.  
PA (NECA-) NETHERLANDS CANCER INST.  
XX  
PI Van't Veer LJ, He Y;  
XX  
DR WPI; 2004-593473/57.  
XX  
PT Classifying a breast cancer patient according to prognosis comprises  
PT determining the similarity between the level of expression of each of  
PT five genes in a cell sample taken from patient, to control levels.  
PS  
PS Disclosure; SEQ ID NO 17; 226pp; English.  
CC  
CC The invention relates to a method of classifying a breast cancer patient  
CC according to prognosis by determining the similarity between the level of  
CC expression of each of five genes for which markers are listed in the  
CC specification, in a cell sample taken from the breast cancer patient, to  
CC control levels of expression for each respective five genes to obtain a  
CC patient similarity value. The methods are useful for classifying a breast  
CC cancer patient according to prognosis. Kits and computer program products  
CC are useful for data analysis using the diagnostic, prognostic and  
CC statistical methods of the invention. This sequence corresponds to a  
CC marker used in the method of the invention.  
XX  
SQ Sequence 4661 BP; 1405 A; 854 C; 919 G; 1483 T; 0 U; 0 Other;  
Query Match 3.4%; Score 19; DB 13; Length 4661;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGAGAAATACAAAGTGAT 383  
Db 917 AGAGAAATACAAAGTGAT 935  
RESULT 29  
AD222652 standard; DNA; 4661 BP.  
ID AD222652;  
XX  
AC AD222652;  
XX  
DT 16-JUN-2005 (first entry)  
XX  
DE Neoblastoma prognosis method target gene SEQ ID NO 27.  
XX  
XX prognosis; nervous system tumor; cytostatic; neoplasm;  
KM neurological disease; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2005030992-A2.  
XX  
PD 07-APR-2005.  
XX  
PF 01-OCT-2004; 2004WO-FR050475.  
XX  
PR 01-OCT-2003; 2003FR-00011483.  
XX  
PA (INMR-) BIOMERIEUX SA.  
PA (BERRA-) CENT BERAARD LEON.  
XX  
PI Combaret V, Krause A, Puitsieux A, Lacroix B;  
XX  
DR WPI; 2005-273392/28.

PT Prognosis of neuroblastoma, based on measuring expression of one or more  
PT specific target genes, for example insulin-like growth factor binding  
PT protein-7, that are differentially expressed between patients with good  
PT and poor prognosis.  
XX  
XX Claim 1; SEQ ID NO 27; 104pp; French.  
PS  
PS The invention describes a method for prognosis of neuroblastoma  
CC comprising: extracting a biological material from a patient sample;  
CC contacting the material with at least one reagent (R) specific for any of  
CC 37 target genes (TG) of, e.g. 2667, 762 and 580 base pairs in length (SEQ  
CC ID Nos: 1-37) fully defined in the specification, provided that when the  
CC gene is any of SEQ ID Nos: 11, 17 or 37, then at least two (R) specific  
CC for different TG are used, and determining expression of at least one TG  
CC (or at least two for SEQ ID Nos: 11, 17 and 37). The method provides a  
CC very reliable differentiation between patients with good or poor  
CC prognoses. This sequence represents a neuroblastoma prognosis method target  
CC gene.  
XX  
SQ Sequence 4661 BP; 1405 A; 854 C; 919 G; 1483 T; 0 U; 0 Other;  
Query Match 3.4%; Score 19; DB 14; Length 4661;  
Best Local Similarity 100.0%; Pred. No. 51;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 365 AGAGAAATACAAAGTGAT 383  
Db 917 AGAGAAATACAAAGTGAT 935  
RESULT 30  
ABA07182  
ID ABA07182 standard; DNA; 4748 BP.  
XX  
AC ABA07182;  
XX  
DT 14-JAN-2002 (first entry)  
XX  
DE Human pancreatic cancer related genomic DNA, SEQ ID NO: 501.  
XX  
DE Human; cytostatic; antidiabetic; antiinflammatory; gastric; osteopathic;  
KM antihormone; antitumor; thyroid-active; gene therapy; antisense therapy;  
KM pancreatic cancer antigen inhibitor; pancreatic cancer; pancreatitis;  
KM diabetes; endocrine disorder; acromegaly; hyperthyroidism;  
KM gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155206-A1.  
XX  
PD 02-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US001353.  
XX  
PR 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
PR 24-FEB-2000; 2000US-0184664P.  
PR 02-MAR-2000; 2000US-0186350P.  
PR 16-MAR-2000; 2000US-0189874P.  
PR 17-MAR-2000; 2000US-0190076P.  
PR 18-APR-2000; 2000US-0198123P.  
PR 19-MAY-2000; 2000US-0205515P.  
PR 07-JUN-2000; 2000US-0209467P.  
PR 28-JUN-2000; 2000US-0214886P.  
PR 30-JUN-2000; 2000US-0215135P.  
PR 07-JUL-2000; 2000US-0216647P.  
PR 07-JUL-2000; 2000US-0216880P.  
PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
PR 26-JUL-2000; 2000US-0220964P.  
PR 14-AUG-2000; 2000US-0224518P.







Best Local Similarity 100.0%; Pred. No. 50;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 493 GATGAGAAACGACATTC 511  
Db 3174 GATGAGAAACGACATTC 3192

## RESULT 31

AAK89814  
ID AAK89814 standard; DNA; 4748 BP.

XX AAK89814;

DT 05-NOV-2001 (first entry)

DE Human digestive system antigen genomic sequence SRQ ID NO: 3390.

XX Human; digestive system antigen; gene therapy; cancer; appendicitis;

KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;

KW digestive system disorder; Meckel's diverticulum; ds.

XX Homo sapiens.

XX WC200155314-A2.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US001324.

XX 31-JAN-2000; 2000US-0179065P.

PR 04-FEB-2000; 2000US-0180628P.

PR 24-FEB-2000; 2000US-0184668P.

PR 02-MAR-2000; 2000US-0186350P.

PR 16-MAR-2000; 2000US-0189874P.

PR 17-MAR-2000; 2000US-0190076P.

PR 18-APR-2000; 2000US-0198123P.

PR 19-MAY-2000; 2000US-0205515P.

PR 07-JUN-2000; 2000US-0209467P.

PR 28-JUN-2000; 2000US-0214886P.

PR 30-JUN-2000; 2000US-0215135P.

PR 07-JUL-2000; 2000US-0216647P.

PR 11-JUL-2000; 2000US-0217487P.

PR 14-JUL-2000; 2000US-0217496P.

PR 26-JUL-2000; 2000US-0220964P.

PR 14-AUG-2000; 2000US-0224518P.

PR 14-AUG-2000; 2000US-0224519P.

PR 14-AUG-2000; 2000US-0225213P.

PR 14-AUG-2000; 2000US-0225214P.

PR 14-AUG-2000; 2000US-0225267P.

PR 14-AUG-2000; 2000US-0225268P.

PR 14-AUG-2000; 2000US-0225270P.

PR 14-AUG-2000; 2000US-0225447P.

PR 06-SEP-2000; 2000US-0230438P.

PR 08-SEP-2000; 2000US-0231242P.

PR 08-SEP-2000; 2000US-0231243P.

PR 08-SEP-2000; 2000US-0231244P.

PR 08-SEP-2000; 2000US-0231413P.

PR 08-SEP-2000; 2000US-0231414P.

PR 08-SEP-2000; 2000US-0232080P.

PR 08-SEP-2000; 2000US-0232081P.

PR 12-SEP-2000; 2000US-0231968P.

PR 14-SEP-2000; 2000US-0232397P.

PR 14-SEP-2000; 2000US-0232398P.

PR 14-SEP-2000; 2000US-0232399P.

PR 14-SEP-2000; 2000US-0232400P.

PR 14-SEP-2000; 2000US-0232401P.

PR 14-SEP-2000; 2000US-0233063P.

PR 14-SEP-2000; 2000US-0233064P.

PR 21-SEP-2000; 2000US-0233065P.

PR 21-SEP-2000; 2000US-0234223P.

PR 25-SEP-2000; 2000US-0234997P.

PR 25-SEP-2000; 2000US-0234998P.

PR 25-SEP-2000; 2000US-0234999P.

PR 26-SEP-2000; 2000US-0235484P.

PR 27-SEP-2000; 2000US-0235834P.

PR 27-SEP-2000; 2000US-0235836P.

PR 29-SEP-2000; 2000US-0236377P.

PR 29-SEP-2000; 2000US-0236378P.

PR 29-SEP-2000; 2000US-0236388P.

PR 29-SEP-2000; 2000US-0236399P.

PR 02-OCT-2000; 2000US-0237037P.

PR 02-OCT-2000; 2000US-0237038P.

PR 02-OCT-2000; 2000US-0237039P.

PR 13-OCT-2000; 2000US-0237040P.

PR 13-OCT-2000; 2000US-0239935P.

PR 20-OCT-2000; 2000US-0240960P.

PR 20-OCT-2000; 2000US-0241221P.

PR 20-OCT-2000; 2000US-0241785P.

PR 20-OCT-2000; 2000US-0241786P.

PR 20-OCT-2000; 2000US-0241787P.

PR 20-OCT-2000; 2000US-0241808P.

PR 20-OCT-2000; 2000US-0241809P.

PR 20-OCT-2000; 2000US-0241810P.

PR 01-NOV-2000; 2000US-0241826P.

PR 08-NOV-2000; 2000US-0246474P.

PR 08-NOV-2000; 2000US-0246475P.

PR 08-NOV-2000; 2000US-0246476P.

PR 08-NOV-2000; 2000US-0246477P.

PR 08-NOV-2000; 2000US-0246478P.

PR 08-NOV-2000; 2000US-0246523P.

PR 08-NOV-2000; 2000US-0246524P.

PR 08-NOV-2000; 2000US-0246525P.

PR 08-NOV-2000; 2000US-0246526P.

PR 08-NOV-2000; 2000US-0246527P.

PR 08-NOV-2000; 2000US-0246528P.

PR 08-NOV-2000; 2000US-0246532P.

PR 08-NOV-2000; 2000US-0246609P.

PR 08-NOV-2000; 2000US-0246610P.

PR 08-NOV-2000; 2000US-0246611P.

PR 08-NOV-2000; 2000US-0246613P.

PR 17-NOV-2000; 2000US-0249207P.

PR 17-NOV-2000; 2000US-0249208P.

PR 17-NOV-2000; 2000US-0249209P.

PR 17-NOV-2000; 2000US-0249210P.

PR 17-NOV-2000; 2000US-0249211P.

PR 17-NOV-2000; 2000US-0249212P.

PR 17-NOV-2000; 2000US-0249213P.

PR 17-NOV-2000; 2000US-0249214P.

PR 17-NOV-2000; 2000US-0249215P.

PR 17-NOV-2000; 2000US-0249216P.

PR 17-NOV-2000; 2000US-0249217P.

PR 17-NOV-2000; 2000US-0249218P.



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PR 17-NOV-2000; 2000US-0249244P.
PR 17-NOV-2000; 2000US-0249245P.
PR 17-NOV-2000; 2000US-0249246P.
PR 17-NOV-2000; 2000US-0249247P.
PR 17-NOV-2000; 2000US-0249248P.
PR 17-NOV-2000; 2000US-0249249P.
PR 17-NOV-2000; 2000US-0249250P.
PR 17-NOV-2000; 2000US-0250160P.
PR 01-DEC-2000; 2000US-0250391P.
PR 05-DEC-2000; 2000US-0251030P.
PR 05-DEC-2000; 2000US-0251988P.
PR 05-DEC-2000; 2000US-0256719P.
PR 06-DEC-2000; 2000US-0254779P.
PR 08-DEC-2000; 2000US-0251856P.
PR 08-DEC-2000; 2000US-0251868P.
PR 08-DEC-2000; 2000US-0251869P.
PR 08-DEC-2000; 2000US-0251989P.
PR 11-DEC-2000; 2000US-0254097P.
PR 05-JAN-2001; 2001US-0259678P.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-502630/55.
XX
XX Polynucleotides encoding digestive system antigens, useful for
XX diagnosing, treating, preventing and/or prognosing disorders of the
XX digestive system, particularly cancer and cancer metastases.
XX
XX Disclosure; SEQ ID NO 3390; 986bp; English.
XX
XX The present invention provides the protein and coding sequences of a
XX number of human digestive system antigens. These can be used in the
XX diagnosis, treatment and prevention of digestive system disorders,
XX including cancer. Meckel's diverticulum, bacterial or parasitic
XX infections, appendicitis, Hirschsprung's disease, chronic colitis or
XX ulcerative colitis. The present sequence is a genomic DNA fragment
XX encoding a digestive system antigen of the invention
XX
XX Sequence 4748 BP; 1189 A; 1294 C; 1326 G; 939 T; 0 U; 0 Other;
XX
XX Query Match 3.4%; Score 19; DB 4; Length 4748;
XX Best Local Similarity 100.0%; Pred. No. 50;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 493 GATGAGAAACAGCATTC 511
XX |||||
XX DB 3174 GATGAGAAACAGCATTC 3192
XX
XX RESULT 32
XX ADJ87640
XX ID ADJ87640 standard; DNA; 4748 BP.
XX
XX AC ADJ87640;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Nervous system disease differentially expressed gene #42.
XX
XX KW ds; nootropic; neuroprotective; neuroleptic; cyostatic;
XX antiparkinsonian; gene therapy; nervous system disorder;
XX Alzheimer's disease; bipolar disorder; cancer; epilepsy;
XX multiple sclerosis; Parkinson's disease; schizophrenia;
XX Stiff-Man syndrome.
XX
XX OS Homo sapiens.
XX
XX PN WO2003103474-A2.
XX
XX PD 18-DEC-2003.

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XX
XX 21-MAY-2003; 2003WO-US016270.
XX
XX 22-MAY-2002; 2002US-0383031P.
XX
XX (INCY-) INCYTE CORP.
XX
XX PI Walker MG, Murry LE;
XX
XX WPI; 2004-122191/12.
XX
XX Claim 1; SEQ ID NO 42; 104bp; English.
XX
XX The invention relates to novel genes that are differentially expressed in
XX disorders of the nervous system, e.g. Alzheimer's disease, epilepsy, etc.
XX The methods and compositions of the present invention are useful for
XX diagnosing, prognosticating and/or treating disorders of the nervous
XX system, such as Alzheimer's disease, bipolar disorders, cancers,
XX epilepsy, multiple sclerosis, Parkinson's disease, schizophrenia and
XX Stiff-Man syndrome. This sequence corresponds to a DNA of the invention.
XX
XX Sequence 4748 BP; 1425 A; 871 C; 948 G; 1504 T; 0 U; 0 Other;
XX
XX Query Match 3.4%; Score 19; DB 12; Length 4748;
XX Best Local Similarity 100.0%; Pred. No. 50;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 365 AGAGAAATACAAAGTGAT 383
XX |||||
XX DB 970 AGAGAAATACAAAGTGAT 988
XX
XX RESULT 33
XX ADF83694
XX ID ADF83694 standard; DNA; 4959 BP.
XX
XX AC ADF83694;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE 4959bp human 21163 nucleic acid.
XX
XX KW 21163; prolly oligopeptidase; cyostatic; neuroprotective; nootropic;
XX cerebroprotective; virocidic; immunosuppressive; dermatological; candidant;
XX cardiovascular; nephrotropic; osteopathic; hypotensive; gene therapy;
XX proliferative disorder; neurodegenerative disease; tissue; glial;
XX neuronal disorder; cerebrovascular disease; infection; T cell;
XX skin disease; heart disorder; blood vessel; red cell;
XX developmental disorder; kidney; breast; prostate; testis; thyroid;
XX pancreas; small intestine; ovary; skeletal muscle; antigen; immunogen;
XX human; gene; ds.
XX
XX OS Homo sapiens.
XX
XX PN WO200251992-A2.
XX
XX PD 04-JUL-2002.
XX
XX PF 20-DEC-2001; 2001WO-US050317.
XX
XX PR 22-DEC-2000; 2000US-0257736P.
XX
XX PR 19-DEC-2001; 2001US-00025950.
XX
XX (MILL-) MILLENIUM PHARM INC.
XX
XX PI Hunter JT, Kapellier-Libermann R;
XX

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DR		WPI, 2003-201195/19.
DR		P-PBDB; ADF83695.
XX		
PT		New prollyl oligopeptidase nucleic acids, designated 21163 nucleic acids,
PT		useful for treating and/or diagnosing e.g. proliferative disorders,
PT		neurodegenerative diseases, glial and neuronal disorders or
XX		cerebrovascular disorders.
XX		
PS		Claim 1; SEQ ID NO 1, 130pp; English.
XX		
CC		The invention relates to novel isolated nucleic acid molecules,
CC		designated 21163 nucleic acid molecules, which encode novel prollyl
CC		oligopeptidase family members. More specifically the invention relates to
CC		21163 nucleic acids comprising either a fully defined 4959 bp or 1914 bp
CC		sequence given in the specification, which encode a prollyl oligopeptidase
CC		having a sequence of 638 amino acids also fully defined in the
CC		specification. The 21163 nucleic acid molecules have the following
CC		activities: cytotaxtic, neuroprotective, nootropic, cerebroprotective,
CC		vincidine, immunosuppressive, dermatological, radiant, cardiovascular,
CC		nephrotropic, osteopethic, and hypotensive. The 21163 nucleic acid
CC		molecules can be used in gene therapy to treat disorders. 21163 nucleic
CC		acids and proteins are useful for treating and/or diagnosing
CC		proliferative disorders (e.g. haematopoietic neoplastic disorders),
CC		neurodegenerative diseases (e.g. Alzheimer's disease, Parkinson's disease
CC		or Pick's disease), disorders that arise in the tissues in which it is
CC		expressed (e.g. splenomegaly, or neoplasms), glial and neuronal disorders
CC		(e.g. cerebral edema or hydrocephalus), cerebrovascular diseases (e.g.
CC		hypoxia, ischemia or infarction), infections (e.g. HIV or AIDS),
CC		disorders involving T cells (e.g. transplant rejection), skin diseases
CC		(e.g. vitiligo, melasma, or lentigo), heart disorders (e.g. heart failure
CC		or hypertensive heart disease), disorders involving blood vessels (e.g.
CC		vascular cell wall injury) and red cells (e.g. anaemia), developmental
CC		disorders (e.g. aplasia or thymic hypoplasia), and disorders of the
CC		kidney, breast, prostate, testis, thyroid, pancreas, small intestine,
CC		ovary, and skeletal muscle. The polypeptides are further useful as
CC		antigens or immunogens to raise or test anti-21163 antibodies. The
CC		polynucleotides may further be used in chromosome mapping, tissue typing,
CC		forensic biology, and as surrogate markers. This polynucleotide sequence
CC		represents a 21163 nucleic acid of the invention.
XX		
SQ		Sequence 4959 BP; 1479 A; 923 C; 1003 G; 1554 T; 0 U; 0 Other;
	Query Match	3.4%; Score 19; DB 10; Length 4959;
	Best Local Similarity	100.0%; Pred. No. 50;
	Matches 19; Conservative	0; Mismatches 0; Indels 0; Gaps 0
OY	365 AGAGAAATCAAAAAGTGAATGAT 383 	
DB	1214 AGAGAAATCAAAAAGTGAATGAT 1232	
RESULT 34		
ID	AAS35890	
XX	AAS35890 standard; DNA; 10093 BP.	
XX		
XX	AAS35890;	
DT	17-DEC-2001	(first entry)
XX		
DSE		
XX		Human cardiovascular system antigen genomic DNA SEQ ID No 1390.
KM		Cardiovascular system antigen; human; mouse; rabbit; goat; horse; cat;
KM		chicken; sheep; immunosuppressive; antidiabetic; vasotropic; dog;
KM		anthrhemetic; antiproliferative; cytostatic; cardiant; neuroprotective;
KM		cerebroprotective; nootropic; antibacterial; vincidine; fungicide; cancer;
KM		ophthalmological; vulnery; gene therapy; autoimmune disease; neoplasm;
KM		hyperproliferative disorder; breast; liver; cardiovascular disorder; de;
KM		cerebrovascular disorder; nervous system disorder; bacterial infection;
KM		fungal infection; viral infection; ocular disorder; endocrine disorder;
KM		gastrintestinal disorder; renal disorder; respiratory disorder;
KM		wound healing; skin aging; organ transplantation; tissue regeneration;
XX		anti-infectility.
XX		



PR 27-SEP-2000; 2000US-0235834P.  
PR 27-SEP-2000; 2000US-0235835P.  
PR 29-SEP-2000; 2000US-0236327P.  
PR 29-SEP-2000; 2000US-0236367P.  
PR 29-SEP-2000; 2000US-0236368P.  
PR 29-SEP-2000; 2000US-0236369P.  
PR 29-SEP-2000; 2000US-0236370P.  
PR 02-OCT-2000; 2000US-0236802P.  
PR 02-OCT-2000; 2000US-0237037P.  
PR 02-OCT-2000; 2000US-0237038P.  
PR 02-OCT-2000; 2000US-0237039P.  
PR 02-OCT-2000; 2000US-0237040P.  
PR 13-OCT-2000; 2000US-0239935P.  
PR 13-OCT-2000; 2000US-0239937P.  
PR 20-OCT-2000; 2000US-0240960P.  
PR 20-OCT-2000; 2000US-0241221P.  
PR 20-OCT-2000; 2000US-0241785P.  
PR 20-OCT-2000; 2000US-0241786P.  
PR 20-OCT-2000; 2000US-0241787P.  
PR 20-OCT-2000; 2000US-0241808P.  
PR 20-OCT-2000; 2000US-0241809P.  
PR 20-OCT-2000; 2000US-0241826P.  
PR 01-NOV-2000; 2000US-0244617P.  
PR 08-NOV-2000; 2000US-0246474P.  
PR 08-NOV-2000; 2000US-0246475P.  
PR 08-NOV-2000; 2000US-0246476P.  
PR 08-NOV-2000; 2000US-0246477P.  
PR 08-NOV-2000; 2000US-0246478P.  
PR 08-NOV-2000; 2000US-0246523P.  
PR 08-NOV-2000; 2000US-0246524P.  
PR 08-NOV-2000; 2000US-0246525P.  
PR 08-NOV-2000; 2000US-0246526P.  
PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
PR 17-NOV-2000; 2000US-0249208P.  
PR 17-NOV-2000; 2000US-0249209P.  
PR 17-NOV-2000; 2000US-0249210P.  
PR 17-NOV-2000; 2000US-0249211P.  
PR 17-NOV-2000; 2000US-0249212P.  
PR 17-NOV-2000; 2000US-0249213P.  
PR 17-NOV-2000; 2000US-0249214P.  
PR 17-NOV-2000; 2000US-0249215P.  
PR 17-NOV-2000; 2000US-0249216P.  
PR 17-NOV-2000; 2000US-0249217P.  
PR 17-NOV-2000; 2000US-0249218P.  
PR 17-NOV-2000; 2000US-0249244P.  
PR 17-NOV-2000; 2000US-0249245P.  
PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
PR 17-NOV-2000; 2000US-0249300P.  
PR 01-DEC-2000; 2000US-0250160P.  
PR 01-DEC-2000; 2000US-0250391P.  
PR 05-DEC-2000; 2000US-0251030P.  
PR 05-DEC-2000; 2000US-0251988P.  
PR 05-DEC-2000; 2000US-025619P.  
PR 06-DEC-2000; 2000US-0251479P.  
PR 08-DEC-2000; 2000US-0251856P.  
PR 08-DEC-2000; 2000US-0251868P.  
PR 08-DEC-2000; 2000US-0251869P.  
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PR 05-JAN-2001; 2001US-0259678P.  
XX  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.

XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX  
XX WPI; 2001-451930/48.  
DR  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for diagnosing, treating and/or preventing disorders of the  
PT cardiovascular system.  
XX  
PS Claim 1, SEQ ID NO 1390; 674bp; English.  
XX  
XX Sequences AAS35741-AA356942 represent genomic DNA molecules, which encode  
CC the cardiovascular system antigen polypeptides of the invention.  
CC Cardiovascular system antigens and their associated polynucleotides are  
CC useful in the diagnosis, treatment and prevention of various types of  
CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,  
CC chickens or sheep. A pathological condition can be determined by  
CC detecting the presence or absence of a mutation in a cardiovascular  
CC system antigen polynucleotide. The treatable disorders include autoimmune  
CC diseases such as rheumatoid arthritis, hyperproliferative disorders such  
CC as neoplasms of the breast or liver, cardiovascular disorders such as  
CC cardiac arrest, cerebrovascular disorders such as cerebral ischaemia,  
CC nervous system disorders such as Alzheimer's disease, infections caused  
CC by bacteria, viruses and fungi, ocular disorders such as corneal  
CC infection, endocrine disorders such as premature labour and infertility,  
CC gastrointestinal disorders such as Crohn's disease, renal disorders such  
CC as glomerulonephritis and respiratory disorders such as asthma and  
CC pleurisy. The polypeptides can also be used to aid wound healing, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, to regenerate tissues and in chemotaxis. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
XX at ftp.wipo.int/pub/published\_pct\_sequences

Query Match 3.4%; Score 19; DB 4; Length 10093;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GATGAGGAAACGACATTC 511  
DB 3174 GATGAGGAAACGACATTC 3192  
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|||||

RESULT 35  
ABA07184 standard; DNA; 10093 BP.  
XX  
AC ABA07184;  
XX  
DT 14-JAN-2002 (first entry)  
XX  
XX Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.  
DE  
XX Human pancreatic cancer related genomic DNA, SEQ ID NO: 503.  
XX  
XX Human; cytostatic; antidiabetic; antiinflammatory; gastric; osteopathic;  
KW antihomone; anticulcer; thyroid-active; gene therapy; antisense therapy;  
KW pancreatic cancer antigen inhibitor; pancreatic cancer; pancreatitis;  
KW diabetes; endocrine disorder; acromegaly; hyperthyroidism;  
KW gastrointestinal disorder; Crohn's disease; duodenal ulcer; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200155206-A1.  
XX  
PD 02-AUG-2001.  
XX  
XX 17-JAN-2001; 2001WO-US001353.  
PF  
XX 31-JAN-2000; 2000US-0179065P.  
PR 04-FEB-2000; 2000US-0180628P.  
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PR 13-OCT-2000; 2000US-0239935P.

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PR 08-NOV-2000; 2000US-0246525P.  
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PR 08-NOV-2000; 2000US-0246527P.  
PR 08-NOV-2000; 2000US-0246528P.  
PR 08-NOV-2000; 2000US-0246532P.  
PR 08-NOV-2000; 2000US-0246609P.  
PR 08-NOV-2000; 2000US-0246610P.  
PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
PR 17-NOV-2000; 2000US-0249207P.  
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PR 17-NOV-2000; 2000US-0249244P.  
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PR 17-NOV-2000; 2000US-0249246P.  
PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
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PR 08-DEC-2000; 2000US-0251990P.  
PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.

(HUMA-) HUMAN GENOME SCI INC.

Rosen CA, Barash SC, Ruben SM;

WPI; 2001-457717/49.

Isolated pancreatic cancer polypeptide for treating, preventing and/or  
prognosing disorders related to the pancreas including pancreatic cancers  
and also for testing and detection e.g. diagnosis.

Disclosure; SEQ ID NO 503; 537pp; English.

The invention relates to an isolated polypeptide comprising an amino acid  
sequence at least 90% identical to 188 amino acid sequences fully defined







PR 08-NOV-2000; 2000US-0246611P.  
PR 08-NOV-2000; 2000US-0246613P.  
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PR 17-NOV-2000; 2000US-0249265P.  
PR 17-NOV-2000; 2000US-0249297P.  
PR 17-NOV-2000; 2000US-0249299P.  
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PR 01-DEC-2000; 2000US-0250160P.  
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PR 08-DEC-2000; 2000US-0251989P.  
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PR 11-DEC-2000; 2000US-0254097P.  
PR 05-JAN-2001; 2001US-0259678P.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Baraah SC, Ruben SM;  
XX  
DR WPI; 2001-502630/55.  
XX  
XX Polynucleotides encoding digestive system antigen, useful for  
PT diagnosing, treating, preventing and/or prognosing disorders of the  
PT digestive system, particularly cancer and cancer metastases.  
XX  
XX  
PS Disclosure; SEQ ID NO 3392; 986bp; English.  
XX  
XX The present invention provides the protein and coding sequences of a  
CC number of human digestive system antigens. These can be used in the  
CC diagnosis, treatment and prevention of digestive system disorders,  
CC including cancer, Meckel's diverticulum, bacterial or parasitic  
CC infections, appendicitis, Hirschsprung's disease, chronic colitis or  
CC ulcerative colitis. The present sequence is a genomic DNA fragment  
CC encoding a digestive system antigen of the invention  
XX  
SQ Sequence 10093 BP; 2782 A; 2562 C; 2726 G; 2023 T; 0 U; 0 Other;  
Query Match 3.4%; Score 19; DB 4; Length 10093;  
Best Local Similarity 100.0%; Pred. No. 49;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX  
DE Human cardiovascular system related genomic DNA #150.  
XX  
XX Human; cardiovascular system related polypeptide; cancer;  
KW proliferative disorder; foetal abnormality; developmental abnormality;  
KW haematopoietic disorder; AIDS; autoimmune disease; rheumatoid arthritis;  
KW inflammation; allergy; neurological disorder; Alzheimer's disease;  
KW Parkinson's disease; cognitive disorder; schizophrenia; asthma;  
KW skin disorder; psoriasis; sepsis; diabetes; atherosclerosis;  
KW cardiovascular disorder; angiogenic disorder; kidney disorder;  
KW gastrointestinal disorder; pregnancy-related disorder;  
KW endocrine disorder; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN US2003059908-A1.  
XX  
PD 27-MAR-2003.  
XX  
XX 07-MAR-2002; 2002US-00091504.  
XX  
XX 31-JAN-2000; 2000US-0179065P.  
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PR 11-JUL-2000; 2000US-0217487P.  
PR 11-JUL-2000; 2000US-0217496P.  
PR 14-JUL-2000; 2000US-0218290P.  
PR 26-JUL-2000; 2000US-0220963P.  
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PR 14-AUG-2000; 2000US-0224519P.  
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PR 14-AUG-2000; 2000US-0225214P.  
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PR 14-AUG-2000; 2000US-0225447P.  
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PR 30-AUG-2000; 2000US-0228924P.  
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PR 01-SEP-2000; 2000US-0229343P.  
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PR 08-SEP-2000; 2000US-0232081P.  
PR 12-SEP-2000; 2000US-0231968P.



PR 05-DEC-2000; 2000US-0251030P.  
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 PR 08-DEC-2000; 2000US-0251989P.  
 PR 08-DEC-2000; 2000US-0251990P.  
 PR 11-DEC-2000; 2000US-0254097P.  
 PR 09-JAN-2001; 2001US-0259678P.  
 PR 17-JAN-2001; 2001US-00764869.  
 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 PI Rosen CA, Ruben SM, Barash SC;  
 XX WPI; 2003-743766/70.  
 XX  
 XX New cardiovascular system related polynucleotides and polypeptides,  
 PT useful for preventing, treating, or ameliorating a medical condition,  
 PT such as cancer of cardiovascular tissues and cancer metastases.  
 XX  
 PS Claim 1; SEQ ID NO 1390; 262pp; English.  
 XX  
 XX The invention relates to human cardiovascular system related polypeptides  
 CC and the polynucleotides encoding them. The polypeptides, polynucleotides  
 CC and antibodies to the polypeptides are useful for diagnosing a  
 CC pathological condition or a susceptibility to a pathological condition,  
 CC for preventing, treating, or ameliorating a medical condition, such as  
 CC cancer of cardiovascular system tissues, proliferative disorders, foetal  
 CC and developmental abnormalities, haematopoietic disorders, diseases of  
 CC the immune system, AIDS, autoimmune diseases (e.g., rheumatoid  
 CC arthritis), inflammation, allergies, neurological disorders (e.g.,  
 CC Alzheimer's disease, Parkinson's disease), cognitive disorders,  
 CC schizophrenia, asthma, skin disorders (e.g., psoriasis), sepsis,  
 CC diabetes, atherosclerosis, cardiovascular disorders, angiogenic  
 CC disorders, kidney disorders, gastrointestinal disorders, pregnancy-  
 CC related disorders, endocrine disorders and infections. The nucleic acids  
 CC are also useful for chromosome identification, radiation hybrid mapping  
 CC or long-range restriction mapping. The polypeptides and polynucleotides  
 CC may also be used as food additives or preservatives to increase or  
 CC decrease storage capabilities, fat content or other nutritional  
 CC components. This sequence represents human cardiovascular system related  
 CC genomic DNA of the invention.  
 CC  
 SO Sequence 10093 BP; 2782 A; 2562 C; 2726 G; 2023 T; 0 U; 0 Other;  
 Query Match 3.4%; Score 19; DB 10; Length 10093;  
 Best Local Similarity 100.0%; Prid. No. 49;  
 Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 493 GATGAGGAAACAGCATTC 511  
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 Db 3174 GATGAGGAAACAGCATTC 3192  
 RESULT 38  
 ADJ08002  
 ID ADJ08002 standard; DNA; 10093 BP.  
 XX  
 AC ADJ08002;  
 XX  
 DT 04-NOV-2004 (first entry)  
 XX  
 XX Human cardiovascular system associated polypeptide-related DNA SeqID1390.  
 XX  
 XX autoimmune disease; rheumatoid arthritis; hyperproliferative disorder;  
 KW breast neoplasms; liver neoplasm; cardiovascular disorder;  
 KW cardiac arrest; cerebrovascular disorder; cerebral ischaemia;  
 KW angiogenesis; nervous system disorder; Alzheimer's disease; infection;  
 KW ocular disorder; corneal infection; wound healing;  
 KW epithelial cell proliferation; skin aging; sunburn;



KW organ transplantation; cell culture; tissue regeneration; chemotaxis;  
KW food additive; preservative; cardiovascular system associated antigen;  
KW nuclear factor kappaB; NFkappaB; promoter element; human; ds.  
XX Homo sapiens.  
PN US2004005575-A1.  
XX 08-JAN-2004.  
PD  
XX  
PF 26-AUG-2002; 2002US-00227577.  
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XX 31-JAN-2000; 2000US-0179065P.  
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PR 07-MAR-2002; 2002US-00091504.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Ruben SM, Barash SC;  
DR WPI; 2004-081713/08.  
XX  
PT New cardiovascular system-related nucleic acid molecule, useful for  
PT diagnosing, preventing or treating diseases of the cardiovascular system,  
PT and in chromosome mapping, drug screening or in pharmacogenomics.  
XX  
PS Disclosure; SEQ ID NO 1390; 262bp; English.  
XX  
XX The invention relates to an isolated nucleic acid molecule encoding a  
CC human cardiovascular system associated polypeptide (or antigens), or its  
CC fragment. Also included recombinant vectors, recombinant host cells, an  
CC isolated human cardiovascular system associated polypeptide (including  
CC its fragment, allelic variant, species homologue or epitope), an isolated  
CC antibody that binds specifically to a human cardiovascular system  
CC associated polypeptide, diagnosing a pathological condition or  
CC susceptibility to a pathological condition (comprising determining the  
CC presence or absence of a mutation in human cardiovascular system  
CC associated nucleic acid and diagnosing a condition based on the presence  
CC or absence of the mutation), identifying a binding partner to human  
CC cardiovascular system associated polypeptides, the gene corresponding to  
CC the human cardiovascular system associated cDNA sequence and identifying  
CC an activity in a biological assay comprising expressing the human  
CC cardiovascular system associated cDNA in a cell, isolating the  
CC supernatant, detecting an activity in a biological assay and identifying  
CC the protein in the supernatant having the activity. The human  
CC cardiovascular system associated nucleic acids and polypeptides are used  
CC to prevent, treat or ameliorate a medical condition (for example in  
CC humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep), for  
CC example autoimmune diseases such as rheumatoid arthritis,  
CC hyperproliferative disorders, for example neoplasms of the breast or  
CC liver, cardiovascular disorders, for example cardiac arrest,  
CC  
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Best Local Similarity 100.0%; Pred. No. 49;  
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QY 493 GATGAGAAACGACATTC 511  
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RESULT 39  
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ID ABK31389 standard; DNA; 10872 BP.  
XX  
AC ABK31389;  
XX  
DT 23-APR-2002 (first entry)  
XX  
XX Signal transduction associated gene modified complementary DNA #116.  
DE  
XX  
XX Human; signal transduction associated gene; cytosine methylation state;  
KW Cpg island; signal transduction associated disease; solid tumour; cancer;  
KW antitumour; cytostatic; mutant; ds.  
XX  
XX Homo sapiens.  
OS Synthetic.  
XX  
XX WO200200926-A2.  
PN  
XX 03-JAN-2002.  
PD  
XX 29-JUN-2001; 2001WO-EP007472.  
PF  
XX

PR 30-JUN-2000; 2000DE-01032529.  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
XX  
XX Olek A, Piepenbrock C, Berlin K;  
XX  
XX WPI; 2002-147896/19.  
DR  
PT Oligonucleotide for diagnosis and therapy of diseases associated with  
PT signal transduction e.g. cancer, comprises chemically modified genomic  
PT sequences of genes associated with signal transduction.  
XX  
PS Claim 1; SEQ ID NO 232; 24bp; English.  
XX  
XX The present invention relates to chemically modified DNA sequences of  
CC signal transduction associated genes. The DNA sequences are chemically  
CC modified using a solution of bisulphite, hydrogen sulphite or disulphite.  
CC Also disclosed are oligonucleotides and/or PNA oligomers for detecting  
CC the cytosine methylation state (Cpg islands) of these genes, and a method  
CC for the diagnosis and/or therapy of genetic and epigenetic parameters of  
CC genes associated with signal transduction. The genomic DNA can be  
CC obtained from cells or cellular components which contain DNA, e.g. cell  
CC lines, biopsies, blood, sputum, stool, urine, cerebral-spinal fluid,  
CC tissue embedded in paraffin such as tissue from eyes, intestine, kidney,  
CC brain, heart, prostate, lung, breast or liver, histologic object slides,  
CC and all their possible combinations. The sequences of the invention are  
CC useful for the diagnosis and therapy of diseases associated with signal  
CC transduction e.g. solid tumours and cancer. ABK3158-ABK3155 represent  
CC chemically pretreated genomic DNA sequences of different genes associated  
CC with signal transduction, or their complementary sequences. Note: The  
CC sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from the  
CC European Patent Office  
XX  
SQ Sequence 10872 BP; 2200 A; 431 C; 3320 G; 4921 T; 0 U; 0 Other;  
XX  
Query Match 3.4%; Score 19; DB 6; Length 10872;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 8782 ATTATCTTCCAAATATAA 8764  
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XX  
AC ABL70336;  
XX  
DT 01-JUN-2002 (first entry)  
XX  
XX Chemically treated cell signalling DNA sequence complementary to#113.  
DE  
XX  
XX Cell signalling; cytosine methylation; cell signalling disease; cancer;  
KW tumour; cytostatic; ds.  
XX  
XX Unidentified.  
OS  
XX  
XX WO200202807-A2.  
PN  
XX 10-JAN-2002.  
PD  
XX 29-JUN-2001; 2001WO-EP007471.  
PF  
XX  
XX 30-JUN-2000; 2000DE-01032529.  
PR 01-SEP-2000; 2000DE-01043826.  
XX  
XX (EPIG-) EPIGENOMICS AG.  
PA  
XX Olek A, Piepenbrock C, Berlin K;  
XX



XX WPI; 2002-154758/20.  
DR  
XX  
PT Nucleic acid, useful for diagnosis and therapy of diseases associated  
PT with cell signalling e.g. cancer, comprises chemically modified genomic  
PT sequences of genes associated with cell signalling.  
XX  
PS Claim 1; SEQ ID NO 226; 24bp + Sequence Listing; English.  
XX  
CC The invention relates to a nucleic acid comprising a sequence of at least  
CC 18 bases of a segment of chemically pretreated DNA of genes associated  
CC with cell signalling. The activity of the modified sequences of the  
CC invention may be described as cytostatic. The object of the invention is  
CC to provide the chemically modified DNA of genes associated with cell  
CC signalling, as well as oligonucleotides and/or PNA-oligomers for  
CC detecting cytosine methylations, as well as a method which is  
CC particularly suitable for the diagnosis and/or therapy of genetic and  
CC epigenetic parameters of genes associated with cell signalling. The  
CC chemically modified DNA provided by the invention is useful for diagnosis  
CC and therapy of diseases such as solid tumours and cancer. The sequences  
CC given in records ABU70111-ABU70626 represent chemically pre-treated  
CC genomic DNA's of genes associated with cell signalling. Note: The  
CC sequence data for this patent is not represented in the printed  
CC specification, but is based on sequence information supplied by the  
CC European Patent Office  
XX  
SQ Sequence 10872 BP; 2200 A; 431 C; 3320 G; 4921 T; 0 U; 0 Other;  
Query Match 3.4%; Score 19; DB 6; Length 10872;  
Best Local Similarity 100.0%; Pred. No. 48;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 8782 ATTATCTTCCAAATATAA 8764  
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OM nucleic - nucleic search, using sw model

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## SUMMARIES

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143	16	2.9	601	3	US-09-949-016-76402	Sequence 76402, A
144	16	2.9	601	3	US-09-949-016-77150	Sequence 77150, A
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153	16	2.9	601	3	US-09-949-016-129509	Sequence 129509, A
154	16	2.9	601	3	US-09-949-016-129580	Sequence 129580, A
155	16	2.9	601	3	US-09-949-016-129651	Sequence 129651, A
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157	16	2.9	601	3	US-09-949-016-129793	Sequence 129793, A
158	16	2.9	601	3	US-09-949-016-129864	Sequence 129864, A
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183	16	2.9	618	3	US-09-710-279-2183	Sequence 2183, Ap
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187	16	2.9	702	3	US-09-107-433-523	Sequence 923, App
188	16	2.9	720	3	US-08-998-416-789	Sequence 789, App
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191	16	2.9	741	3	US-08-264-042-2	Sequence 2, Appl1
192	16	2.9	745	3	US-09-023-655-523	Sequence 523, App
193	16	2.9	747	3	US-09-134-000C-928	Sequence 928, App
194	16	2.9	754	3	US-09-286-981B-21	Sequence 21, Appl
195	16	2.9	754	3	US-10-254-995-21	Sequence 21, Appl
196	16	2.9	763	3	US-09-056-019C-19	Sequence 19, Appl
197	16	2.9	768	3	US-08-264-042-3	Sequence 3, Appl1
198	16	2.9	768	3	US-09-489-039A-4076	Sequence 4076, Ap
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201	16	2.9	818	3	US-08-956-171E-742	Sequence 742, App
202	16	2.9	818	3	US-08-781-986A-742	Sequence 742, App
203	16	2.9	825	3	US-08-998-416-525	Sequence 525, App
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216	16	2.9	1275	3	US-10-254-995-28	Sequence 28, Appl
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230	16	2.9	1866	3	US-09-614-957D-31	Sequence 31, Appl
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232	16	2.9	1874	3	US-09-614-957D-5	Sequence 5, Appl1
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234	16	2.9	2017	3	US-09-436-983-1	Sequence 1, Appl1
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236	16	2.9	2232	6	PCT-US96-05320A-113	Sequence 113, App
237	16	2.9	2340	3	US-09-949-016-4358	Sequence 4358, Ap
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242	16	2.9	2594	3	US-10-160-167-1	Sequence 1, Appl1
243	16	2.9	2732	3	US-09-933-999A-37	Sequence 37, Appl



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245	16	2.9	2775	3	US-09-270-767-5	Sequence 5, Appl1	c 318	16	2.9	5740	3	US-09-921-380-3	Sequence 3, Appl1
246	16	2.9	3023	3	US-09-308-022-4	Sequence 4, Appl1	c 319	16	2.9	5826	3	US-09-630-931A-11	Sequence 11, Appl1
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248	16	2.9	3225	3	US-09-358-856C-2	Sequence 2, Appl1	c 321	16	2.9	5838	2	US-08-944-916-3	Sequence 3, Appl1
249	16	2.9	3249	2	US-08-507-455-4	Sequence 4, Appl1	c 322	16	2.9	5838	2	US-08-814-877-3	Sequence 3, Appl1
250	16	2.9	3253	3	US-09-710-279-3887	Sequence 3887, Ap	c 323	16	2.9	5838	3	US-09-272-432A-3	Sequence 3, Appl1
251	16	2.9	3400	3	US-09-793-372-1	Sequence 1, Appl1	c 324	16	2.9	6043	3	US-09-630-929-4	Sequence 4, Appl1
252	16	2.9	3462	3	US-09-742-373-10	Sequence 10, Appl	c 325	16	2.9	6071	3	US-09-630-931A-12	Sequence 12, Appl1
253	16	2.9	3462	3	US-10-394-058-10	Sequence 10, Appl	c 326	16	2.9	6061	2	US-08-929-867-6	Sequence 6, Appl1
254	16	2.9	3501	3	US-09-633-145-3	Sequence 3, Appl1	c 327	16	2.9	6503	3	US-09-767-515-1	Sequence 1, Appl1
C 255	16	2.9	3532	3	US-09-710-279-3752	Sequence 3752, Ap	c 328	16	2.9	6501	3	US-09-767-515-2	Sequence 31, Appl1
C 256	16	2.9	3543	3	US-09-710-279-4149	Sequence 4149, Ap	c 329	16	2.9	6971	3	US-09-495-880A-31	Sequence 18, Appl
257	16	2.9	3801	3	US-09-640-882-1	Sequence 1, Appl1	c 330	16	2.9	7055	3	US-09-495-880A-18	Sequence 18, Appl1
C 258	16	2.9	3803	2	US-07-623-953-1	Sequence 1, Appl1	c 331	16	2.9	7326	9	5304637-21	Patent No. 5304637
C 259	16	2.9	3803	2	US-07-640-476-1	Sequence 1, Appl1	c 332	16	2.9	7336	2	US-08-418-085-3	Sequence 3, Appl1
260	16	2.9	3818	3	US-09-799-451-542	Sequence 542, App	c 333	16	2.9	7336	3	US-09-099-011A-3	Sequence 3, Appl1
261	16	2.9	3822	3	US-08-675-566-8	Sequence 8, Appl1	c 334	16	2.9	7336	3	US-08-470-369-21	Sequence 21, Appl1
262	16	2.9	3840	3	US-09-710-279-3187	Sequence 3187, Ap	c 335	16	2.9	7336	3	US-09-098-877B-3	Sequence 3, Appl1
263	16	2.9	3861	3	US-08-675-566-11	Sequence 11, Appl	c 336	16	2.9	7379	3	US-08-675-566-13	Sequence 13, Appl
264	16	2.9	3881	3	US-09-744-016A-15	Sequence 15, Appl	c 337	16	2.9	7424	3	US-09-596-002-8	Sequence 8, Appl1
265	16	2.9	3888	3	US-08-675-566-12	Sequence 12, Appl	c 338	16	2.9	7507	2	US-08-975-763-1	Sequence 1, Appl1
266	16	2.9	3955	3	US-08-675-566-10	Sequence 10, Appl	c 339	16	2.9	7566	2	US-08-232-016-23	Sequence 23, Appl1
267	16	2.9	3975	3	US-09-744-016A-13	Sequence 13, Appl	c 340	16	2.9	7639	2	US-08-232-016-22	Sequence 22, Appl
268	16	2.9	3977	2	US-07-794-400-2	Sequence 2, Appl1	c 341	16	2.9	7783	3	US-09-495-880A-3	Sequence 3, Appl1
269	16	2.9	3977	2	US-07-794-400-13	Sequence 13, Appl	c 342	16	2.9	7811	2	US-08-549-680A-5	Sequence 5, Appl1
270	16	2.9	3977	2	US-08-041-648-1	Sequence 1, Appl1	c 343	16	2.9	8906	3	US-09-027-169-5	Sequence 5, Appl1
271	16	2.9	3977	2	US-08-217-529-1	Sequence 1, Appl1	c 344	16	2.9	9652	3	US-10-007-527A-7	Sequence 7, Appl1
272	16	2.9	3977	2	US-08-397-470-2	Sequence 2, Appl1	c 345	16	2.9	9737	3	US-09-479-122-22	Sequence 22, Appl
273	16	2.9	3977	2	US-08-397-470-13	Sequence 13, Appl	c 346	16	2.9	9737	3	US-09-479-122-22	Sequence 22, Appl
274	16	2.9	3996	3	US-09-949-016-3026	Sequence 2026, Ap	c 347	16	2.9	9737	3	US-09-479-122-28	Sequence 28, Appl
275	16	2.9	4009	3	US-08-675-566-9	Sequence 9, Appl1	c 348	16	2.9	9737	3	US-09-484-997-22	Sequence 22, Appl
276	16	2.9	4045	3	US-09-809-517A-37	Sequence 37, Appl	c 349	16	2.9	9737	3	US-09-484-997-23	Sequence 23, Appl
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C 278	16	2.9	4055	3	US-09-620-312D-706	Sequence 706, App	c 351	16	2.9	9737	3	US-09-481-355-22	Sequence 22, Appl
C 279	16	2.9	4103	3	US-09-949-016-98	Sequence 98, Appl	c 352	16	2.9	9737	3	US-09-481-355-23	Sequence 23, Appl
C 280	16	2.9	4109	3	US-09-949-016-4227	Sequence 4227, Ap	c 353	16	2.9	9737	3	US-09-481-355-28	Sequence 28, Appl
C 281	16	2.9	4245	2	US-08-929-967-4	Sequence 4, Appl1	c 354	16	2.9	9737	3	US-09-481-355-28	Sequence 28, Appl
C 282	16	2.9	4338	2	US-08-015-986A-1	Sequence 1, Appl1	c 355	16	2.9	9737	3	US-09-481-355-28	Sequence 28, Appl
C 283	16	2.9	4338	2	US-08-446-363-1	Sequence 1, Appl1	c 356	16	2.9	9737	3	US-09-481-355-28	Sequence 28, Appl
C 284	16	2.9	4411	2	US-08-929-967-5	Sequence 5, Appl1	c 357	16	2.9	9737	3	US-09-481-355-28	Sequence 28, Appl
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286	16	2.9	4503	3	US-08-975-566-7	Sequence 7, Appl1	c 359	16	2.9	9737	3	US-09-455-659A-28	Sequence 28, Appl
287	16	2.9	4544	3	US-08-956-171E-517	Sequence 517, App	c 360	16	2.9	9737	3	US-09-484-996-22	Sequence 22, Appl
288	16	2.9	4544	3	US-08-781-986A-517	Sequence 517, App	c 361	16	2.9	9737	3	US-09-484-996-23	Sequence 23, Appl
289	16	2.9	4755	3	US-09-837-863-34	Sequence 34, Appl1	c 362	16	2.9	9737	3	US-09-484-996-28	Sequence 28, Appl
290	16	2.9	5000	3	US-09-147-522-5	Sequence 5, Appl1	c 363	16	2.9	9737	3	US-09-479-123-22	Sequence 22, Appl
291	16	2.9	5096	2	US-08-106-433A-3	Sequence 3, Appl1	c 364	16	2.9	9737	3	US-09-479-123-23	Sequence 23, Appl
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294	16	2.9	5110	2	US-08-106-433A-6	Sequence 6, Appl1	c 367	16	2.9	9737	3	US-09-484-317A-23	Sequence 23, Appl
295	16	2.9	5110	2	US-08-106-433A-7	Sequence 7, Appl1	c 368	16	2.9	9737	3	US-09-484-317A-28	Sequence 28, Appl
296	16	2.9	5110	2	US-08-106-433A-8	Sequence 8, Appl1	c 369	16	2.9	9737	3	US-09-276-820A-22	Sequence 22, Appl
297	16	2.9	5110	2	US-08-106-433A-9	Sequence 9, Appl1	c 370	16	2.9	9737	3	US-09-276-820A-23	Sequence 23, Appl
298	16	2.9	5110	2	US-08-106-433A-10	Sequence 10, Appl	c 371	16	2.9	9737	3	US-09-376-820A-28	Sequence 28, Appl
299	16	2.9	5110	2	US-08-106-433A-11	Sequence 11, Appl	c 372	16	2.9	9871	3	US-09-479-122-24	Sequence 24, Appl
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301	16	2.9	5110	2	US-08-106-433A-13	Sequence 13, Appl	c 374	16	2.9	9871	3	US-09-481-355-24	Sequence 24, Appl
302	16	2.9	5110	2	US-08-106-433A-14	Sequence 14, Appl	c 375	16	2.9	9871	3	US-09-481-355-24	Sequence 24, Appl
303	16	2.9	5110	2	US-08-106-433A-15	Sequence 15, Appl	c 376	16	2.9	9871	3	US-09-455-659A-24	Sequence 24, Appl
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305	16	2.9	5201	3	US-09-640-882-1	Sequence 3, Appl1	c 378	16	2.9	9871	3	US-09-479-123-24	Sequence 24, Appl
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C 307	16	2.9	5241	3	US-08-809-513A-2	Sequence 2, Appl1	c 380	16	2.9	9871	3	US-09-376-820A-24	Sequence 24, Appl
308	16	2.9	5262	3	US-09-298-367B-5	Sequence 5, Appl1	c 381	16	2.9	10060	3	US-09-479-122-25	Sequence 25, Appl1
309	16	2.9	5498	3	US-09-744-016A-29	Sequence 29, Appl	c 382	16	2.9	10060	3	US-09-484-997-25	Sequence 25, Appl1
310	16	2.9	5525	3	US-09-744-016A-20	Sequence 20, Appl	c 383	16	2.9	10060	3	US-09-481-355-25	Sequence 25, Appl1
311	16	2.9	5528	3	US-09-744-016A-32	Sequence 32, Appl	c 384	16	2.9	10060	3	US-09-481-355-25	Sequence 25, Appl1
312	16	2.9	5555	3	US-09-744-016A-17	Sequence 17, Appl	c 385	16	2.9	10060	3	US-09-455-659A-25	Sequence 25, Appl
313	16	2.9	5557	3	US-09-744-016A-23	Sequence 23, Appl	c 386	16	2.9	10060	3	US-09-484-996-25	Sequence 25, Appl1
314	16	2.9	5611	3	US-09-744-016A-26	Sequence 26, Appl	c 387	16	2.9	10060	3	US-09-479-123-25	Sequence 25, Appl1
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C 316	16	2.9	5670	3	US-09-630-931A-14	Sequence 14, Appl	c 389	16	2.9	10060	3	US-09-276-820A-25	Sequence 25, Appl



390	16	2.9	10554	3	US-09-949-016-12320	Sequence 12320, A	463	16	2.9	105001	3	US-09-949-002-627	Sequence 627, App
391	16	2.9	10554	3	US-09-949-016-16084	Sequence 16084, A	464	16	2.9	105002	3	US-09-949-002-821	Sequence 821, App
392	16	2.9	10580	2	US-08-196-259-1	Sequence 1, Appl1	465	16	2.9	107329	3	US-09-949-016-12663	Sequence 12663, A
393	16	2.9	10580	2	US-08-956-171E-364	Sequence 364, App	466	16	2.9	107329	3	US-09-949-016-12664	Sequence 12664, A
394	16	2.9	10813	3	US-08-781-986A-364	Sequence 364, App	467	16	2.9	107330	3	US-09-949-016-15408	Sequence 15408, A
395	16	2.9	10891	3	US-09-134-001C-2243	Sequence 2243, App	468	16	2.9	107330	3	US-09-949-016-15409	Sequence 15409, A
396	16	2.9	11186	3	US-09-949-016-13399	Sequence 13399, A	469	16	2.9	107330	3	US-09-949-016-15410	Sequence 15410, A
397	16	2.9	11201	3	US-09-973-278-707	Sequence 707, App	470	16	2.9	107330	3	US-09-949-016-15411	Sequence 15411, A
398	16	2.9	11241	3	US-10-007-527A-6	Sequence 6, Appl1	471	16	2.9	107750	3	US-09-949-016-15412	Sequence 15412, A
399	16	2.9	11662	3	US-09-949-016-13148	Sequence 13148, A	472	16	2.9	107751	3	US-09-949-016-15413	Sequence 15413, A
400	16	2.9	11673	3	US-09-949-016-13671	Sequence 13671, A	473	16	2.9	107751	3	US-09-949-016-15414	Sequence 15414, A
401	16	2.9	11690	3	US-09-949-016-16592	Sequence 16592, A	474	16	2.9	107751	3	US-09-949-016-15415	Sequence 15415, A
402	16	2.9	13825	3	US-09-634-238-59	Sequence 29, Appl	475	16	2.9	107925	3	US-09-949-016-15416	Sequence 15416, A
403	16	2.9	14602	2	US-08-597-236-1	Sequence 1, Appl1	476	16	2.9	107925	3	US-09-949-016-15417	Sequence 15417, A
404	16	2.9	14602	2	US-08-746-682A-1	Sequence 12169, A	477	16	2.9	107926	3	US-09-949-016-15405	Sequence 15405, A
405	16	2.9	15053	3	US-09-949-016-12169	Sequence 12169, A	478	16	2.9	107926	3	US-09-949-016-15406	Sequence 15406, A
406	16	2.9	15503	3	US-09-949-016-17151	Sequence 17151, A	479	16	2.9	107926	3	US-09-949-016-15407	Sequence 15407, A
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408	16	2.9	19910	3	US-09-949-002-638	Sequence 638, App	481	16	2.9	111459	3	US-09-949-016-14397	Sequence 14397, A
409	16	2.9	21513	3	US-09-949-016-16695	Sequence 769, App	482	16	2.9	111459	3	US-09-949-016-17379	Sequence 17379, A
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417	16	2.9	24201	3	US-09-949-016-13874	Sequence 13874, A	490	16	2.9	133559	3	US-09-949-016-12816	Sequence 12816, A
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423	16	2.9	29558	3	US-09-949-016-15607	Sequence 15607, A	496	16	2.9	145320	3	US-09-949-016-12787	Sequence 12787, A
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426	16	2.9	30246	3	US-08-956-171E-56	Sequence 56, Appl	499	16	2.9	161900	3	US-09-949-016-12685	Sequence 12685, A
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432	16	2.9	33827	2	US-09-949-002-760	Sequence 760, App	505	16	2.9	235452	3	US-09-949-016-16101	Sequence 16101, A
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437	16	2.9	36047	3	US-09-949-016-13966	Sequence 13966, A	510	16	2.9	314798	3	US-09-949-016-13539	Sequence 13539, A
438	16	2.9	44377	3	US-09-949-016-11840	Sequence 11840, A	511	16	2.9	314798	3	US-09-539-333D-1	Sequence 3, Appl1
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441	16	2.9	46340	3	US-09-719-554-66	Sequence 66, App	514	16	2.9	363033	3	US-09-949-016-15754	Sequence 15754, A
442	16	2.9	49744	3	US-09-927-091-4	Sequence 4, Appl1	515	16	2.9	466589	3	US-09-949-016-12900	Sequence 12900, A
443	16	2.9	51620	3	US-09-949-016-12848	Sequence 12848, A	516	16	2.9	476044	3	US-09-949-016-12412	Sequence 12412, A
444	16	2.9	51621	3	US-09-949-016-16503	Sequence 16503, A	517	15	2.7	19	3	US-09-495-880A-1	Sequence 1, Appl1
445	16	2.9	58879	3	US-09-949-016-16052	Sequence 16052, A	518	15	2.7	29	3	US-08-988-234-4	Sequence 4, Appl1
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449	16	2.9	66480	3	US-09-949-016-14817	Sequence 14817, A	522	15	2.7	146	3	US-09-513-999C-12227	Sequence 12227, A
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452	16	2.9	69764	3	US-09-949-016-15638	Sequence 15638, A	525	15	2.7	168	3	US-09-513-999C-25877	Sequence 25877, A
453	16	2.9	72604	3	US-09-268-992-7	Sequence 7, Appl1	526	15	2.7	189	3	US-08-956-171E-1192	Sequence 1192, App
454	16	2.9	72604	3	US-09-657-474-7	Sequence 7, Appl1	527	15	2.7	189	3	US-08-781-986A-1192	Sequence 1192, App
455	16	2.9	74940	3	US-09-949-016-17112	Sequence 17112, A	528	15	2.7	189	3	US-09-248-796A-8280	Sequence 8280, App
456	16	2.9	88490	3	US-09-949-016-12758	Sequence 12758, A	529	15	2.7	189	3	US-09-248-796A-13343	Sequence 13343, A
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459	16	2.9	96866	3	US-09-949-016-13768	Sequence 13768, A	532	15	2.7	245	3	US-09-513-999C-34334	Sequence 34344, App
460	16	2.9	100928	3	US-09-949-016-16926	Sequence 16926, A	533	15	2.7	246	3	US-09-248-796A-8514	Sequence 8514, App
461	16	2.9	101981	3	US-09-949-016-13995	Sequence 13995, A	534	15	2.7	255	3	US-09-270-767-25671	Sequence 25671, A
462	16	2.9	101982	3	US-09-949-016-12590	Sequence 12590, A	535	15	2.7	263	3	US-09-621-976-10772	Sequence 10772, A



C 536	15	2.7	278	3	US-09-313-294A-1203	Sequence 1203, Ap	609	15	2.7	601	3	US-09-949-016-66476	Sequence 66476, A
C 537	15	2.7	295	3	US-09-513-999C-20237	Sequence 20237, A	C 610	15	2.7	601	3	US-09-949-016-70825	Sequence 70825, A
C 538	15	2.7	318	3	US-09-248-796A-9A13	Sequence 9A13, Ap	C 611	15	2.7	601	3	US-09-949-016-70826	Sequence 70826, A
C 539	15	2.7	321	3	US-09-107-532A-1330	Sequence 1330, Ap	C 612	15	2.7	601	3	US-09-949-016-72589	Sequence 72589, A
C 540	15	2.7	332	3	US-09-270-767-10299	Sequence 10299, A	C 613	15	2.7	601	3	US-09-949-016-73809	Sequence 73809, A
C 541	15	2.7	340	3	US-08-836-075A-71	Sequence 71, Appl	C 614	15	2.7	601	3	US-09-949-016-76029	Sequence 76029, A
C 542	15	2.7	349	2	US-08-275-225-10	Sequence 10, Appl	C 615	15	2.7	601	3	US-09-949-016-81689	Sequence 81689, A
C 543	15	2.7	359	3	US-09-513-999C-3544	Sequence 3544, Ap	C 616	15	2.7	601	3	US-09-949-016-81690	Sequence 81690, A
C 544	15	2.7	394	3	US-09-513-999C-1282	Sequence 1292, Ap	C 617	15	2.7	601	3	US-09-949-016-81691	Sequence 81691, A
C 545	15	2.7	394	3	US-09-621-976-730	Sequence 3730, Ap	C 618	15	2.7	601	3	US-09-949-016-81692	Sequence 81692, A
C 546	15	2.7	402	3	US-09-134-000C-518	Sequence 518, App	C 619	15	2.7	601	3	US-09-949-016-83024	Sequence 83024, A
C 547	15	2.7	403	3	US-09-513-999C-3060	Sequence 3060, Ap	C 620	15	2.7	601	3	US-09-949-016-83025	Sequence 83025, A
C 548	15	2.7	409	3	US-09-621-976-18894	Sequence 18894, A	C 621	15	2.7	601	3	US-09-949-016-85145	Sequence 85145, A
C 549	15	2.7	439	2	US-08-644-729-27	Sequence 27, Appl	C 622	15	2.7	601	3	US-09-949-016-94491	Sequence 94491, A
C 550	15	2.7	460	3	US-09-280-116-57	Sequence 67, Appl	C 623	15	2.7	601	3	US-09-949-016-94503	Sequence 94503, A
C 551	15	2.7	461	3	US-09-513-999C-22049	Sequence 22049, A	C 624	15	2.7	601	3	US-09-949-016-95019	Sequence 95019, A
C 552	15	2.7	466	3	US-09-270-767-7715	Sequence 6715, Ap	C 625	15	2.7	601	3	US-09-949-016-95131	Sequence 95131, A
C 553	15	2.7	466	3	US-09-270-767-21997	Sequence 21997, A	C 626	15	2.7	601	3	US-09-949-016-103705	Sequence 103705, A
C 554	15	2.7	470	3	US-09-513-999C-2356	Sequence 2356, Ap	C 627	15	2.7	601	3	US-09-949-016-115305	Sequence 115305, A
C 555	15	2.7	485	3	US-09-621-976-3929	Sequence 2329, Ap	C 628	15	2.7	601	3	US-09-949-016-119339	Sequence 119339, A
C 556	15	2.7	485	3	US-09-280-116-39	Sequence 39, Appl	C 629	15	2.7	601	3	US-09-949-016-119351	Sequence 119351, A
C 557	15	2.7	488	3	US-09-621-976-11110	Sequence 11110, A	C 630	15	2.7	601	3	US-09-949-016-119352	Sequence 119352, A
C 558	15	2.7	501	3	US-10-178-449A-5	Sequence 5, Appl1	C 631	15	2.7	601	3	US-09-949-016-123805	Sequence 123805, A
C 559	15	2.7	510	3	US-09-270-767-928	Sequence 928, App	C 632	15	2.7	601	3	US-09-949-016-126569	Sequence 126569, A
C 560	15	2.7	510	3	US-09-270-767-16210	Sequence 16210, A	C 633	15	2.7	601	3	US-09-949-016-126570	Sequence 126570, A
C 561	15	2.7	516	3	US-09-248-796A-8513	Sequence 8513, Ap	C 634	15	2.7	601	3	US-09-949-016-127070	Sequence 127070, A
C 562	15	2.7	525	3	US-09-601-198-11	Sequence 11, Appl	C 635	15	2.7	601	3	US-09-949-016-127071	Sequence 127071, A
C 563	15	2.7	537	3	US-09-107-532A-1541	Sequence 1541, Ap	C 636	15	2.7	601	3	US-09-949-016-137393	Sequence 137393, A
C 564	15	2.7	537	3	US-09-107-532A-2913	Sequence 2913, Ap	C 637	15	2.7	601	3	US-09-949-016-137394	Sequence 137394, A
C 565	15	2.7	537	3	US-09-134-000C-2403	Sequence 2403, Ap	C 638	15	2.7	601	3	US-09-949-016-137922	Sequence 137922, A
C 566	15	2.7	537	3	US-09-710-279-3099	Sequence 3099, Ap	C 639	15	2.7	601	3	US-09-949-016-140842	Sequence 140842, A
C 567	15	2.7	549	3	US-09-489-039A-6026	Sequence 6026, Ap	C 640	15	2.7	601	3	US-09-949-016-147519	Sequence 147519, A
C 568	15	2.7	549	3	US-09-248-796A-179	Sequence 179, App	C 641	15	2.7	601	3	US-09-949-016-147579	Sequence 147579, A
C 569	15	2.7	552	3	US-09-107-433-2199	Sequence 2199, Ap	C 642	15	2.7	601	3	US-09-949-016-150903	Sequence 150903, A
C 570	15	2.7	556	3	US-09-018-584A-25	Sequence 25, Appl	C 643	15	2.7	601	3	US-09-949-016-150926	Sequence 150926, A
C 571	15	2.7	556	3	US-09-784-423-25	Sequence 423, Appl	C 644	15	2.7	601	3	US-09-949-016-151547	Sequence 151547, A
C 572	15	2.7	558	3	US-09-134-001C-456	Sequence 456, App	C 645	15	2.7	601	3	US-09-949-016-153570	Sequence 153570, A
C 573	15	2.7	562	3	US-09-621-976-10663	Sequence 10663, A	C 646	15	2.7	601	3	US-09-949-016-155178	Sequence 155178, A
C 574	15	2.7	573	3	US-08-956-171E-7	Sequence 7, Appl1	C 647	15	2.7	601	3	US-09-949-016-155515	Sequence 155515, A
C 575	15	2.7	573	3	US-08-781-986A-7	Sequence 7, Appl1	C 648	15	2.7	601	3	US-09-949-016-155614	Sequence 155614, A
C 576	15	2.7	577	3	US-09-270-767-77324	Sequence 27324, A	C 649	15	2.7	601	3	US-09-949-016-155884	Sequence 155884, A
C 577	15	2.7	597	3	US-09-107-532A-907	Sequence 907, App	C 650	15	2.7	601	3	US-09-949-016-155885	Sequence 155885, A
C 578	15	2.7	601	3	US-09-949-016-17615	Sequence 17615, A	C 651	15	2.7	601	3	US-09-949-016-155886	Sequence 155886, A
C 579	15	2.7	601	3	US-09-949-016-18766	Sequence 18766, A	C 652	15	2.7	601	3	US-09-949-016-155958	Sequence 155958, A
C 580	15	2.7	601	3	US-09-949-016-18767	Sequence 18767, A	C 653	15	2.7	601	3	US-09-949-016-155959	Sequence 155959, A
C 581	15	2.7	601	3	US-09-949-016-19372	Sequence 19372, A	C 654	15	2.7	601	3	US-09-949-016-155960	Sequence 155960, A
C 582	15	2.7	601	3	US-09-949-016-24053	Sequence 24053, A	C 655	15	2.7	601	3	US-09-949-016-156642	Sequence 156642, A
C 583	15	2.7	601	3	US-09-949-016-24054	Sequence 24054, A	C 656	15	2.7	601	3	US-09-949-016-160566	Sequence 160566, A
C 584	15	2.7	601	3	US-09-949-016-26347	Sequence 26347, A	C 657	15	2.7	601	3	US-09-949-016-160567	Sequence 160567, A
C 585	15	2.7	601	3	US-09-949-016-27713	Sequence 27713, A	C 658	15	2.7	601	3	US-09-949-016-162033	Sequence 162033, A
C 586	15	2.7	601	3	US-09-949-016-30340	Sequence 30340, A	C 659	15	2.7	601	3	US-09-949-016-162034	Sequence 162034, A
C 587	15	2.7	601	3	US-09-949-016-32166	Sequence 32166, A	C 660	15	2.7	601	3	US-09-949-016-162149	Sequence 162149, A
C 588	15	2.7	601	3	US-09-949-016-33180	Sequence 33180, A	C 661	15	2.7	601	3	US-09-949-016-164199	Sequence 164199, A
C 589	15	2.7	601	3	US-09-949-016-34253	Sequence 34253, A	C 662	15	2.7	601	3	US-09-949-016-164640	Sequence 164640, A
C 590	15	2.7	601	3	US-09-949-016-34333	Sequence 34333, A	C 663	15	2.7	601	3	US-09-949-016-165805	Sequence 165805, A
C 591	15	2.7	601	3	US-09-949-016-36637	Sequence 36637, A	C 664	15	2.7	601	3	US-09-949-016-166835	Sequence 166835, A
C 592	15	2.7	601	3	US-09-949-016-36638	Sequence 36638, A	C 665	15	2.7	601	3	US-09-949-016-166836	Sequence 166836, A
C 593	15	2.7	601	3	US-09-949-016-37618	Sequence 37618, A	C 666	15	2.7	601	3	US-09-949-016-176756	Sequence 176756, A
C 594	15	2.7	601	3	US-09-949-016-37619	Sequence 37619, A	C 667	15	2.7	601	3	US-09-949-016-177229	Sequence 177229, A
C 595	15	2.7	601	3	US-09-949-016-37620	Sequence 37620, A	C 668	15	2.7	601	3	US-09-949-016-179230	Sequence 179230, A
C 596	15	2.7	601	3	US-09-949-016-39620	Sequence 39620, A	C 669	15	2.7	601	3	US-09-949-016-181223	Sequence 181223, A
C 597	15	2.7	601	3	US-09-949-016-39940	Sequence 39940, A	C 670	15	2.7	601	3	US-09-949-016-181746	Sequence 181746, A
C 598	15	2.7	601	3	US-09-949-016-40173	Sequence 40173, A	C 671	15	2.7	601	3	US-09-949-016-181865	Sequence 181865, A
C 599	15	2.7	601	3	US-09-949-016-41140	Sequence 41140, A	C 672	15	2.7	601	3	US-09-949-016-181984	Sequence 181984, A
C 600	15	2.7	601	3	US-09-949-016-44246	Sequence 44246, A	C 673	15	2.7	601	3	US-09-949-016-188935	Sequence 188935, A
C 601	15	2.7	601	3	US-09-949-016-44809	Sequence 44809, A	C 674	15	2.7	601	3	US-09-949-016-188936	Sequence 188936, A
C 602	15	2.7	601	3	US-09-949-016-44810	Sequence 44810, A	C 675	15	2.7	601	3	US-09-949-016-188937	Sequence 188937, A
C 603	15	2.7	601	3	US-09-949-016-52185	Sequence 52185, A	C 676	15	2.7	601	3	US-09-949-016-188938	Sequence 188938, A
C 604	15	2.7	601	3	US-09-949-016-52810	Sequence 52810, A	C 677	15	2.7	601	3	US-09-949-016-190049	Sequence 190049, A
C 605	15	2.7	601	3	US-09-949-016-53344	Sequence 53344, A	C 678	15	2.7	601	3	US-09-949-016-195457	Sequence 195457, A
C 606	15	2.7	601	3	US-09-949-016-57548	Sequence 57548, A	C 679	15	2.7	601	3	US-09-949-016-195458	Sequence 195458, A
C 607	15	2.7	601	3	US-09-949-016-57549	Sequence 57549, A	C 680	15	2.7	601	3	US-09-949-016-196377	Sequence 196377, A
C 608	15	2.7	601	3	US-09-949-016-63374	Sequence 63374, A	C 681	15	2.7	601	3	US-09-949-016-196378	Sequence 196378, A



C 682	15	2.7	601	3	US-09-949-016-197770	Sequence 197770,
C 683	15	2.7	601	3	US-09-949-016-197771	Sequence 197771,
684	15	2.7	601	3	US-09-949-016-202467	Sequence 202467,
685	15	2.7	601	3	US-09-949-016-203961	Sequence 203961,
686	15	2.7	601	3	US-09-949-016-203962	Sequence 203962,
C 687	15	2.7	601	3	US-09-949-016-204352	Sequence 204352,
C 688	15	2.7	601	3	US-09-949-001-504	Sequence 104, App
C 689	15	2.7	601	3	US-09-949-001-560	Sequence 267, App
690	15	2.7	601	3	US-09-949-002-2967	Sequence 4564, Ap
691	15	2.7	601	3	US-09-949-002-4573	Sequence 4573, Ap
692	15	2.7	601	3	US-09-949-002-4574	Sequence 4574, Ap
693	15	2.7	601	3	US-09-949-002-4574	Sequence 4575, Ap
694	15	2.7	601	3	US-09-949-002-4575	Sequence 4575, Ap
695	15	2.7	601	3	US-09-949-002-4576	Sequence 4577, Ap
696	15	2.7	601	3	US-09-949-002-4577	Sequence 4586, Ap
697	15	2.7	606	3	US-09-270-767-5486	Sequence 20768, A
698	15	2.7	606	3	US-09-270-767-20768	Sequence 98, Appl
C 699	15	2.7	655	3	US-09-023-655-98	Sequence 6302, Ap
C 700	15	2.7	672	3	US-09-270-767-6302	Sequence 21584, A
C 701	15	2.7	672	3	US-09-270-767-21584	Sequence 2047, Ap
702	15	2.7	675	3	US-09-134-000C-2047	Sequence 3782, Ap
703	15	2.7	696	3	US-09-543-681A-3782	Sequence 1281, Ap
704	15	2.7	700	3	US-09-735-271-1281	Sequence 736, App
705	15	2.7	716	3	US-08-998-416-736	Sequence 9029, Ap
706	15	2.7	757	3	US-09-270-767-9029	Sequence 24311, A
707	15	2.7	757	3	US-09-270-767-24311	Sequence 11704, A
C 708	15	2.7	768	3	US-08-961-083-17	Sequence 17, Appl
709	15	2.7	775	3	US-09-536-784-17	Sequence 17, Appl
710	15	2.7	775	3	US-09-765-271-17	Sequence 17, Appl
711	15	2.7	775	3	US-09-765-271-17	Sequence 17, Appl
712	15	2.7	775	3	US-09-765-272A-17	Sequence 163, App
713	15	2.7	776	3	US-09-328-475C-163	Sequence 851, App
C 714	15	2.7	781	3	US-09-016-434-851	Sequence 2922, Ap
715	15	2.7	801	3	US-09-543-681A-2922	Sequence 1731, Ap
716	15	2.7	815	3	US-09-533-559-1731	Sequence 11, Appl
717	15	2.7	822	3	US-09-925-637-11	Sequence 736, App
718	15	2.7	837	3	US-09-583-110-736	Sequence 14191, A
C 719	15	2.7	839	3	US-09-270-767-14191	Sequence 1869, Ap
C 720	15	2.7	855	3	US-09-248-796A-1869	Sequence 3794, Ap
C 721	15	2.7	861	3	US-09-107-433-1492	Sequence 1492, Ap
722	15	2.7	889	3	US-09-533-559-225	Sequence 585, App
C 723	15	2.7	903	3	US-09-134-001C-585	Sequence 1143, Ap
C 724	15	2.7	909	3	US-09-710-279-1143	Sequence 2795, Ap
C 725	15	2.7	918	3	US-09-134-001C-2795	Sequence 1215, Ap
C 726	15	2.7	935	3	US-08-162-475A-3	Sequence 2492, Ap
727	15	2.7	942	3	US-09-710-279-1215	Sequence 1, Appl
C 728	15	2.7	957	3	US-09-328-352-2492	Sequence 12, Appl
C 729	15	2.7	966	2	US-08-162-475A-1	Sequence 12, Appl
730	15	2.7	966	2	US-08-181-271A-12	Sequence 12, Appl
731	15	2.7	968	2	US-08-449-315-12	Sequence 12, Appl
732	15	2.7	968	2	US-08-444-803-12	Sequence 12, Appl
733	15	2.7	968	2	US-08-444-803-12	Sequence 12, Appl
734	15	2.7	968	2	US-08-449-043-12	Sequence 12, Appl
735	15	2.7	968	2	US-08-456-265A-12	Sequence 12, Appl
736	15	2.7	968	2	US-08-455-416-12	Sequence 12, Appl
737	15	2.7	968	2	US-08-455-244-12	Sequence 12, Appl
738	15	2.7	968	2	US-08-454-876-12	Sequence 12, Appl
739	15	2.7	968	2	US-08-457-364-12	Sequence 12, Appl
740	15	2.7	968	2	US-08-456-262-12	Sequence 12, Appl
741	15	2.7	968	2	US-08-456-240-12	Sequence 12, Appl
742	15	2.7	968	2	US-08-455-736-12	Sequence 12, Appl
743	15	2.7	968	2	US-08-971-217-12	Sequence 12, Appl
744	15	2.7	968	2	US-09-350-600-12	Sequence 12, Appl
745	15	2.7	968	3	US-09-906-234-12	Sequence 12, Appl
746	15	2.7	969	3	US-09-712-016-46	Sequence 46, Appl
747	15	2.7	969	3	US-09-134-000C-3015	Sequence 3015, Ap
C 748	15	2.7	969	3	US-09-280-197-13	Sequence 13, Appl
749	15	2.7	978	3	US-09-710-279-697	Sequence 1329, Ap
750	15	2.7	978	3	US-10-197-220-119	Sequence 119, App
751	15	2.7	1026	3	US-09-533-559-4489	Sequence 4489, Ap
C 752	15	2.7	1044	3	US-09-495-406-12	Sequence 12, Appl
753	15	2.7	1044	3	US-09-816-028A-16	Sequence 16, Appl
754	15	2.7	1044	3	US-09-816-028A-16	Sequence 16, Appl

755	15	2.7	1044	3	US-10-303-162-16	Sequence 16, Appl
756	15	2.7	1044	3	US-10-303-134-16	Sequence 16, Appl
757	15	2.7	1044	3	US-10-303-118-16	Sequence 16, Appl
758	15	2.7	1044	3	US-10-303-128-16	Sequence 20, Appl
759	15	2.7	1056	3	US-09-816-028A-20	Sequence 20, Appl
760	15	2.7	1056	3	US-10-303-162-20	Sequence 20, Appl
761	15	2.7	1056	3	US-10-303-134-20	Sequence 20, Appl
762	15	2.7	1056	3	US-10-303-118-20	Sequence 20, Appl
763	15	2.7	1056	3	US-10-303-128-20	Sequence 20, Appl
C 764	15	2.7	1068	3	US-09-602-878A-671	Sequence 671, App
765	15	2.7	1074	3	US-09-710-279-409	Sequence 409, App
766	15	2.7	1113	3	US-09-859-822-3	Sequence 3, Appl
767	15	2.7	1116	3	US-09-134-000C-2694	Sequence 2694, Ap
C 768	15	2.7	1139	3	US-08-858-207A-29	Sequence 29, Appl
C 769	15	2.7	1173	3	US-09-826-509-530	Sequence 530, App
C 770	15	2.7	1191	3	US-09-248-796A-5820	Sequence 5820, Ap
771	15	2.7	1212	3	US-09-248-796A-2550	Sequence 2520, Ap
772	15	2.7	1281	3	US-09-327-487A-3	Sequence 4, Appl
773	15	2.7	1284	3	US-09-107-532A-2655	Sequence 2655, Ap
774	15	2.7	1305	2	US-08-307-499-36	Sequence 36, Appl
775	15	2.7	1323	3	US-09-289-268-36	Sequence 6598, Ap
776	15	2.7	1338	3	US-09-469-039A-6638	Sequence 331, App
C 777	15	2.7	1338	3	US-08-956-171E-331	Sequence 331, App
778	15	2.7	1341	3	US-08-781-986A-331	Sequence 1333, App
779	15	2.7	1352	6	PCT-US92-02091-7	Sequence 7, Appl
C 780	15	2.7	1352	6	US-09-004-838-25	Sequence 25, Appl
C 781	15	2.7	1365	3	US-09-087-277-3	Sequence 3, Appl
782	15	2.7	1393	3	US-09-658-499-3	Sequence 33, Appl
783	15	2.7	1399	3	US-08-956-171E-335	Sequence 335, App
784	15	2.7	1399	3	US-08-781-986A-335	Sequence 2048, Ap
785	15	2.7	1419	3	US-09-134-000C-2048	Sequence 96, Appl
C 786	15	2.7	1427	3	US-09-004-838-96	Sequence 31, Appl
C 787	15	2.7	1432	3	US-09-640-838-31	Sequence 332, App
788	15	2.7	1440	3	US-09-561-756-31	Sequence 31, Appl
C 789	15	2.7	1440	3	US-09-227-721-31	Sequence 31, Appl
C 790	15	2.7	1440	3	US-09-954-697-31	Sequence 8279, Ap
791	15	2.7	1452	3	US-09-248-796A-8279	Sequence 9, Appl
792	15	2.7	1458	3	US-09-334-938-9	Sequence 2, Appl
793	15	2.7	1458	3	US-09-516-914-2	Sequence 2602, Ap
794	15	2.7	1458	3	US-09-328-352-2602	Sequence 1, Appl
795	15	2.7	1458	3	US-09-286-691-1	Sequence 1, Appl
C 796	15	2.7	1458	3	US-09-687-147-1	Sequence 704, App
797	15	2.7	1558	3	US-09-248-796A-704	Sequence 5, Appl
798	15	2.7	1581	6	PCT-US92-02091-5	Sequence 11, App
800	15	2.7	1602	3	US-09-356-806-117	Sequence 21, Appl
C 801	15	2.7	1614	3	US-09-344-882-21	Sequence 21, Appl
C 802	15	2.7	1614	3	US-10-293-865-21	Sequence 5473, Ap
803	15	2.7	1642	3	US-09-270-767-5473	Sequence 20755, A
804	15	2.7	1642	3	US-09-270-767-5473	Sequence 267, App
C 805	15	2.7	1670	3	US-09-071-035-267	Sequence 8, Appl
C 806	15	2.7	1670	3	US-09-910-430-17	Sequence 1, Appl
C 807	15	2.7	1670	3	US-10-206-576-67	Sequence 1, Appl
C 808	15	2.7	1670	3	US-10-002-344A-1	Sequence 1, Appl
C 809	15	2.7	1678	3	US-08-665-220-1	Sequence 1, Appl
810	15	2.7	1700	2	US-09-952-768-1	Sequence 1, Appl
811	15	2.7	1700	3	US-09-952-768-1	Sequence 1, Appl
812	15	2.7	1700	3	US-09-952-768-1	Sequence 1, Appl
813	15	2.7	1700	3	US-09-952-768-1	Sequence 1, Appl
814	15	2.7	1700	3	US-10-668-955-1	Sequence 26193, A
815	15	2.7	1703	3	US-09-270-767-26193	Sequence 1, Appl
816	15	2.7	1704	3	US-09-962-834A-1	Sequence 1, Appl
817	15	2.7	1706	3	US-09-462-720-1	Sequence 1, Appl
818	15	2.7	1742	3	US-09-073-009-3	Sequence 3, Appl
C 819	15	2.7	1742	3	US-09-073-010-3	Sequence 3, Appl
C 820	15	2.7	1760	3	US-09-993-874-3	Sequence 19, Appl
C 821	15	2.7	1799	3	US-09-326-115C-19	Sequence 220, App
822	15	2.7	1799	3	US-09-620-312D-439	Sequence 439, App
C 823	15	2.7	1816	3	US-09-709-451-301	Sequence 301, App
C 824	15	2.7	1824	2	US-08-101-435-3	Sequence 3, Appl
825	15	2.7	1831	2	US-09-543-681A-1126	Sequence 1126, Ap
826	15	2.7	1848	3	US-10-104-047-117	Sequence 117, App
827	15	2.7	1866	3	US-10-104-047-117	Sequence 117, App



C 828	15	2.7	1878	3	US-09-248-796A-1624	Sequence 1624, Ap	C 901	15	2.7	3001	3	US-09-539-333D-224	Sequence 224, App
C 829	15	2.7	1896	3	US-09-543-681A-3070	Sequence 3070, Ap	C 902	15	2.7	3003	3	US-08-945-722-12	Sequence 12, Appl
830	15	2.7	1913	3	US-09-949-016-3601	Sequence 3601, Ap	C 903	15	2.7	3009	3	US-09-710-279-3896	Sequence 3896, Ap
831	15	2.7	1920	3	US-08-682-767-22	Sequence 22, Appl	C 904	15	2.7	3033	3	US-08-945-722-14	Sequence 14, Appl
832	15	2.7	1920	3	US-09-328-352-3660	Sequence 3660, Ap	C 905	15	2.7	3045	3	US-09-949-016-701	Sequence 701, App
C 833	15	2.7	1920	3	US-09-614-221A-457	Sequence 457, App	C 906	15	2.7	3074	3	US-09-087-277-1	Sequence 1, Appl
C 834	15	2.7	1920	3	US-09-447-497-4	Sequence 4, Appl	C 907	15	2.7	3074	3	US-09-658-499-1	Sequence 1, Appl
C 835	15	2.7	1921	3	US-08-682-767-21	Sequence 21, Appl	C 908	15	2.7	3126	3	US-09-710-279-4371	Sequence 4371, Ap
C 836	15	2.7	1932	3	US-09-447-497-2	Sequence 1, Appl	C 909	15	2.7	3206	3	US-09-774-528-287	Sequence 287, App
C 837	15	2.7	1952	3	US-09-976-594-63	Sequence 63, Appl	C 910	15	2.7	3206	3	US-10-120-988-287	Sequence 287, App
838	15	2.7	1952	3	US-09-919-039-61	Sequence 61, Appl	C 911	15	2.7	3231	3	US-08-945-722-18	Sequence 18, Appl
839	15	2.7	1966	3	US-08-714-918-84	Sequence 84, Appl	C 912	15	2.7	3253	3	US-09-710-279-3654	Sequence 3654, Ap
840	15	2.7	1966	3	US-09-265-315-44	Sequence 44, Appl	C 913	15	2.7	3276	3	US-08-633-768A-4	Sequence 4, Appl
841	15	2.7	1966	3	US-09-265-315-44	Sequence 44, Appl	C 914	15	2.7	3276	3	US-09-280-197-4	Sequence 4, Appl
842	15	2.7	1966	3	US-09-265-315-44	Sequence 44, Appl	C 915	15	2.7	3276	3	US-09-423-126-8	Sequence 8, Appl
843	15	2.7	1966	3	US-09-528-709-94	Sequence 94, Appl	C 916	15	2.7	3302	3	US-09-710-279-4016	Sequence 4016, Ap
C 844	15	2.7	1966	3	US-09-527-745-44	Sequence 44, Appl	C 917	15	2.7	3305	3	US-09-710-279-4002	Sequence 4002, Ap
C 845	15	2.7	1966	3	US-09-543-681A-3594	Sequence 3594, Ap	C 918	15	2.7	3312	3	US-09-710-279-3465	Sequence 3465, Ap
C 846	15	2.7	2097	3	US-09-487-558B-373	Sequence 373, App	C 919	15	2.7	3315	3	US-09-710-279-3820	Sequence 3820, Ap
C 847	15	2.7	2112	3	US-09-437-277-2	Sequence 2, Appl	C 920	15	2.7	3321	2	US-08-484-438-5	Sequence 5, Appl
C 848	15	2.7	2112	3	US-09-710-279-4414	Sequence 4414, Ap	C 921	15	2.7	3354	3	US-09-710-279-3763	Sequence 3763, Ap
C 849	15	2.7	2126	2	US-08-545-745-1	Sequence 1, Appl	C 922	15	2.7	3359	3	US-09-248-796A-923	Sequence 923, App
C 850	15	2.7	2149	3	US-09-023-655-539	Sequence 939, App	C 923	15	2.7	3420	3	US-09-513-505-1	Sequence 1, Appl
C 851	15	2.7	2151	3	US-09-328-352-3912	Sequence 3912, Ap	C 924	15	2.7	3431	3	US-09-710-279-4435	Sequence 4435, Ap
C 852	15	2.7	2152	3	US-08-724-378D-1	Sequence 1, Appl	C 925	15	2.7	3478	3	US-09-513-505-3	Sequence 3, Appl
C 853	15	2.7	2213	3	US-09-949-016-4499	Sequence 4499, Ap	C 926	15	2.7	3511	3	US-09-949-016-4656	Sequence 4656, Ap
C 854	15	2.7	2262	3	US-09-167-109-2	Sequence 2, Appl	C 927	15	2.7	3535	2	US-08-618-408B-1	Sequence 1, Appl
C 855	15	2.7	2276	3	US-09-927-738-37	Sequence 27, Appl	C 928	15	2.7	3536	3	US-09-949-002-273	Sequence 273, App
C 856	15	2.7	2315	3	US-08-961-527-194	Sequence 194, App	C 929	15	2.7	3583	3	US-09-949-002-31	Sequence 31, Appl
C 857	15	2.7	2347	3	US-10-104-047-1449	Sequence 1449, Ap	C 930	15	2.7	3588	3	US-09-976-594-74	Sequence 74, Appl
C 858	15	2.7	2373	2	US-08-445-586-1	Sequence 1, Appl	C 931	15	2.7	3635	3	US-09-710-279-4392	Sequence 4392, Ap
C 859	15	2.7	2379	3	US-09-107-532A-1487	Sequence 1487, Ap	C 932	15	2.7	3635	2	US-08-553-436A-5	Sequence 5, Appl
C 860	15	2.7	2430	3	US-09-949-016-1201	Sequence 1201, Ap	C 933	15	2.7	3631	3	US-09-710-279-3338	Sequence 3338, Ap
C 861	15	2.7	2513	3	US-09-270-767-10733	Sequence 10733, A	C 934	15	2.7	3748	2	US-10-104-047-1031	Sequence 1031, Ap
C 862	15	2.7	2529	3	US-08-945-722-17	Sequence 17, Appl	C 935	15	2.7	3817	3	US-10-104-047-1	Sequence 1, Appl
C 863	15	2.7	2576	3	US-10-197-220-32	Sequence 32, Appl	C 936	15	2.7	3964	3	US-08-961-527-136	Sequence 136, App
C 864	15	2.7	2577	3	US-10-197-220-32	Sequence 32, Appl	C 937	15	2.7	4071	3	US-09-770-170-5	Sequence 5, Appl
C 865	15	2.7	2578	3	US-08-945-722-19	Sequence 19, Appl	C 938	15	2.7	4156	3	US-10-104-047-321	Sequence 321, App
C 866	15	2.7	2631	3	US-10-104-047-52	Sequence 52, Appl	C 939	15	2.7	4173	2	US-08-770-544-1	Sequence 1, Appl
C 867	15	2.7	2637	3	US-09-492-709A-204	Sequence 204, App	C 940	15	2.7	4173	3	US-09-579-259-1	Sequence 1, Appl
C 868	15	2.7	2682	3	US-09-949-016-5604	Sequence 5604, Ap	C 941	15	2.7	4173	3	US-09-650-324A-1	Sequence 1, Appl
C 869	15	2.7	2686	3	US-09-228-986-3	Sequence 3, Appl	C 942	15	2.7	4173	3	US-10-039-112A-1	Sequence 1, Appl
C 870	15	2.7	2686	3	US-10-101-464A-3	Sequence 3, Appl	C 943	15	2.7	4371	3	US-09-462-1136-8	Sequence 8, Appl
C 871	15	2.7	2696	3	US-09-949-016-298	Sequence 298, App	C 944	15	2.7	4934	3	US-09-221-017B-985	Sequence 985, App
C 872	15	2.7	2722	3	US-09-919-497-37	Sequence 37, Appl	C 945	15	2.7	4977	3	US-09-071-035-257	Sequence 257, App
C 873	15	2.7	2783	3	US-09-620-312D-107	Sequence 107, App	C 946	15	2.7	4977	3	US-09-071-035-261	Sequence 261, App
C 874	15	2.7	2790	3	US-09-134-000C-3019	Sequence 3019, Ap	C 947	15	2.7	4977	3	US-09-071-035-265	Sequence 265, App
C 875	15	2.7	2836	3	US-09-073-009-4	Sequence 4, Appl	C 948	15	2.7	4977	3	US-10-206-576-257	Sequence 257, App
C 876	15	2.7	2836	3	US-09-073-010-4	Sequence 4, Appl	C 949	15	2.7	4977	3	US-10-206-576-261	Sequence 261, App
C 877	15	2.7	2844	3	US-09-614-221A-81	Sequence 81, Appl	C 950	15	2.7	4977	3	US-10-206-576-265	Sequence 265, App
C 878	15	2.7	2872	3	US-09-327-487A-2	Sequence 2, Appl	C 951	15	2.7	4988	3	US-09-501-171-5	Sequence 5, Appl
C 879	15	2.7	2901	3	US-09-949-016-4707	Sequence 4707, Ap	C 952	15	2.7	5111	3	US-09-004-838-118	Sequence 118, App
C 880	15	2.7	2906	3	US-09-907-794A-291	Sequence 291, App	C 953	15	2.7	5244	3	US-09-134-000C-2594	Sequence 2594, App
C 881	15	2.7	2906	3	US-09-905-125A-291	Sequence 291, App	C 954	15	2.7	5245	3	US-09-976-594-546	Sequence 546, App
C 882	15	2.7	2906	3	US-09-902-775A-291	Sequence 291, App	C 955	15	2.7	5245	3	US-09-976-594-545	Sequence 546, App
C 883	15	2.7	2906	3	US-09-906-700-291	Sequence 291, App	C 956	15	2.7	5245	3	US-09-949-016-4210	Sequence 4210, Ap
C 884	15	2.7	2906	3	US-09-903-603A-291	Sequence 291, App	C 957	15	2.7	5252	3	US-09-949-016-338	Sequence 338, App
C 885	15	2.7	2906	3	US-09-904-920A-291	Sequence 291, App	C 958	15	2.7	5252	3	US-10-131-827-8827	Sequence 8827, Ap
C 886	15	2.7	2906	3	US-09-909-064-591	Sequence 291, App	C 959	15	2.7	5252	3	US-10-131-827-8828	Sequence 8828, Ap
C 887	15	2.7	2906	3	US-09-905-381A-291	Sequence 291, App	C 960	15	2.7	5444	3	US-09-632-580A-3	Sequence 3, Appl
C 888	15	2.7	2906	3	US-09-906-618-291	Sequence 291, App	C 961	15	2.7	5444	2	US-08-484-438-1	Sequence 1, Appl
C 889	15	2.7	2906	3	US-09-906-646-291	Sequence 291, App	C 962	15	2.7	5631	3	US-09-487-558B-101	Sequence 101, App
C 890	15	2.7	2906	3	US-09-904-462-291	Sequence 291, App	C 963	15	2.7	5852	2	US-07-467-106-2	Sequence 2, Appl
C 891	15	2.7	2906	3	US-09-902-736A-291	Sequence 291, App	C 964	15	2.7	6022	3	US-09-949-016-15582	Sequence 15582, A
C 892	15	2.7	2906	3	US-09-991-181-500	Sequence 500, App	C 965	15	2.7	6273	3	US-08-961-527-21	Sequence 21, Appl
C 893	15	2.7	2906	3	US-09-990-444-500	Sequence 500, App	C 966	15	2.7	6348	3	US-09-976-594-756	Sequence 756, App
C 894	15	2.7	2906	3	US-09-906-722A-291	Sequence 291, App	C 967	15	2.7	6348	3	US-09-919-039-366	Sequence 366, App
C 895	15	2.7	2906	3	US-09-997-333-500	Sequence 500, App	C 968	15	2.7	6371	3	US-08-836-325-13	Sequence 13, Appl
C 896	15	2.7	2906	3	US-09-992-598-500	Sequence 500, App	C 969	15	2.7	6371	3	US-09-457-571-13	Sequence 13, Appl
C 897	15	2.7	2937	3	US-09-469-200E-8	Sequence 8, Appl	C 970	15	2.7	6404	3	US-08-836-325-14	Sequence 14, Appl
C 898	15	2.7	2937	3	US-10-172-527A-9	Sequence 9, Appl	C 971	15	2.7	6404	3	US-09-457-571-14	Sequence 14, Appl
C 899	15	2.7	2975	3	US-08-945-722-13	Sequence 13, Appl	C 972	15	2.7	6572	3	US-09-620-312D-823	Sequence 823, App
C 900	15	2.7	3001	3	US-09-539-333D-223	Sequence 223, App	C 973	15	2.7	7655	2	US-08-619-554-1	Sequence 1, Appl



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974 15 2.7 7887 3 US-09-614-221A-563 Sequence 563, App
975 15 2.7 8145 3 US-08-961-527-122 Sequence 122, App
976 15 2.7 8630 3 US-09-973-278-677 Sequence 677, App
977 15 2.7 9179 3 US-08-956-171E-100 Sequence 100, App
978 15 2.7 9179 3 US-08-781-986A-100 Sequence 100, App
979 15 2.7 9338 3 US-09-949-016-13864 Sequence 13864, A
980 15 2.7 9506 3 US-09-949-016-16449 Sequence 16449, A
981 15 2.7 10088 3 US-08-956-171E-32 Sequence 32, Appl
982 15 2.7 10088 3 US-08-781-986A-32 Sequence 32, Appl
983 15 2.7 10228 3 US-09-949-016-12151 Sequence 12151, A
984 15 2.7 11459 3 US-09-462-136-7 Sequence 7, Appl
985 15 2.7 11474 3 US-09-495-406-1 Sequence 1, Appl
986 15 2.7 11474 3 US-09-816-028A-1 Sequence 1, Appl
987 15 2.7 11474 3 US-10-303-162-1 Sequence 1, Appl
988 15 2.7 11474 3 US-10-303-134-1 Sequence 1, Appl
989 15 2.7 11474 3 US-10-303-118-1 Sequence 1, Appl
990 15 2.7 11474 3 US-09-343-128-1 Sequence 1, Appl
991 15 2.7 11581 3 US-09-949-016-15173 Sequence 15173, A
992 15 2.7 11858 3 US-09-949-016-12443 Sequence 12443, A
993 15 2.7 11858 3 US-09-949-016-12443 Sequence 12443, A
994 15 2.7 12284 3 US-09-949-016-15243 Sequence 15243, A
995 15 2.7 12460 3 US-09-949-016-13009 Sequence 13009, A
996 15 2.7 12645 3 US-09-949-016-12306 Sequence 12306, A
997 15 2.7 13534 3 US-09-902-540-1078 Sequence 1078, A
998 15 2.7 14176 2 US-08-307-499-1 Sequence 1, Appl
999 15 2.7 14176 2 US-08-307-499-1 Sequence 1, Appl
c1000 15 2.7 14176 2 US-09-299-268-1 Sequence 1, Appl
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## ALIGNMENTS

RESULT 1  
US-09-949-016-12756

; Sequence 12756, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 12756

; LENGTH: 136264

; TYPE: DNA

; ORGANISM: Human

; PEPTIDE:

; NAME/KEY: misc\_feature

; LOCATION: (1)...(136264)

; OTHER INFORMATION: n = A,T,C or G

US-09-949-016-12756

Query Match

Best Local Similarity 100.0%; Pred. No. 1.8;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 173 AAATTATCTTCCAAATATAAA 193

Db 98332 AAATTATCTTCCAAATATAAA 98352

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 3  
US-09-949-016-14432

; Sequence 14432, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
US-09-949-016-14433

; Sequence 14433, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

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; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
US-09-949-016-14433

; Sequence 14433, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; FILE REFERENCE: CL001307

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; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

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Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
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; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
US-09-949-016-14433

; Sequence 14433, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

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; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
US-09-949-016-14433

; Sequence 14433, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

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; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 207 TGTTCGAGTGAATGTAATG 226

Db 18287 TGTTCGAGTGAATGTAATG 18306

Qy 173 AAATTATCTTCCAAATATAAA 193  
Db 98332 AAATTATCTTCCAAATATAAA 98352

RESULT 4  
US-09-949-016-14433

; Sequence 14433, Application US/09949016  
; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; FILE REFERENCE: CL001307

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03

; PRIOR APPLICATION NUMBER: 60/231,498

; PRIOR FILING DATE: 2000-09-08

; NUMBER OF SEQ ID NOS: 207012

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 14432

; LENGTH: 34172

; TYPE: DNA

; ORGANISM: Human

US-09-949-016-14432

Query Match

Best Local Similarity 100.0%; Pred. No. 5.8;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;



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; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14433
; LENGTH: 103934
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
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; LOCATION: (1)..(103934)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-14433
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Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      67687 TGTGTGAGTGTGATTAATG 67706
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US-09-134-000C-2462
; Sequence 2462, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; TITLE OF INVENTION: ENTEROCOCCUS FAECALIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2462
; LENGTH: 1863
; TYPE: DNA
; ORGANISM: Enterococcus faecalis
US-09-134-000C-2462
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Best Local Similarity 100.0%; Pred. No. 20;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      1491 TCCTGATTAGACGAGA 1509
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US-09-949-016-2387
; Sequence 2387, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
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; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2387
; LENGTH: 4663
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-2387
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Best Local Similarity 100.0%; Pred. No. 19;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      365 AGAGAAATACAAAGTGAT 383
Db      917 AGAGAAATACAAAGTGAT 935
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US-09-949-016-14129
; Sequence 14129, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14129
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; TYPE: DNA
; ORGANISM: Human
US-09-949-016-14129
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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db      25006 AGAGAAATACAAAGTGAT 25024
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US-09-949-016-13363/C
; Sequence 13363, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
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; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
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; SEQ ID NO 13363
; LENGTH: 47799
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-13363

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Best Local Similarity 100.0%; Pred. No. 18;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      216 GATTGTAATGTTTGAAGA 234
DB      6023 GATTGTAATGTTTGAAGA 6005

RESULT 9
US-09-949-016-122048/c
; Sequence 122048, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 122048
; LENGTH: 601
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-122048

Query Match          3.2%; Score 18; DB 3; Length 601;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      397 TCTAGAAATTCAGAAAGA 414
DB      475 TCTAGAAATTCAGAAAGA 458

RESULT 10
US-08-271-948-1
; Sequence 1, Application US/08271948
; Patent No. 6303769
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. 6303769e1 Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; APPLICATION NUMBER: US 08/271,948
; FILING DATE: Apple Macintosh
```

```

; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/271,948
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Seese, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hLERRK-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1002
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1..75
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 76..999
US-08-271-948-1

Query Match          3.2%; Score 18; DB 3; Length 1002;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      397 TCTAGAAATTCAGAAAGA 414
DB      369 TCTAGAAATTCAGAAAGA 386

RESULT 11
US-08-739-333-1
; Sequence 1, Application US/08739333
; Patent No. 6479459
; GENERAL INFORMATION:
; APPLICANT: Cerretti, Douglas P.
; APPLICANT: Reddy, Pranhitha
; TITLE OF INVENTION: No. 6479459e1 Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/739,333
; FILING DATE: 29-OCT-1996
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,948
; FILING DATE: 08-JUL-1994
```



ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2823  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1002 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hULK-5  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1002  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1..75  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 76..999  
US-08-739-333-1

Query Match 3.2%; Score 18; DB 3; Length 1002;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTAGATTTCAGAGAA 414  
|||||  
Db 369 TCTAGATTTCAGAGAA 386

RESULT 12  
US-09-754-105-1  
Sequence 1, Application US/09754105  
Patent No. 6492140  
GENERAL INFORMATION:  
APPLICANT: Cerretti, Douglas  
APPLICANT: Reddy, Pranhitha  
TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING CYTOKINE DESIGNATED LERK-5  
FILE REFERENCE: 28232  
CURRENT APPLICATION NUMBER: US/09/754,105  
CURRENT FILING DATE: 2001-01-03  
PRIOR APPLICATION NUMBER: 09/329,531  
PRIOR FILING DATE: 1999-06-10  
NUMBER OF SEQ ID NOS: 3  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 1002  
TYPE: DNA  
ORGANISM: homo sapiens  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: (76)..()  
NAME/KEY: CDS  
LOCATION: (1)..(999)  
NAME/KEY: sig\_peptide  
LOCATION: (1)..(75)  
US-09-754-105-1

Query Match 3.2%; Score 18; DB 3; Length 1002;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTAGATTTCAGAGAA 414  
|||||  
|||||

Db 369 TCTAGATTTCAGAGAA 386

RESULT 13  
US-09-978-339-1  
Sequence 1, Application US/09978339  
Patent No. 6596852  
GENERAL INFORMATION:  
APPLICANT: Cerretti, Douglas P.  
Reddy, Pranhitha  
TITLE OF INVENTION: No. 6596852el Cytokine Designated lerk-5  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: Washington  
COUNTRY: US  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Macintosh  
OPERATING SYSTEM: Apple 7.1  
SOFTWARE: Microsoft Word, Version 5.1a  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/978,339  
FILING DATE: 15-Oct-2001  
CLASSIFICATION: <Unknown>  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/271,948  
FILING DATE: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Seese, Kathryn A.  
REGISTRATION NUMBER: 32,172  
REFERENCE/DOCKET NUMBER: 2823  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206) 587-0430  
TELEFAX: (206) 233-0644  
TELEX: 756822  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1002 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHEICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: hULK-5  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1002  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 1..75  
NAME/KEY: mat\_peptide  
LOCATION: 76..999  
SEQUENCE DESCRIPTION: SEQ ID NO: 1:  
US-09-978-339-1

Query Match 3.2%; Score 18; DB 3; Length 1002;

Best Local Similarity 100.0%; Pred. No. 63;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTAGATTTCAGAGAA 414  
|||||  
Db 369 TCTAGATTTCAGAGAA 386

RESULT 14  
PCT-US95-08534-1



```
; Sequence 1, Application PC/TUS9508534
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; TITLE OF INVENTION: Novel Cytokine Designated Lerk-5
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: Washington
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Apple 7.1
; SOFTWARE: Microsoft Word, Version 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08534
; FILING DATE: 06-JUL-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,948
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Anderson, Kathryn A.
; REGISTRATION NUMBER: 32,172
; REFERENCE/DOCKET NUMBER: 2823-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1002 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA to mRNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: hULK-5
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 1..1002
; FEATURE:
; NAME/KEY: sig.peptide
; LOCATION: 1..75
; FEATURE:
; NAME/KEY: mat.peptide
; LOCATION: 76..999
; PCT-US95-08534-1

Query Match 3.2%; Score 18; DB 6; Length 1002;
Best Local Similarity 100.0%; Pred. No. 63;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTAGATTTCAGAAAGAA 414
DB 369 TCTAGATTTCAGAAAGAA 386

RESULT 15
US-08-436-044-3
; Sequence 3, Application US/08436044
; Patent No. 5624899
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
```

```
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,044
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902D3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1953 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-436-044-3

Query Match 3.2%; Score 18; DB 2; Length 1953;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 397 TCTAGATTTCAGAAAGAA 414
DB 400 TCTAGATTTCAGAAAGAA 417

RESULT 16
US-08-436-054-3
; Sequence 3, Application US/08436054
; Patent No. 5864020
; GENERAL INFORMATION:
; APPLICANT: Bennett, Brian D.
; APPLICANT: Matthews, William
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,054
; FILING DATE: 05-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/277722
; FILING DATE: 20-JUL-1994
; ATTORNEY/AGENT INFORMATION:
```



NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 902D1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1953 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-436-054-3

Query Match 3.2%; Score 18; DB 2; Length 1953;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAA 414  
DB 400 TCTGAATTTCAGAA 417

RESULT 17  
PCT-US95-08812-3  
Sequence 3, Application PC/TUS9508812  
GENERAL INFORMATION:  
APPLICANT: Genentech, Inc.  
TITLE OF INVENTION: HTK LIGAND  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US95/08812  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lee, Wendy M.  
REGISTRATION NUMBER: 00,000  
REFERENCE/DOCKET NUMBER: 902PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415/225-1994  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1953 bases  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
PCT-US95-08812-3

Query Match 3.2%; Score 18; DB 6; Length 1953;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAA 414  
DB 400 TCTGAATTTCAGAA 417

RESULT 18  
US-09-370-807-7  
Sequence 7, Application US/09370807  
Patent No. 6297034  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Rebecca E.  
APPLICANT: Falco, S. Carl  
APPLICANT: Rafaleki, J. Antoni  
TITLE OF INVENTION: N-End Rule Pathway Enzymes  
FILE REFERENCE: BB-1199  
CURRENT APPLICATION NUMBER: US/09/370,807  
CURRENT FILING DATE: 1999-08-09  
EARLIER APPLICATION NUMBER: 60/096,225  
EARLIER FILING DATE: August 12, 1998  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 7  
LENGTH: 2407  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-370-807-7

Query Match 3.2%; Score 18; DB 3; Length 2407;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 CTGCTGATTGAGCAG 130  
DB 22 CTGCTGATTGAGCAG 39

RESULT 19  
US-09-921-259-7  
Sequence 7, Application US/09921259  
Patent No. 6465234  
GENERAL INFORMATION:  
APPLICANT: Cahoon, Rebecca E.  
APPLICANT: Falco, S. Carl  
APPLICANT: Rafaleki, J. Antoni  
APPLICANT: Sakai, Hajime  
TITLE OF INVENTION: N-End Rule Pathway Enzymes  
FILE REFERENCE: BB-1199  
CURRENT APPLICATION NUMBER: US/09/921,259  
CURRENT FILING DATE: 2001-08-02  
PRIOR APPLICATION NUMBER: 60/096,225  
PRIOR FILING DATE: August 12, 1998  
NUMBER OF SEQ ID NOS: 16  
SOFTWARE: Microsoft Office 97  
SEQ ID NO 7  
LENGTH: 2407  
TYPE: DNA  
ORGANISM: Oryza sativa  
US-09-921-259-7

Query Match 3.2%; Score 18; DB 3; Length 2407;  
Best Local Similarity 100.0%; Pred. No. 61;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 CTGCTGATTGAGCAG 130  
DB 22 CTGCTGATTGAGCAG 39

RESULT 20  
US-09-949-016-582  
Sequence 582, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED



```

1  TITLE OF INVENTION:  WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
2  FILE REFERENCE:  CL001307
3  CURRENT APPLICATION NUMBER:  US/09/949,016
4  CURRENT FILING DATE:  2000-04-14
5  PRIOR APPLICATION NUMBER:  60/241,755
6  PRIOR FILING DATE:  2000-10-20
7  PRIOR APPLICATION NUMBER:  60/237,768
8  PRIOR FILING DATE:  2000-10-03
9  PRIOR APPLICATION NUMBER:  60/231,498
10 PRIOR FILING DATE:  2000-09-08
11 NUMBER OF SEQ ID NOS:  207012
12 SOFTWARE:  FastSeq for Windows Version 4.0
13 SEQ ID NO 582
14 LENGTH:  2902
15 TYPE:  DNA
16 ORGANISM:  Human
17 US-09-949-016-582

```

Query Match	3.2%;	Score 18;	DB 3;	Length 2902;
Best Local Similarity	100.0%;	Pred. No. 61;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	397	TCTAGAA	TT	TCAGA	GAA	414
Db	376	TCTAGAA	TT	TCAGA	GAA	393

RESULT 21  
US-09-949-016-3424

```

; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

```

Query Match	3.2%	Score 18;	DB 3;	Length 3356;
Best Local Similarity	100.0%;	Pred 10;	60;	
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

Qy 397 TCTAGAAATTCAGAAGAA 414  
|||||  
Db 377 TCTAGAAATTCAGAAGAA 394

RESULT 22  
 US-08-436-044-1  
 Sequence 1, Application US/08436044  
 Patent No. 5624899  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Brian D.  
 APPLICANT: Matthews, William  
 TITLE OF INVENTION: HTR LIGAND  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSES: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 /

CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genetech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,044  
 FILING DATE: 05-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/277722  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 00,000  
 REFERENCE/DOCKET NUMBER: 90D3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1994  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 1:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4342 bases  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear

US-08-436-044-1

Query Match	3.2%;	Score 18;	DB 2;	Length 4342;
Best Local Similarity	100.0%;	Pred. No. 60;		
Matches 18;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	397	TCTAGAA	TT	CAGAAGAA	414
Db	538	TCTAGAA	TT	CAGAAGAA	555

RESULT 23  
 US-08-436-054-1  
 Sequence 1, Application US/08436054  
 Patent No. 5864020  
 GENERAL INFORMATION:  
 APPLICANT: Bennett, Brian D.  
 APPLICANT: Matthews, William  
 TITLE OF INVENTION: HTK LIGAND  
 NUMBER OF SEQUENCES: 7  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: datin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/436,054  
 FILING DATE: 05-MAY-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/277722  
 FILING DATE: 20-JUL-1994  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Lee, Wendy M.  
 REGISTRATION NUMBER: 00,000  
 REFERENCE/DOCKET NUMBER: 902D1



```

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4342 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-436-054-1

Query Match          3.2%; Score 18; DB 2; Length 4342;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAGAA 414
    |||
Db 538 TCTGAATTTCAGAGAA 555

RESULT 24
PCT-US95-08812-1
; Sequence 1, Application PC/TUS9508812
; GENERAL INFORMATION:
; APPLICANT: Genentech, Inc.
; TITLE OF INVENTION: HTK LIGAND
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08812
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 00,000
; REFERENCE/DOCKET NUMBER: 902PCT
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4342 bases
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
PCT-US95-08812-1

Query Match          3.2%; Score 18; DB 6; Length 4342;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAGAA 414
    |||
Db 538 TCTGAATTTCAGAGAA 555

RESULT 25
```

```

US-09-949-016-12324
; Sequence 12324, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12324
; LENGTH: 47818
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(47818)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12324

Query Match          3.2%; Score 18; DB 3; Length 47818;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAGAA 414
    |||
Db 24398 TCTGAATTTCAGAGAA 24415

RESULT 26
US-09-949-016-15166
; Sequence 15166, Application US/09949016
; Patent No. 681239
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15166
; LENGTH: 48480
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(48480)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-15166

Query Match          3.2%; Score 18; DB 3; Length 48480;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 397 TCTGAATTTCAGAGAA 414
    |||
Db 24398 TCTGAATTTCAGAGAA 24415
```



```
RESULT 27
US-09-949-016-12705
; Sequence 12705, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12705
; LENGTH: 271134
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(271134)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-12705

Query Match      3.2%; Score 18; DB 3; Length 271134;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      209 TTGAGTGATTGTAATG 226
DB      20533 TTGGAGTGATTGTAATG 20550

RESULT 28
US-09-949-016-17550
; Sequence 17550, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17550
; LENGTH: 305491
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(305491)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-17550

Query Match      3.2%; Score 18; DB 3; Length 305491;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      209 TTGAGTGATTGTAATG 226
DB      20604 TTGGAGTGATTGTAATG 20621

RESULT 29
US-09-790-988-1
; Sequence 1, Application US/09790988
; Patent No. 6632935
; GENERAL INFORMATION:
; APPLICANT: SHIGENOBU, SHUJI
; APPLICANT: WATANABE, HIDEMI
; APPLICANT: HATORI, MASAHIRA
; APPLICANT: SAKAKI, YOSHIYUKI
; TITLE OF INVENTION: GENOME DNA OF BACTERIAL SYMBIONT OF APHIDS
; FILE REFERENCE: 081356/0159
; CURRENT APPLICATION NUMBER: US/09/790,988
; PRIOR FILING DATE: 2001-02-23
; PRIOR APPLICATION NUMBER: JP2000-107160
; PRIOR FILING DATE: 2000-04-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 640681
; TYPE: DNA
; ORGANISM: Buchnera sp.
US-09-790-988-1

Query Match      3.2%; Score 18; DB 3; Length 640681;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      218 TTGTAATGTTTAGAG 235
DB      608575 TTGTAATGTTTAGAG 608592

RESULT 30
US-08-956-171E-2335
; Sequence 2335, Application US/08956171E
; Patent No. 6593114
; GENERAL INFORMATION:
; APPLICANT: Charles Kunach
;           Gil H. Choi
;           Patrick S. Dillon
;           Craig A. Rosen
;           Steven C. Barash
;           Michael R. Fannon
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5256
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/956,171E
; FILING DATE: 20-Oct-1997
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/009,861
; FILING DATE: January 5, 1996
; APPLICATION NUMBER: 08/781,986
; FILING DATE: January 3, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark J. Hyman
```



```

;
; REGISTRATION NUMBER: 46,789
; REFERENCE/DOCKET NUMBER: PB248P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (240) 314-1224
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 2335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2335:
US-08-956-171B-2335
```

```

Query Match          3.0%; Score 17; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      489 GATTGATGAGGAACAG 505
Db      36 GATTGATGAGGAACAG 52
```

```

RESULT 31
US-08-781-986A-2335
; Sequence 2335, Application US/08781986A
; Patent No. 6737248
; GENERAL INFORMATION:
; APPLICANT: Charles Kunsch
; TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
; NUMBER OF SEQUENCES: 5255
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Human Genome Sciences, Inc.
; STREET: 9410 Key West Avenue
; CITY: Rockville
; STATE: Maryland
; COUNTRY: USA
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
; COMPUTER: HP Vectra 486/33
; OPERATING SYSTEM: MSDOS version 6.2
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/781,986A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Benson, Bob
; REGISTRATION NUMBER: 30,446
; REFERENCE/DOCKET NUMBER: PB248PP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 2335:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; US-08-781-986A-2335
```

```

Query Match          3.0%; Score 17; DB 3; Length 193;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      489 GATTGATGAGGAACAG 505
Db      36 GATTGATGAGGAACAG 52
```

```

RESULT 32
US-08-836-075A-73/C
; Sequence 73, Application US/08836075A
; Patent No. 6180768
; GENERAL INFORMATION:
; APPLICANT: MAERTENS, GEERT
; APPLICANT: STUYVER, LIEVEN
; TITLE OF INVENTION: NEW SEQUENCES OF HEPATITIS C VIRUS GENOTYPES
; TITLE OF INVENTION: AND THEIR USE AS PROPHYLACTIC, THERAPEUTIC AND DIAGNOSTIC
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433
; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: USA
; ZIP: 77210-4433
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Microsoft Word 6.0 / ASCII text output
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/836,075A
; FILING DATE: 21 Apr 1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP95/04155
; FILING DATE: 23 Oct 1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 94870166.9
; FILING DATE: 21 Oct 1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95870076.7
; FILING DATE: 28 Jun 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: KAMMERER, PATRICIA A.
; REGISTRATION NUMBER: 29,775
; REFERENCE/DOCKET NUMBER: INNS:004
; INFORMATION FOR SEQ ID NO: 73:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 340 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; MOLECULAR TYPE: cDNA
; TOPOLOGY: linear
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; US-08-836-075A-73

Query Match          3.0%; Score 17; DB 3; Length 340;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      144 TGAATGTATGCAGTTC 160
Db      91 TGAATGTATGCAGTTC 75
```

```

RESULT 33
US-09-495-050A-136
; Sequence 136, Application US/09495050A
; Patent No. 6492505
; GENERAL INFORMATION:
; APPLICANT: Roopa, Reddy
; APPLICANT: Guegler, Karl, J.
; TITLE OF INVENTION: COMPOSITION FOR DETECTION OF GENES ENCODING MEMBRANE-ASSOCIATED
; FILE REFERENCE: PA-0013 US
; CURRENT APPLICATION NUMBER: US/09/495,050A
; CURRENT FILING DATE: 2000-01-31
; PRIOR APPLICATION NUMBER: 60/118,318
```



```
/ PRIOR FILING DATE: February 1, 1999
/ NUMBER OF SEQ ID NOS: 305
/ SOFTWARE: PERL Program
/ SEQ ID NO 136
/ LENGTH: 502
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: misc feature
/ OTHER INFORMATION: Incyte ID No. 6492505 1468040CT1
US-09-495-050A-136

Query Match      3.0%; Score 17; DB 3; Length 502;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      182  TCCAAATATAATGATT 198
Db      194  TCCAAATATAATGATT 210

RESULT 34
US-09-276-531-62
/ Sequence 62, Application US/09276531
/ Patent No. 6183968
/ GENERAL INFORMATION:
/ APPLICANT: Bandman, Olga
/ APPLICANT: Lal, Preeti
/ APPLICANT: Hillman, Jennifer L.
/ APPLICANT: Yue, Henry
/ APPLICANT: Reddy, Roopa
/ APPLICANT: Guegler, Karl J.
/ APPLICANT: Baughn, Mariah R.
/ TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING
/ NUMBER OF SEQUENCES: 114
/ NUMBER OF SEQUENCES: 114
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
/ STREET: 3174 PORTER DRIVE
/ CITY: PALO ALTO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94304
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/276,531
/ FILING DATE: Herewith
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 60/079,677
/ FILING DATE: March 27, 1998
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lynn E. Murry, Ph.D.
/ REGISTRATION NUMBER: 42,918
/ REFERENCE/DOCKET NUMBER: PA-0008 US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 855-0555
/ TELEFAX: (650) 845-4166
/ INFORMATION FOR SEQ ID NO: 62:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 552 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ IMMEDIATE SOURCE:
/ LIBRARY: PANCTU02
/ CLONE: 1468040
/ US-09-276-531-62

Query Match      3.0%; Score 17; DB 3; Length 552;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      182  TCCAAATATAATGATT 198
Db      198  TCCAAATATAATGATT 214

RESULT 35
US-09-216-430C-5
/ Sequence 5, Application US/09216430C
/ Patent No. 6734283
/ GENERAL INFORMATION:
/ APPLICANT: Chau, Vincent
/ TITLE OF INVENTION: Human Proteins Responsible for NEDD8 Activation and Conjugation
/ FILE REFERENCE: 103576-127
/ CURRENT APPLICATION NUMBER: US/09/216,430C
/ CURRENT FILING DATE: 1998-12-18
/ PRIOR APPLICATION NUMBER: PCT/US98/27141
/ PRIOR FILING DATE: 1998-12-18
/ PRIOR APPLICATION NUMBER: US 60/068,209
/ PRIOR FILING DATE: 1998-08-12
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 558
/ TYPE: DNA
/ ORGANISM: Human
/ FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(558)
/ OTHER INFORMATION: NEDD8-conjugating enzyme 2 (NCE2)
/ NAME/KEY: CDS
/ LOCATION: (1)..(558)
/ OTHER INFORMATION:
/ US-09-216-430C-5

Query Match      3.0%; Score 17; DB 3; Length 558;
Best Local Similarity 100.0%; Pred. No. 2e+02;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Cy      347  TTAAGAGGTGCAGAA 363
Db      113  TTAAGAGGTGCAGAA 129

RESULT 36
US-09-949-016-35539
/ Sequence 35539, Application US/09949016
/ Patent No. 6812319
/ GENERAL INFORMATION:
/ APPLICANT: VENTER, J. Craig et al.
/ TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
/ WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
/ FILE REFERENCE: C1001307
/ CURRENT APPLICATION NUMBER: US/09/949,016
/ CURRENT FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: 60/241,755
/ PRIOR FILING DATE: 2000-10-20
/ PRIOR APPLICATION NUMBER: 60/237,768
/ PRIOR FILING DATE: 2000-10-03
/ PRIOR APPLICATION NUMBER: 60/231,498
/ PRIOR FILING DATE: 2000-09-08
/ NUMBER OF SEQ ID NOS: 207012
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35539
/ LENGTH: 601
/ TYPE: DNA
/ ORGANISM: Human
/ US-09-949-016-35539
```



Query Match 3.0%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 237 TCATATGATGTATGG 253  
DB 408 TCATATGATGTATGG 424

RESULT 37  
US-09-949-016-52869  
; Sequence 52869, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 52869  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-52869

Query Match 3.0%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GATGAGGAACAGCATT 509  
DB 349 GATGAGGAACAGCATT 365

RESULT 38  
US-09-949-016-63465  
; Sequence 63465, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63465  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-63465

Query Match 3.0%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 AATTATCTCCAAATA 190

DB |||||  
565 AATTATCTCCAAATA 581

RESULT 39  
US-09-949-016-63466  
; Sequence 63466, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 63466  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-63466

Query Match 3.0%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 174 AATTATCTCCAAATA 190  
DB 217 AATTATCTCCAAATA 233

RESULT 40  
US-09-949-016-64068/c  
; Sequence 64068, Application US/09949016  
; Patent No. 6812339  
; GENERAL INFORMATION:  
; APPLICANT: VENTER, J. Craig et al.  
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
; FILE REFERENCE: C1001307  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 64068  
; LENGTH: 601  
; TYPE: DNA  
; ORGANISM: Human  
US-09-949-016-64068

Query Match 3.0%; Score 17; DB 3; Length 601;  
Best Local Similarity 100.0%; Pred. No. 2e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 185 AAAATAAATGATTCAA 201  
DB 507 AAAATAAATGATTCAA 491

Search completed: April 11, 2006, 21:50:20



Job time : 256.298 secs

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OM nucleic - nucleic search, using sw model

Run on: April 12, 2006, 04:34:11 ; Search time 1516.89 Seconds  
(without alignments)  
3052.864 Million cell updates/sec

Title: US-10-712-654-34

Perfect score: 560

Sequence: 1 aacactggtacatctgcgcg.....ggagcatgagattacacg 560

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 9793542 seqs, 4134689005 residues

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  - 3: /cgn2\_6/ptodata/1/pubpna/US09A\_PUBCOMB.seq:\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	32	5.7	32	5	US-10-068-238-3
2	30	5.4	30	5	US-10-068-238-4
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4	29	5.2	29	10	US-11-018-377-67
5	26	4.6	26	5	US-10-068-238-14
6	25	4.5	25	5	US-10-068-238-13
7	24	4.3	24	6	US-10-376-323-65
8	24	4.3	24	10	US-11-018-377-65
9	23	4.1	23	6	US-10-376-323-66
10	23	4.1	23	10	US-11-018-377-66
11	23	3.6	552	4	US-09-925-065A-648674
12	20	3.6	552	4	US-09-925-065A-648675
13	19	3.4	537	4	US-09-925-065A-223976
14	19	3.4	537	4	US-09-925-065A-223977
15	19	3.4	540	4	US-09-925-065A-223977
16	19	3.4	555	7	US-10-282-122A-643642
17	19	3.4	646	4	US-09-925-065A-906587
18	19	3.4	646	4	US-09-925-065A-912775
19	19	3.4	1004	7	US-10-425-114-19356
20	19	3.4	1092	7	US-10-425-114-11482
21	19	3.4	1343	7	US-10-424-599-85136
22	19	3.4	1914	5	US-10-025-950-3
23	19	3.4	1917	6	US-10-303-664A-35

24	19	3.4	2301	6	US-10-369-493-27237	Sequence 27237, A
25	19	3.4	4661	3	US-09-795-651-100	Sequence 100, App
26	19	3.4	4661	6	US-10-172-118-17	Sequence 17, Appl
27	19	3.4	4661	7	US-10-342-887-17	Sequence 17, Appl
28	19	3.4	4959	5	US-10-025-950-1	Sequence 1, Appl1
29	19	3.4	4959	6	US-10-303-664A-34	Sequence 34, Appl1
30	19	3.4	5970	7	US-10-437-963-17397	Sequence 17397, A
31	19	3.4	10093	3	US-09-764-869-1390	Sequence 1390, App
32	19	3.4	10093	5	US-10-091-504-1390	Sequence 1390, App
33	19	3.4	10093	6	US-10-227-577-1390	Sequence 1390, App
34	19	3.4	10872	7	US-10-221-613-250	Sequence 250, App
35	19	3.4	13311	3	US-09-754-468-14	Sequence 14, Appl
36	19	3.4	32768	3	US-09-070-927A-399	Sequence 399, App
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41	18	3.2	369	4	US-09-925-065A-539146	Sequence 539146, A
42	18	3.2	369	4	US-09-925-065A-539147	Sequence 539147, A
43	18	3.2	369	4	US-09-925-065A-539148	Sequence 539148, A
44	18	3.2	498	4	US-09-925-065A-144381	Sequence 144381, A
45	18	3.2	507	5	US-10-027-632-181086	Sequence 181086, A
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47	18	3.2	507	6	US-10-027-632-181087	Sequence 181087, A
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53	18	3.2	579	4	US-09-925-065A-217603	Sequence 217603, A
54	18	3.2	631	7	US-10-424-559-121945	Sequence 121945, A
55	18	3.2	632	4	US-09-925-065A-725515	Sequence 725515, A
56	18	3.2	632	4	US-09-925-065A-800539	Sequence 800539, A
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61	18	3.2	684	4	US-09-925-065A-543177	Sequence 543177, A
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63	18	3.2	697	8	US-10-363-345A-30616	Sequence 30616, A
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65	18	3.2	697	9	US-10-363-483A-30616	Sequence 30616, A
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78	18	3.2	914	4	US-09-925-065A-57028	Sequence 57028, A
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83	18	3.2	1002	7	US-10-384-339C-26	Sequence 26, Appl1
84	18	3.2	1024	7	US-10-477-974-10	Sequence 10, Appl1
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86	18	3.2	1188	7	US-10-282-112A-38489	Sequence 38489, A
87	18	3.2	1306	7	US-10-424-599-16972	Sequence 16972, A
88	18	3.2	1306	7	US-10-425-114-19306	Sequence 19306, A
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93	18	3.2	1474	4	US-09-925-065A-631119	Sequence 631119, A
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149	17	3.0	263	3	US-09-815-242-2320
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156	17	3.0	364	4	US-09-925-065A-95723
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165	17	3.0	430	7	US-10-085-783A-20368
166	17	3.0	437	5	US-10-027-632-19030
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247	17	3.0	624	5	US-10-027-632-215973	Sequence 215973,	320	17	3.0	1561	7	US-10-437-963-32968	Sequence 32968, A
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c 259	17	3.0	634	4	US-09-925-065A-98887	Sequence 98887, A	c 332	17	3.0	1930	4	US-09-925-065A-692913	Sequence 692913,
c 260	17	3.0	641	4	US-09-925-065A-453509	Sequence 453509,	c 333	17	3.0	1930	4	US-09-925-065A-692914	Sequence 692914,
c 261	17	3.0	649	7	US-10-437-963-40227	Sequence 40227, A	c 334	17	3.0	1930	4	US-09-925-065A-692915	Sequence 692915,
c 262	17	3.0	652	5	US-10-027-632-166798	Sequence 166798,	c 335	17	3.0	1937	5	US-10-157-669-2	Sequence 2,
c 263	17	3.0	652	6	US-10-027-632-166798	Sequence 166798,	336	17	3.0	1937	5	US-10-157-669-16	Sequence 16, Appl1
c 264	17	3.0	652	7	US-10-425-114-34163	Sequence 34163, A	337	17	3.0	1953	3	US-09-971-392-206	Sequence 206, App
c 265	17	3.0	738	3	US-09-815-242-4406	Sequence 4406, Ap	338	17	3.0	1978	5	US-10-157-669-13	Sequence 13, Appl1
c 266	17	3.0	741	3	US-09-815-242-8025	Sequence 8025, Ap	c 339	17	3.0	2006	6	US-10-021-660-59	Sequence 59, Appl1
c 267	17	3.0	741	3	US-09-815-242-8705	Sequence 8705, Ap	c 340	17	3.0	2006	6	US-10-295-027-29	Sequence 29, Appl1
c 268	17	3.0	741	3	US-09-815-242-9002	Sequence 9002, Ap	c 341	17	3.0	2006	7	US-10-211-462-84	Sequence 84, Appl1
c 269	17	3.0	741	7	US-10-282-122A-7765	Sequence 7765, Ap	c 342	17	3.0	2006	8	US-10-416-203A-2	Sequence 2, Appl1
c 270	17	3.0	741	8	US-10-857-625-290	Sequence 290, App	c 343	17	3.0	2019	6	US-10-172-118-1349	Sequence 1349, Ap
c 271	17	3.0	765	5	US-10-027-632-128074	Sequence 128074,	c 344	17	3.0	2019	7	US-10-342-887-1349	Sequence 53, Appl1
c 272	17	3.0	765	6	US-10-027-632-128074	Sequence 128074,	c 345	17	3.0	2019	7	US-10-764-425-53	Sequence 154, App
c 273	17	3.0	787	4	US-10-425-115-26871	Sequence 26871, A	c 346	17	3.0	2019	9	US-10-848-755A-154	Sequence 102, Ap
c 274	17	3.0	793	4	US-09-925-065A-941998	Sequence 941998,	c 347	17	3.0	2040	5	US-10-102-52A-1702	Sequence 65438, Ap
c 275	17	3.0	793	4	US-10-029-386-20458	Sequence 20458, A	c 348	17	3.0	2187	4	US-09-925-065A-65338	Sequence 77384, A
c 276	17	3.0	802	5	US-10-027-632-164564	Sequence 164564,	c 349	17	3.0	2724	4	US-09-925-065A-77384	Sequence 77385, A
c 277	17	3.0	822	6	US-10-027-632-164564	Sequence 164564,	c 350	17	3.0	2724	4	US-09-925-065A-77385	Sequence 77386, A
c 278	17	3.0	822	6	US-10-027-632-164564	Sequence 164564,	c 351	17	3.0	2724	4	US-09-925-065A-77386	Sequence 1015, Ap
c 279	17	3.0	829	5	US-10-037-270-640	Sequence 640, App	c 352	17	3.0	2796	10	US-11-097-143-1015	Sequence 683424,
c 280	17	3.0	829	6	US-10-117-722-640	Sequence 640, App	c 353	17	3.0	2937	4	US-09-925-065A-683424	Sequence 29347, A
c 281	17	3.0	829	6	US-10-122-851-156	Sequence 26868, A	c 354	17	3.0	3156	7	US-10-320-797-218	Sequence 218, App
c 282	17	3.0	830	8	US-10-425-115-26868	Sequence 94389, A	c 355	17	3.0	3159	9	US-10-450-763-29347	Sequence 53, Appl1
c 283	17	3.0	846	4	US-09-925-065A-94389	Sequence 94389, A	c 356	17	3.0	3195	8	US-10-857-625-54	Sequence 53, App
c 284	17	3.0	846	4	US-09-925-065A-94389	Sequence 94389, A	c 357	17	3.0	3231	9	US-10-481-032A-533	Sequence 407, App
c 285	17	3.0	855	7	US-10-425-114-4342	Sequence 4342, Ap	c 358	17	3.0	3398	9	US-10-481-032A-407	Sequence 17244, A
c 286	17	3.0	855	7	US-09-738-626-2272	Sequence 2272, Ap	c 359	17	3.0	3398	7	US-10-437-963-77244	Sequence 1949, Ap
c 287	17	3.0	863	4	US-09-925-065A-18901	Sequence 18901, A	c 360	17	3.0	3682	4	US-09-925-065A-1949	Sequence 1950, Ap
c 288	17	3.0	929	8	US-10-470-048B-117	Sequence 117, App	c 361	17	3.0	3682	4	US-09-925-065A-1950	Sequence 1951, Ap
c 289	17	3.0	933	8	US-09-815-242-6570	Sequence 6570, Ap	c 362	17	3.0	3682	4	US-09-925-065A-1951	Sequence 1952, Ap
c 290	17	3.0	943	7	US-10-424-599-14741	Sequence 14741, A	c 363	17	3.0	3682	4	US-09-925-065A-1952	Sequence 1953, Ap
c 291	17	3.0	960	8	US-10-425-115-182244	Sequence 182244,	c 364	17	3.0	3682	4	US-09-925-065A-1953	Sequence 1954, Ap
c 292	17	3.0	974	7	US-10-425-114-12904	Sequence 12904, A	c 365	17	3.0	3682	4	US-09-925-065A-1954	Sequence 1954, Ap
c 293	17	3.0	974	7	US-10-425-114-21001	Sequence 21001, A	c 366	17	3.0	3682	4	US-09-925-065A-45661	Sequence 45661, A
c 294	17	3.0	1006	9	US-10-450-763-1263	Sequence 7263, Ap	c 367	17	3.0	4001	5	US-10-172-086-76	Sequence 76, Appl1
c 295	17	3.0	1008	9	US-10-450-763-1367	Sequence 51, Appl1	c 368	17	3.0	4224	8	US-10-480-446-76	Sequence 76, Appl1
c 296	17	3.0	1033	3	US-09-840-787-51	Sequence 51, Appl1	c 369	17	3.0	4224	8	US-10-437-963-44719	Sequence 44719, A
c 297	17	3.0	1074	3	US-09-949-192-50	Sequence 50, Appl1	c 370	17	3.0	4260	6	US-10-369-493-34937	Sequence 34937, A
c 298	17	3.0	1074	10	US-11-090-448-50	Sequence 27852,	c 371	17	3.0	4280	2	US-08-781-986A-81	Sequence 81, Appl1
c 299	17	3.0	1098	4	US-09-925-065A-278552	Sequence 27852,	c 372	17	3.0	4280	2	US-10-329-624-81	Sequence 81, Appl1
c 300	17	3.0	1099	7	US-10-424-599-56472	Sequence 36472, A	c 373	17	3.0	4371	9	US-10-450-763-29348	Sequence 29348, A
c 301	17	3.0	1104	4	US-09-925-065A-680915	Sequence 680915,	c 374	17	3.0	4410	10	US-11-097-143-31295	Sequence 31295, A
c 302	17	3.0	1113	3	US-09-738-626-2380	Sequence 2380, Ap	c 375	17	3.0	5051	9	US-10-461-862-26	Sequence 26, Appl1
c 303	17	3.0	1142	5	US-10-027-632-118722	Sequence 118722,	c 376	17	3.0	5051	6	US-10-339-782-1	Sequence 1, Appl1
c 304	17	3.0	1142	6	US-10-027-632-118722	Sequence 118722,	c 377	17	3.0	5473	8	US-10-857-625-53	Sequence 53, Appl1
c 305	17	3.0	1164	7	US-10-424-599-35459	Sequence 35459, A	c 378	17	3.0	5833	7	US-10-461-862-32	Sequence 32, Appl1
c 306	17	3.0	1170	7	US-10-424-599-35459	Sequence 35459, A	c 379	17	3.0	6033	9	US-10-240-454-32	Sequence 32, Appl1
c 307	17	3.0	1181	7	US-10-302-172-252	Sequence 252, App	c 380	17	3.0	6251	7	US-08-781-986A-25	Sequence 25, Appl1
c 308	17	3.0	1197	4	US-09-925-065A-554889	Sequence 554889,	c 381	17	3.0	6251	7	US-10-329-624-25	Sequence 25, Appl1
c 309	17	3.0	1236	6	US-10-254-995-34	Sequence 34, Appl1	c 382	17	3.0	6450	9	US-10-450-763-29349	Sequence 29349, A
c 310	17	3.0	1236	10	US-11-062-080-34	Sequence 34, Appl1	c 383	17	3.0	6577	10	US-11-097-143-31294	Sequence 31294, A
c 311	17	3.0	1271	3	US-09-037-460-1	Sequence 1, Appl1	c 384	17	3.0	6676	10	US-11-097-143-31295	Sequence 23356, A
c 312	17	3.0	1271	9	US-10-951-866-1	Sequence 1, Appl1	c 385	17	3.0	7658	8	US-10-857-625-52	Sequence 52, Appl1
c 313	17	3.0	1350	9	US-10-767-701-12185	Sequence 12185, A	c 386	17	3.0	8033	8	US-09-070-927A-121	Sequence 121, App
c 314	17	3.0	1364	5	US-10-016-349A-49	Sequence 49, Appl1	c 387	17	3.0	10999	10	US-11-097-143-2725	Sequence 2725, Ap
c 315	17	3.0	1469	5	US-10-198-846-13539	Sequence 13539, A	c 388	17	3.0	12100	3	US-09-754-468-21	Sequence 21, Appl1



C 389	17	3.0	12100	3	US-09-754-468-22	Sequence 22, Appl	462	16	2.9	201	7	US-10-741-601-11472	Sequence 11472, A
C 390	17	3.0	12100	3	US-09-754-468-24	Sequence 24, Appl	463	16	2.9	201	7	US-10-741-601-11486	Sequence 11486, A
C 391	17	3.0	12100	3	US-09-754-468-26	Sequence 26, Appl	464	16	2.9	201	7	US-10-741-601-11498	Sequence 11498, A
C 392	17	3.0	13480	10	US-11-097-143-3157	Sequence 3157, Ap	465	16	2.9	201	8	US-10-719-993-16344	Sequence 16344, A
C 393	17	3.0	13521	10	US-11-097-143-26146	Sequence 26146, A	466	16	2.9	201	8	US-10-741-600-88929	Sequence 88929, A
C 394	17	3.0	15505	10	US-11-097-143-26143	Sequence 26143, A	467	16	2.9	207	7	US-10-424-599-40367	Sequence 40367, A
C 395	17	3.0	17213	6	US-10-311-455-9456	Sequence 1456, Ap	468	16	2.9	213	7	US-10-767-701-16720	Sequence 16720, A
C 396	17	3.0	18512	6	US-10-311-455-949	Sequence 949, Ap	469	16	2.9	227	3	US-09-895-828-137	Sequence 137, Ap
C 397	17	3.0	23695	6	US-10-433-793-12	Sequence 12, Appl	470	16	2.9	227	5	US-10-114-666-137	Sequence 137, Ap
C 398	17	3.0	28118	6	US-10-282-174-402	Sequence 402, App	471	16	2.9	238	3	US-09-938-842A-2913	Sequence 2913, Ap
C 399	17	3.0	28118	6	US-10-282-174-403	Sequence 403, App	472	16	2.9	238	3	US-09-938-842A-2913	Sequence 2913, Ap
C 400	17	3.0	28118	8	US-10-600-009-402	Sequence 402, App	473	16	2.9	249	3	US-10-070-927A-864	Sequence 864, App
C 401	17	3.0	28118	8	US-10-600-009-403	Sequence 403, App	474	16	2.9	260	7	US-10-424-599-100622	Sequence 100622, A
C 402	17	3.0	28180	5	US-10-114-170-242	Sequence 242, App	475	16	2.9	272	7	US-10-424-599-51540	Sequence 51540, A
C 403	17	3.0	37154	8	US-10-741-601-5667	Sequence 5667, Ap	476	16	2.9	282	7	US-10-424-599-51540	Sequence 51540, A
C 404	17	3.0	37154	8	US-10-741-601-5667	Sequence 5667, Ap	477	16	2.9	282	7	US-10-424-599-51540	Sequence 51540, A
C 405	17	3.0	43672	5	US-10-087-192-607	Sequence 607, App	478	16	2.9	282	7	US-10-085-783A-33661	Sequence 33661, A
C 406	17	3.0	45121	3	US-09-997-722-10	Sequence 10, Appl	479	16	2.9	290	7	US-10-437-963-8945	Sequence 8945, Ap
C 407	17	3.0	55875	7	US-10-322-696-139	Sequence 139, App	480	16	2.9	291	8	US-10-425-115-77320	Sequence 77320, A
C 408	17	3.0	68209	7	US-10-741-601-5758	Sequence 5758, Ap	481	16	2.9	300	7	US-10-085-783A-49245	Sequence 49245, A
C 409	17	3.0	68209	8	US-10-719-993-7029	Sequence 7029, Ap	482	16	2.9	300	9	US-10-779-543-7096	Sequence 7096, Ap
C 410	17	3.0	68611	5	US-10-087-192-1882	Sequence 1882, Ap	483	16	2.9	302	3	US-09-764-891-6647	Sequence 6647, Ap
C 411	17	3.0	94672	5	US-10-087-192-1069	Sequence 1069, Ap	484	16	2.9	302	3	US-10-091-572-511	Sequence 511, App
C 412	17	3.0	96595	6	US-10-034-650-34	Sequence 34, Appl	485	16	2.9	307	5	US-09-764-891-573	Sequence 573, App
C 413	17	3.0	96596	3	US-09-997-722-130	Sequence 130, App	486	16	2.9	307	5	US-10-091-572-511	Sequence 511, App
C 414	17	3.0	98300	9	US-10-722-939-2	Sequence 2, Appl	487	16	2.9	307	5	US-10-091-572-511	Sequence 511, App
C 415	17	3.0	121129	7	US-10-322-281-587	Sequence 587, App	488	16	2.9	324	9	US-10-450-763-3300	Sequence 3300, Ap
C 416	17	3.0	130030	8	US-10-719-993-6986	Sequence 6986, Ap	489	16	2.9	324	9	US-10-450-763-3300	Sequence 3300, Ap
C 417	17	3.0	134442	9	US-10-461-862-23	Sequence 23, Appl	490	16	2.9	329	3	US-09-998-598-184	Sequence 184, App
C 418	17	3.0	136436	9	US-10-756-149-3773	Sequence 3773, Ap	491	16	2.9	330	3	US-09-998-598-184	Sequence 184, App
C 419	17	3.0	177556	3	US-09-952-213D-6	Sequence 6, Appl	492	16	2.9	334	8	US-10-425-115-171128	Sequence 171128, A
C 420	17	3.0	177556	10	US-11-033-666-6	Sequence 6, Appl	493	16	2.9	340	7	US-10-437-963-33439	Sequence 33439, A
C 421	17	3.0	193757	8	US-10-719-993-6939	Sequence 6939, Ap	494	16	2.9	341	6	US-10-392-808-12	Sequence 808, Ap
C 422	17	3.0	301477	7	US-10-322-281-456	Sequence 456, App	495	16	2.9	344	7	US-10-424-599-11936	Sequence 11936, A
C 423	17	3.0	321491	5	US-10-087-192-532	Sequence 532, App	496	16	2.9	348	4	US-09-925-065A-178204	Sequence 178204, A
C 424	17	3.0	325791	3	US-09-768-185A-1	Sequence 1, Appl	497	16	2.9	348	4	US-09-925-065A-178205	Sequence 178205, A
C 425	17	3.0	350764	5	US-10-087-192-1864	Sequence 1864, Ap	498	16	2.9	348	4	US-09-925-065A-178206	Sequence 178206, A
C 426	17	3.0	382256	9	US-10-820-226-1	Sequence 1, Appl	499	16	2.9	356	5	US-09-925-065A-178207	Sequence 178207, A
C 427	17	3.0	382259	10	US-11-029-984-1	Sequence 1, Appl	500	16	2.9	356	6	US-10-027-632-13331	Sequence 13331, A
C 428	17	3.0	599001	9	US-10-317-869A-4	Sequence 4, Appl	501	16	2.9	356	6	US-10-027-632-13331	Sequence 13331, A
C 429	17	3.0	640681	3	US-09-790-988-1	Sequence 1, Appl	502	16	2.9	361	9	US-10-911-704-27	Sequence 27, Appl
C 430	17	3.0	786452	8	US-10-719-993-6822	Sequence 6822, Ap	503	16	2.9	364	7	US-10-424-599-112332	Sequence 112332, A
C 431	17	3.0	908766	9	US-10-795-159-685	Sequence 685, App	504	16	2.9	368	4	US-09-925-065A-578584	Sequence 578584, A
C 432	17	3.0	908766	9	US-10-719-993-6940	Sequence 6940, Ap	505	16	2.9	368	4	US-09-925-065A-578585	Sequence 578585, A
C 433	17	3.0	1830121	7	US-10-329-670-1	Sequence 1, Appl	506	16	2.9	373	8	US-10-357-930-21106	Sequence 21106, A
C 434	17	3.0	1830121	8	US-10-158-865-1	Sequence 1, Appl	507	16	2.9	378	3	US-10-357-930-21106	Sequence 21106, A
C 435	17	3.0	1830121	9	US-10-981-687-1	Sequence 1, Appl	508	16	2.9	380	4	US-09-960-352-5909	Sequence 5909, Ap
C 436	17	3.0	2940917	5	US-10-027-632-174763	Sequence 174763, A	509	16	2.9	380	9	US-10-756-149-3179	Sequence 3179, Ap
C 437	17	3.0	2940917	6	US-10-027-632-174763	Sequence 174763, A	510	16	2.9	385	3	US-09-917-800A-1135	Sequence 1135, Ap
C 438	17	3.0	3309400	3	US-09-738-626-1	Sequence 1, Appl	511	16	2.9	385	6	US-10-388-934-455	Sequence 934, App
C 439	17	3.0	3673778	6	US-10-312-841-2	Sequence 2, Appl	512	16	2.9	388	8	US-10-388-934-455	Sequence 934, App
C 440	17	2.9	25	7	US-10-681-773-73629	Sequence 73629, A	513	16	2.9	388	8	US-10-357-930-21106	Sequence 21106, A
C 441	16	2.9	25	8	US-10-719-900-23474	Sequence 23474, A	514	16	2.9	390	7	US-10-424-599-115721	Sequence 115721, A
C 442	16	2.9	25	8	US-10-719-900-582615	Sequence 582615, A	515	16	2.9	392	3	US-09-878-178-1420	Sequence 1420, Ap
C 443	16	2.9	25	8	US-10-719-900-765662	Sequence 765662, A	516	16	2.9	392	5	US-10-046-935-1420	Sequence 1420, Ap
C 444	16	2.9	25	8	US-10-719-900-806530	Sequence 806530, A	517	16	2.9	392	5	US-10-146-502-1420	Sequence 1420, Ap
C 445	16	2.9	25	8	US-10-719-900-901442	Sequence 901442, A	518	16	2.9	394	8	US-10-425-115-51665	Sequence 51665, A
C 446	16	2.9	25	8	US-10-719-900-901442	Sequence 901442, A	519	16	2.9	397	4	US-09-925-065A-845905	Sequence 845905, A
C 447	16	2.9	25	10	US-11-036-317-26562	Sequence 26562, A	520	16	2.9	398	4	US-09-925-065A-85567	Sequence 85567, A
C 448	16	2.9	25	10	US-11-036-317-201076	Sequence 201076, A	521	16	2.9	400	8	US-10-357-930-211078	Sequence 211078, A
C 449	16	2.9	25	10	US-11-036-317-201076	Sequence 201076, A	522	16	2.9	400	8	US-10-357-930-211078	Sequence 211078, A
C 450	16	2.9	25	10	US-11-036-317-201076	Sequence 201076, A	523	16	2.9	401	3	US-09-795-668-339	Sequence 339, App
C 451	16	2.9	25	10	US-11-060-756-118430	Sequence 118430, A	524	16	2.9	401	3	US-09-795-668-339	Sequence 339, App
C 452	16	2.9	25	10	US-11-060-756-118430	Sequence 118430, A	525	16	2.9	401	3	US-09-795-668-339	Sequence 339, App
C 453	16	2.9	25	10	US-11-060-756-118430	Sequence 118430, A	526	16	2.9	401	3	US-09-795-668-339	Sequence 339, App
C 454	16	2.9	30	8	US-10-484-232-2	Sequence 2, Appl	527	16	2.9	403	7	US-10-935-011-339	Sequence 339, App
C 455	16	2.9	60	3	US-09-908-975-20219	Sequence 20219, A	528	16	2.9	404	4	US-10-425-115-51665	Sequence 51665, A
C 456	16	2.9	114	7	US-10-242-535A-4672	Sequence 4672, Ap	529	16	2.9	404	4	US-09-925-065A-825222	Sequence 825222, A
C 457	16	2.9	114	7	US-10-085-783A-4672	Sequence 4672, Ap	530	16	2.9	405	8	US-10-914-031-339	Sequence 339, App
C 458	16	2.9	129	8	US-10-674-124A-6439	Sequence 6439, Ap	531	16	2.9	405	9	US-10-450-763-7475	Sequence 7475, Ap
C 459	16	2.9	142	7	US-10-437-963-80382	Sequence 80382, A	532	16	2.9	407	8	US-10-357-930-211078	Sequence 211078, A
C 460	16	2.9	151	6	US-10-029-386-19059	Sequence 19059, A	533	16	2.9	408	4	US-09-925-065A-497600	Sequence 497600, A
C 461	16	2.9	152	6	US-10-029-386-22023	Sequence 22023, A	534	16	2.9	408	4	US-09-925-065A-497601	Sequence 497601, A
C 462	16	2.9	176	8	US-10-674-124A-8162	Sequence 8162, Ap	535	16	2.9	408	4	US-09-925-065A-497602	Sequence 497602, A



C 535	16	2.9	415	3	US-09-764-891-2134	Sequence 2134, Ap	C 608	16	2.9	510	6	US-10-027-632-303817	Sequence 303817, A
C 536	16	2.9	418	8	US-10-696-639-1767	Sequence 1767, Ap	C 609	16	2.9	511	3	US-09-918-995-54081	Sequence 24081, A
C 537	16	2.9	427	8	US-09-864-408A-1789	Sequence 1789, Ap	C 610	16	2.9	516	4	US-09-925-065A-399558	Sequence 399558, A
C 538	16	2.9	434	6	US-10-131-827-8493	Sequence 8493, Ap	C 611	16	2.9	516	4	US-09-925-065A-578576	Sequence 578576, A
C 539	16	2.9	436	7	US-10-242-535A-5205	Sequence 25205, A	C 612	16	2.9	517	7	US-10-437-963-97127	Sequence 97127, A
C 540	16	2.9	436	7	US-10-085-783A-5205	Sequence 25205, A	C 613	16	2.9	518	4	US-09-925-065A-24476	Sequence 24476, A
C 541	16	2.9	444	5	US-10-066-543-2634	Sequence 2634, Ap	C 614	16	2.9	520	4	US-09-925-065A-650727	Sequence 650727, A
C 542	16	2.9	444	5	US-10-425-115-24275	Sequence 24275, A	C 615	16	2.9	523	4	US-09-925-065A-400400	Sequence 400400, A
C 543	16	2.9	446	8	US-10-357-930-35207	Sequence 35207, A	C 616	16	2.9	523	4	US-09-925-065A-400401	Sequence 400401, A
C 544	16	2.9	446	8	US-10-357-930-44049	Sequence 44049, A	C 617	16	2.9	524	4	US-09-925-065A-816820	Sequence 816820, A
C 545	16	2.9	453	3	US-09-969-034-1822	Sequence 1822, Ap	C 618	16	2.9	526	4	US-09-925-065A-328777	Sequence 328777, A
C 546	16	2.9	453	7	US-10-469-285-629	Sequence 629, App	C 619	16	2.9	526	4	US-09-925-065A-328778	Sequence 328778, A
C 547	16	2.9	454	4	US-09-925-065A-575088	Sequence 575088, A	C 620	16	2.9	526	4	US-09-925-065A-328779	Sequence 328779, A
C 548	16	2.9	458	7	US-10-437-963-94549	Sequence 94549, A	C 621	16	2.9	526	4	US-09-925-065A-334218	Sequence 334218, A
C 549	16	2.9	459	7	US-10-767-701-27740	Sequence 27740, A	C 622	16	2.9	526	4	US-09-925-065A-400402	Sequence 400402, A
C 550	16	2.9	459	8	US-10-674-124A-2958	Sequence 2958, Ap	C 623	16	2.9	526	4	US-09-925-065A-400403	Sequence 400403, A
C 551	16	2.9	460	8	US-10-357-930-9628	Sequence 9628, Ap	C 624	16	2.9	526	4	US-09-925-065A-400403	Sequence 400403, A
C 552	16	2.9	460	8	US-10-357-930-9628	Sequence 9628, Ap	C 625	16	2.9	526	4	US-09-925-065A-478091	Sequence 478091, A
C 553	16	2.9	461	8	US-10-357-930-30830	Sequence 30830, A	C 626	16	2.9	526	5	US-10-198-846-9184	Sequence 9184, Ap
C 554	16	2.9	461	8	US-10-357-930-39799	Sequence 39799, A	C 627	16	2.9	527	4	US-10-021-323-10428	Sequence 10428, A
C 555	16	2.9	462	7	US-10-424-599-68621	Sequence 68621, A	C 628	16	2.9	527	4	US-09-925-065A-113241	Sequence 113241, A
C 556	16	2.9	465	5	US-09-925-065A-737902	Sequence 737902, A	C 629	16	2.9	531	7	US-10-021-323-14610	Sequence 14610, A
C 557	16	2.9	465	5	US-10-016-349A-18	Sequence 18, App1	C 630	16	2.9	535	5	US-10-027-632-57445	Sequence 57445, A
C 558	16	2.9	467	4	US-09-925-065A-559059	Sequence 559059, A	C 631	16	2.9	535	6	US-10-027-632-57445	Sequence 57445, A
C 559	16	2.9	468	4	US-09-925-065A-178016	Sequence 178016, A	C 632	16	2.9	535	4	US-09-925-065A-341696	Sequence 341696, A
C 560	16	2.9	468	4	US-09-925-065A-178017	Sequence 178017, A	C 633	16	2.9	536	4	US-09-925-065A-341697	Sequence 341697, A
C 561	16	2.9	471	3	US-09-864-761-10116	Sequence 10116, A	C 634	16	2.9	536	4	US-09-925-065A-486790	Sequence 486790, A
C 562	16	2.9	472	4	US-09-925-065A-268530	Sequence 268530, A	C 635	16	2.9	537	4	US-09-925-065A-121661	Sequence 121661, A
C 563	16	2.9	472	5	US-10-027-632-57063	Sequence 57063, A	C 636	16	2.9	537	5	US-10-027-632-1966	Sequence 1966, Ap
C 564	16	2.9	472	6	US-10-027-632-57063	Sequence 57063, A	C 637	16	2.9	537	6	US-10-027-632-1966	Sequence 1966, Ap
C 565	16	2.9	475	4	US-09-925-065A-342396	Sequence 342396, A	C 638	16	2.9	538	3	US-09-777-564-1258	Sequence 1258, Ap
C 566	16	2.9	480	7	US-10-283-122A-16277	Sequence 16277, A	C 639	16	2.9	538	5	US-10-015-219-1258	Sequence 1258, Ap
C 567	16	2.9	482	4	US-09-925-065A-139580	Sequence 139580, A	C 640	16	2.9	539	4	US-09-925-065A-481182	Sequence 481182, A
C 568	16	2.9	482	6	US-10-131-827-8457	Sequence 8457, Ap	C 641	16	2.9	539	5	US-10-027-632-5208	Sequence 5208, Ap
C 569	16	2.9	487	4	US-09-925-065A-295140	Sequence 29514, Ap	C 642	16	2.9	539	6	US-10-027-632-5208	Sequence 5208, Ap
C 570	16	2.9	491	3	US-09-918-995-35552	Sequence 35552, A	C 643	16	2.9	542	4	US-09-925-065A-376604	Sequence 376604, A
C 571	16	2.9	493	4	US-09-925-065A-477107	Sequence 477307, A	C 644	16	2.9	542	4	US-09-925-065A-376605	Sequence 376605, A
C 572	16	2.9	493	4	US-09-925-065A-477308	Sequence 477308, A	C 645	16	2.9	542	4	US-09-925-065A-376611	Sequence 376611, A
C 573	16	2.9	494	5	US-10-027-632-45207	Sequence 45207, A	C 646	16	2.9	542	4	US-09-925-065A-376619	Sequence 376619, A
C 574	16	2.9	494	5	US-10-027-632-45208	Sequence 45208, A	C 647	16	2.9	542	4	US-09-925-065A-750852	Sequence 750852, A
C 575	16	2.9	494	6	US-10-027-632-45207	Sequence 45207, A	C 648	16	2.9	542	4	US-09-925-065A-823047	Sequence 823047, A
C 576	16	2.9	494	6	US-10-027-632-45208	Sequence 45208, A	C 649	16	2.9	542	4	US-09-925-065A-823048	Sequence 823048, A
C 577	16	2.9	495	8	US-10-357-930-5726A	Sequence 572676, A	C 650	16	2.9	543	6	US-10-029-386-5303	Sequence 5303, Ap
C 578	16	2.9	495	4	US-09-925-065A-408434	Sequence 408434, A	C 651	16	2.9	545	4	US-09-925-065A-589089	Sequence 589089, A
C 579	16	2.9	496	5	US-10-027-632-191517	Sequence 191517, A	C 652	16	2.9	546	5	US-10-027-632-191929	Sequence 219829, A
C 580	16	2.9	496	6	US-10-027-632-191517	Sequence 191517, A	C 653	16	2.9	546	5	US-10-027-632-191930	Sequence 219830, A
C 581	16	2.9	496	6	US-10-450-763-13740	Sequence 13740, A	C 654	16	2.9	546	6	US-10-027-632-191929	Sequence 219829, A
C 582	16	2.9	498	4	US-09-925-065A-216435	Sequence 216435, A	C 655	16	2.9	547	4	US-10-027-632-216830	Sequence 216830, A
C 583	16	2.9	498	4	US-09-925-065A-766117	Sequence 766117, A	C 656	16	2.9	547	4	US-09-925-065A-178594	Sequence 178594, A
C 584	16	2.9	498	8	US-10-425-115-140886	Sequence 140886, A	C 657	16	2.9	547	5	US-10-027-632-44666	Sequence 44666, A
C 585	16	2.9	499	4	US-09-925-065A-108240	Sequence 108240, A	C 658	16	2.9	547	6	US-10-027-632-44666	Sequence 44666, A
C 586	16	2.9	499	4	US-09-925-065A-108241	Sequence 108241, A	C 659	16	2.9	548	9	US-10-644-765-1119	Sequence 1119, App
C 587	16	2.9	499	4	US-09-925-065A-108242	Sequence 108242, A	C 660	16	2.9	549	4	US-09-925-065A-151722	Sequence 151722, A
C 588	16	2.9	499	4	US-09-925-065A-108243	Sequence 108243, A	C 661	16	2.9	549	4	US-09-925-065A-151722	Sequence 151722, A
C 589	16	2.9	499	4	US-09-925-065A-836343	Sequence 836343, A	C 662	16	2.9	550	4	US-09-925-065A-199926	Sequence 199926, A
C 590	16	2.9	499	4	US-09-925-065A-836344	Sequence 836344, A	C 663	16	2.9	551	4	US-09-925-065A-187227	Sequence 187227, A
C 591	16	2.9	499	5	US-10-027-632-269630	Sequence 269630, A	C 664	16	2.9	551	4	US-09-925-065A-187227	Sequence 187227, A
C 592	16	2.9	499	6	US-10-027-632-37637	Sequence 37637, A	C 665	16	2.9	551	4	US-09-925-065A-728948	Sequence 728948, A
C 593	16	2.9	502	5	US-10-027-632-37637	Sequence 37637, A	C 666	16	2.9	551	4	US-09-925-065A-728949	Sequence 728949, A
C 594	16	2.9	502	5	US-10-027-632-37637	Sequence 37637, A	C 667	16	2.9	552	4	US-09-925-065A-254258	Sequence 254258, A
C 595	16	2.9	502	6	US-10-027-632-37637	Sequence 37637, A	C 668	16	2.9	552	4	US-09-925-065A-591076	Sequence 591076, A
C 596	16	2.9	502	6	US-10-027-632-37637	Sequence 37637, A	C 669	16	2.9	552	7	US-10-424-599-117489	Sequence 117489, A
C 597	16	2.9	503	4	US-09-764-875-287	Sequence 287, App	C 670	16	2.9	555	4	US-09-925-065A-123380	Sequence 123380, A
C 598	16	2.9	503	4	US-09-925-065A-571757	Sequence 571757, A	C 671	16	2.9	555	4	US-09-925-065A-643922	Sequence 643922, A
C 599	16	2.9	505	4	US-09-925-065A-204670	Sequence 204670, A	C 672	16	2.9	556	4	US-09-925-065A-424105	Sequence 424105, A
C 600	16	2.9	510	4	US-09-925-065A-344810	Sequence 344810, A	C 673	16	2.9	556	4	US-09-925-065A-424106	Sequence 424106, A
C 601	16	2.9	510	5	US-10-027-632-88514	Sequence 88514, A	C 674	16	2.9	556	4	US-09-925-065A-424107	Sequence 424107, A
C 602	16	2.9	510	5	US-10-027-632-88515	Sequence 88515, A	C 675	16	2.9	556	4	US-09-925-065A-568927	Sequence 568927, A
C 603	16	2.9	510	5	US-10-027-632-303816	Sequence 303816, A	C 676	16	2.9	557	4	US-09-925-065A-781102	Sequence 781102, A
C 604	16	2.9	510	5	US-10-027-632-303817	Sequence 303817, A	C 677	16	2.9	559	4	US-09-925-065A-143499	Sequence 143499, A
C 605	16	2.9	510	6	US-10-027-632-88514	Sequence 88514, A	C 678	16	2.9	559	4	US-09-925-065A-143500	Sequence 143500, A
C 606	16	2.9	510	6	US-10-027-632-88515	Sequence 88515, A	C 679	16	2.9	559	5	US-10-027-632-188801	Sequence 188801, A
C 607	16	2.9	510	6	US-10-027-632-303816	Sequence 303816, A	C 680	16	2.9	559	5	US-10-027-632-188802	Sequence 188802, A



C 681	16	2.9	559	6	US-10-027-632-188801	Sequence 188801,	C 754	16	2.9	600	9	US-10-972-079-40830	Sequence 40830, A
C 682	16	2.9	559	6	US-10-027-632-188802	Sequence 188802,	C 755	16	2.9	600	9	US-10-972-079-40831	Sequence 40831, A
C 683	16	2.9	561	4	US-09-925-065A-54533	Sequence 54533, A	C 756	16	2.9	600	9	US-10-972-079-40832	Sequence 40832, A
C 684	16	2.9	561	7	US-10-333-184-124	Sequence 124, App	C 757	16	2.9	600	9	US-10-972-079-40833	Sequence 40833, A
C 685	16	2.9	564	4	US-09-925-065A-113553	Sequence 113553,	C 758	16	2.9	600	9	US-10-972-079-44574	Sequence 44574, A
C 686	16	2.9	564	4	US-09-925-065A-857749	Sequence 857749,	C 759	16	2.9	600	9	US-10-972-079-44575	Sequence 44575, A
C 687	16	2.9	565	4	US-09-925-065A-858893	Sequence 858893,	C 760	16	2.9	600	9	US-10-972-079-53118	Sequence 53118, A
C 688	16	2.9	566	4	US-09-925-065A-664073	Sequence 664073,	C 761	16	2.9	600	9	US-10-972-079-53119	Sequence 53119, A
C 689	16	2.9	567	4	US-09-925-065A-267821	Sequence 267821,	C 762	16	2.9	600	9	US-10-972-079-64258	Sequence 64258, A
C 690	16	2.9	567	4	US-09-925-065A-360017	Sequence 360017,	C 763	16	2.9	600	9	US-10-972-079-64259	Sequence 64259, A
C 691	16	2.9	567	4	US-09-925-065A-360016	Sequence 360016,	C 764	16	2.9	600	9	US-10-972-079-80168	Sequence 80168, A
C 692	16	2.9	567	4	US-09-925-065A-360018	Sequence 360018,	C 765	16	2.9	600	9	US-10-972-079-80169	Sequence 80169, A
C 693	16	2.9	567	6	US-10-029-386-20447	Sequence 20447, A	C 766	16	2.9	600	10	US-11-060-756-3438	Sequence 3438, A
C 694	16	2.9	569	6	US-10-029-386-13425	Sequence 13425, A	C 767	16	2.9	600	10	US-11-060-756-3439	Sequence 3439, A
C 695	16	2.9	571	5	US-10-027-632-94306	Sequence 94306, A	C 768	16	2.9	600	10	US-11-060-756-3499	Sequence 3499, A
C 696	16	2.9	571	5	US-10-027-632-305347	Sequence 305347, A	C 769	16	2.9	600	10	US-11-060-756-3499	Sequence 3499, A
C 697	16	2.9	571	6	US-10-027-632-94306	Sequence 94306, A	C 770	16	2.9	600	10	US-11-060-756-3499	Sequence 3499, A
C 698	16	2.9	571	6	US-10-027-632-305347	Sequence 305347, A	C 771	16	2.9	600	10	US-11-060-756-3499	Sequence 3499, A
C 699	16	2.9	575	4	US-09-925-065A-594223	Sequence 594223,	C 772	16	2.9	601	4	US-09-925-065A-750985	Sequence 750985,
C 700	16	2.9	575	4	US-10-972-079-73594	Sequence 73594, A	C 773	16	2.9	601	4	US-09-925-065A-750986	Sequence 750986,
C 701	16	2.9	576	4	US-09-925-065A-766118	Sequence 766118, A	C 774	16	2.9	601	9	US-10-893-315-1516	Sequence 1516, Ap
C 702	16	2.9	576	9	US-10-972-079-95330	Sequence 95330, A	C 775	16	2.9	601	9	US-10-893-315-1719	Sequence 1719, Ap
C 703	16	2.9	577	9	US-09-925-065A-425923	Sequence 425923,	C 776	16	2.9	602	4	US-09-925-065A-748615	Sequence 748615,
C 704	16	2.9	577	4	US-09-925-065A-619252	Sequence 619252,	C 777	16	2.9	602	4	US-09-925-065A-748616	Sequence 748616,
C 705	16	2.9	577	4	US-09-925-065A-619253	Sequence 619253,	C 778	16	2.9	602	4	US-09-925-065A-888628	Sequence 888628,
C 706	16	2.9	579	4	US-09-925-065A-619542	Sequence 619542,	C 779	16	2.9	603	4	US-09-925-065A-888697	Sequence 888697,
C 707	16	2.9	579	4	US-09-925-065A-620365	Sequence 620365,	C 780	16	2.9	603	4	US-09-925-065A-891144	Sequence 891144,
C 708	16	2.9	580	4	US-09-925-065A-184183	Sequence 184183,	C 781	16	2.9	605	4	US-09-925-065A-317401	Sequence 317401,
C 709	16	2.9	580	4	US-09-925-065A-207013	Sequence 207013,	C 782	16	2.9	605	4	US-09-925-065A-510702	Sequence 510702,
C 710	16	2.9	580	4	US-09-925-065A-207014	Sequence 207014,	C 783	16	2.9	605	4	US-09-925-065A-764529	Sequence 764529,
C 711	16	2.9	580	4	US-09-925-065A-207015	Sequence 207015,	C 784	16	2.9	605	4	US-09-925-065A-764605	Sequence 764605,
C 712	16	2.9	580	4	US-09-925-065A-207016	Sequence 207016,	C 785	16	2.9	606	4	US-09-925-065A-870981	Sequence 870981,
C 713	16	2.9	580	5	US-10-027-632-144850	Sequence 144850,	C 786	16	2.9	606	4	US-10-425-115-82128	Sequence 82128, A
C 714	16	2.9	580	6	US-10-027-632-144850	Sequence 144850,	C 787	16	2.9	607	4	US-09-925-065A-887773	Sequence 887773,
C 715	16	2.9	582	4	US-09-925-065A-436648	Sequence 436648,	C 788	16	2.9	607	4	US-10-027-632-254367	Sequence 254367,
C 716	16	2.9	583	4	US-09-925-065A-341698	Sequence 341698,	C 789	16	2.9	608	5	US-10-027-632-254367	Sequence 254367,
C 717	16	2.9	583	4	US-09-925-065A-495763	Sequence 495763,	C 790	16	2.9	608	5	US-10-027-632-254367	Sequence 254367,
C 718	16	2.9	583	4	US-09-925-065A-495764	Sequence 495764,	C 791	16	2.9	608	6	US-10-027-632-254366	Sequence 254366,
C 719	16	2.9	584	4	US-09-925-065A-169496	Sequence 169496,	C 792	16	2.9	608	6	US-10-027-632-254366	Sequence 254366,
C 720	16	2.9	584	8	US-10-767-795-5571	Sequence 5571, Ap	C 793	16	2.9	608	6	US-10-027-632-254366	Sequence 254366,
C 721	16	2.9	585	4	US-09-925-065A-434114	Sequence 434114,	C 794	16	2.9	608	6	US-10-027-632-254367	Sequence 254367,
C 722	16	2.9	585	4	US-09-925-065A-434115	Sequence 434115,	C 795	16	2.9	608	7	US-10-021-333-15408	Sequence 15408, A
C 723	16	2.9	586	4	US-09-925-065A-477189	Sequence 477189,	C 796	16	2.9	608	7	US-09-925-065A-753481	Sequence 753481,
C 724	16	2.9	587	6	US-10-029-386-8333	Sequence 8322, Ap	C 797	16	2.9	609	4	US-10-027-632-233557	Sequence 233557,
C 725	16	2.9	590	6	US-10-029-386-9630	Sequence 9630, Ap	C 798	16	2.9	609	5	US-10-027-632-233557	Sequence 233557,
C 726	16	2.9	591	4	US-09-925-065A-395761	Sequence 395761,	C 799	16	2.9	609	6	US-10-027-632-233557	Sequence 233557,
C 727	16	2.9	591	4	US-09-925-065A-545449	Sequence 545449,	C 800	16	2.9	610	4	US-09-925-065A-562602	Sequence 562602,
C 728	16	2.9	591	5	US-10-027-632-193563	Sequence 193563,	C 801	16	2.9	612	4	US-09-925-065A-583831	Sequence 583831,
C 729	16	2.9	591	6	US-10-027-632-193563	Sequence 193563,	C 802	16	2.9	612	5	US-10-027-632-5922	Sequence 5922, Ap
C 730	16	2.9	592	4	US-09-925-065A-4259075	Sequence 4259075,	C 803	16	2.9	612	5	US-10-027-632-5922	Sequence 5922, Ap
C 731	16	2.9	592	4	US-09-925-065A-639224	Sequence 639224,	C 804	16	2.9	612	5	US-10-027-632-5924	Sequence 5924, Ap
C 732	16	2.9	592	4	US-09-925-065A-645938	Sequence 645938,	C 805	16	2.9	612	5	US-10-027-632-5925	Sequence 5925, Ap
C 733	16	2.9	593	4	US-09-925-065A-792594	Sequence 792594,	C 806	16	2.9	612	5	US-10-027-632-5926	Sequence 5926, Ap
C 734	16	2.9	593	4	US-09-925-065A-266664	Sequence 266664,	C 807	16	2.9	612	6	US-10-027-632-5923	Sequence 5923, Ap
C 735	16	2.9	593	5	US-10-027-632-209547	Sequence 209547,	C 808	16	2.9	612	6	US-10-027-632-5923	Sequence 5923, Ap
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## ALIGNMENTS

RESULT 1  
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; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 32
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-3

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; Sequence 4, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James

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; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
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; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; TITLE OF INVENTION: MOLECULE ASSAYS AND METHODS OF MAKING AND USING THEREOF
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 8
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US-10-376-323-67

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RESULT 4  
US-11-018-377-67

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; Sequence 67, Application US/11018377
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; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasieleski, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ASSAYS AND METHODS FOR MAKING AND USING THEREOF
; FILE REFERENCE: 034047.023CIP1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22

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; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 91
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US-11-018-377-67

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; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 26
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-14

Query Match          4.6%; Score 26; DB 5; Length 26;
Best Local Similarity 100.0%; Pred. No. 0.0084;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      87 TGAGCAACGACGAGGTACTTAAGAGG 112
Db      1 TGAGCAACGACGAGGTACTTAAGAGG 26

RESULT 6
US-10-068-238-13
; Sequence 13, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
```

```
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-13

Query Match          4.5%; Score 25; DB 5; Length 25;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      61 CGCGTAAGAGAGTCTTAATATCG 85
Db      1 CGCGTAAGAGAGTCTTAATATCG 25

RESULT 7
US-10-376-323-65
; Sequence 65, Application US/10376323
; Publication No. US20030211527A1
; GENERAL INFORMATION:
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood Jr., David A.
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
; TITLE OF INVENTION: MOLECULE ASSAYS AND METHODS OF MAKING AND USING THEREOF
; FILE REFERENCE: P68364US0
; CURRENT APPLICATION NUMBER: US/10/376,323
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 88
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 65
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: BACAPB4U
US-10-376-323-65

Query Match          4.3%; Score 24; DB 6; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      446 CAGATAATGCATGCTGCTTTAG 469
Db      1 CAGATAATGCATGCTGCTTTAG 24

RESULT 8
US-11-018-377-65
; Sequence 65, Application US/11018377
; Publication No. US20050095644A1
; GENERAL INFORMATION:
; APPLICANT: U.S. Army Medical Research and Materiel Command
; APPLICANT: Hartman, Laurie J.
; APPLICANT: Norwood, David A.
; APPLICANT: Wasielecki, Leonard
; TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID MOLECULE
; TITLE OF INVENTION: ASSAYS AND METHODS FOR MAKING AND USING THEREOF
; FILE REFERENCE: 034047.023C1P1
; CURRENT APPLICATION NUMBER: US/11/018,377
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: US 10/376,323
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/361,455
; PRIOR FILING DATE: 2002-03-04
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 65
; LENGTH: 24
; TYPE: DNA
; ORGANISM: Artificial
```



```
FEATURE:
OTHER INFORMATION: BACAPB4U
US-11-018-377-65

Query Match      4.3%; Score 24; DB 10; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.095;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      446 CAGATAATGATCGCTTGGCTTTAG 469
      |||
Db      1 CAGATAATGATCGCTTGGCTTTAG 24

RESULT 9
US-10-376-323-66/c
Sequence 66, Application US/10376323
Publication No. US20030211527A1
GENERAL INFORMATION:
APPLICANT: Hartman, Laurie J.
APPLICANT: Norwood Jr., David A.
TITLE OF INVENTION: INTERNAL POSITIVE CONTROL FOR PROBE-BASED NUCLEIC ACID
FILE REFERENCE: P68364USO
CURRENT APPLICATION NUMBER: US/10/376,323
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/361,455
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 88
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 66
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: BACAPB4L
US-10-376-323-66

Query Match      4.1%; Score 23; DB 6; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      511 CGTGTATGTTGAATGCTCATCC 533
      |||
Db      23 CGTGTATGTTGAATGCTCATCC 1

RESULT 10
US-11-018-377-66/c
Sequence 66, Application US/11018377
Publication No. US20050095644A1
GENERAL INFORMATION:
APPLICANT: U.S. Army Medical Research and Materiel Command
APPLICANT: Hartman, Laurie J.
APPLICANT: Norwood, David A.
APPLICANT: Wasielecki, Leonard
TITLE OF INVENTION: ASSAYS AND METHODS FOR MAKING AND USING THEREOF
FILE REFERENCE: 034047.023CIP1
CURRENT APPLICATION NUMBER: US/11/018,377
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: US 10/376,323
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/361,455
PRIOR FILING DATE: 2002-03-04
NUMBER OF SEQ ID NOS: 91
SOFTWARE: PatentIn version 3.3
SEQ ID NO 66
LENGTH: 23
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: BACAPB4L
US-11-018-377-66
```

```
Query Match      4.1%; Score 23; DB 10; Length 23;
Best Local Similarity 100.0%; Pred. No. 0.32;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      511 CGTGTATGTTGAATGCTCATCC 533
      |||
Db      23 CGTGTATGTTGAATGCTCATCC 1

RESULT 11
US-09-925-065A-648674
Sequence 648674, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 648674
LENGTH: 552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-925-065A-648674

Query Match      3.6%; Score 20; DB 4; Length 552;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      361 GAAGAGAGAAATACAAAGT 380
      |||
Db      350 GAAGAGAGAAATACAAAGT 369

RESULT 12
US-09-925-065A-648675
Sequence 648675, Application US/09925065A
Publication No. US20050228172A9
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single
FILE REFERENCE: 108827.135
CURRENT APPLICATION NUMBER: US/09/925,065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 60/243,096
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 60/252,147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250,092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261,766
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US 60/289,846
PRIOR FILING DATE: 2001-05-09
NUMBER OF SEQ ID NOS: 957086
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 648675
LENGTH: 552
```



```
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-648675

Query Match
Best Local Similarity 100.0%; Pred. No. 15;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 361 GAAGAGAGAAATACAAAGT 380
Db 350 GAAGAGAGAAATACAAAGT 369

RESULT 13
US-09-925-065A-223976/c
; Sequence 223976, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; SOFTWARE: FastSeq for Windows Version 4.0
; NUMBER OF SEQ ID NOS: 957086
; SEQ ID NO 223976
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-223976

Query Match
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 216 GATTGTAAATGTTTAGAA 234
Db 74 GATTGTAAATGTTTAGAA 56

RESULT 14
US-09-925-065A-223977/c
; Sequence 223977, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 223977
; LENGTH: 537
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-643642/c
; Sequence 643642, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SEQ ID NO 643642
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 643642
; LENGTH: 540
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-643642

Query Match
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 360 AGAAGAGAGAAATACAAA 378
Db 476 AGAAGAGAGAAATACAAA 458

RESULT 16
US-10-282-122A-12273
; Sequence 12273, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA.034A
```



```
;; CURRENT APPLICATION NUMBER: US/10/282,122A
;; CURRENT FILING DATE: 2003-02-20
;; PRIOR APPLICATION NUMBER: 60/191,078
;; PRIOR FILING DATE: 2000-03-21
;; PRIOR APPLICATION NUMBER: 60/206,848
;; PRIOR FILING DATE: 2000-05-23
;; PRIOR APPLICATION NUMBER: 60/207,727
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: 60/230,335
;; PRIOR FILING DATE: 2000-09-06
;; PRIOR APPLICATION NUMBER: 60/230,347
;; PRIOR FILING DATE: 2000-09-09
;; PRIOR APPLICATION NUMBER: 60/242,578
;; PRIOR FILING DATE: 2000-10-23
;; PRIOR APPLICATION NUMBER: 60/253,625
;; PRIOR FILING DATE: 2000-11-27
;; PRIOR APPLICATION NUMBER: 60/257,931
;; PRIOR FILING DATE: 2000-12-22
;; PRIOR APPLICATION NUMBER: 60/267,636
;; PRIOR FILING DATE: 2001-02-09
;; PRIOR APPLICATION NUMBER: 60/269,308
;; PRIOR FILING DATE: 2001-02-16
;; Remaining Prior Application data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 78614
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 12273
;; LENGTH: 555
;; TYPE: DNA
;; ORGANISM: Bacteroides fragilis
US-10-282-122A-12273
```

```
Query Match          3.4%; Score 19; DB 7; Length 555;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      268 GAAGTAGCTGAAGCTTCA 286
Db      277 GAAGTAGCTGAAGCTTCA 295
```

```
RESULT 17
US-09-925-065A-906587/c
; Sequence 906587, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 906587
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-906587
```

```
Query Match          3.4%; Score 19; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      216 GATTGTAATGTTTAGAA 234
Db      168 GATTGTAATGTTTAGAA 150
```

```
RESULT 18
US-09-925-065A-912775
; Sequence 912775, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 912775
; LENGTH: 646
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-912775
```

```
Query Match          3.4%; Score 19; DB 4; Length 646;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      216 GATTGTAATGTTTAGAA 234
Db      479 GATTGTAATGTTTAGAA 497
```

```
RESULT 19
US-10-425-114-19356
; Sequence 19356, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jindong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E.
; APPLICANT: Tabaska, Jack E.
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 19356
; LENGTH: 1004
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: LIB3139-076-C2_F11
US-10-425-114-19356
```

```
Query Match          3.4%; Score 19; DB 7; Length 1004;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      299 CATATATGAGACATTAGT 317
```



```
Db          932 CATATAATGACATTAGT 950
|||||
RESULT 20
US-10-425-114-11482
; Sequence 11482, Application US/10425114
; Publication No. US20040034888A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(5313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 11482
; LENGTH: 1092
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: 701064513_FLI
US-10-425-114-11482

Query Match          3.4%; Score 19; DB 7; Length 1092;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          299 CATATAATGACATTAGT 317
|||||
Db          1044 CATATAATGACATTAGT 1062

RESULT 21
US-10-424-599-89136
; Sequence 89136, Application US/10424599
; Publication No. US20040031072A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J
; APPLICANT: Kovalic, David K
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Soy Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53223)B
; CURRENT APPLICATION NUMBER: US/10/424,599
; NUMBER OF SEQ ID NOS: 2003-04-28
; SEQ ID NO 89136
; LENGTH: 1343
; TYPE: DNA
; ORGANISM: Glycine max
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT3847_51499C.1
US-10-424-599-89136

Query Match          3.4%; Score 19; DB 7; Length 1343;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          299 CATATAATGACATTAGT 317
|||||
Db          1211 CATATAATGACATTAGT 1229

RESULT 22
US-10-025-950-3
; Sequence 3, Application US/10025950
```

```
; Publication No. US20030096392A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 2163, A No. US20030096392A1 Human Prolyl
; FILE REFERENCE: 035800/242196
; CURRENT APPLICATION NUMBER: US/10/025,950
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,736
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1914
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-025-950-3

Query Match          3.4%; Score 19; DB 5; Length 1914;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          365 AGAGAAATACAAAAGTGAT 383
|||||
Db          764 AGAGAAATACAAAAGTGAT 782

RESULT 23
US-10-303-664A-35
; Sequence 35, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; APPLICANT: Tsai, Fong-Ying
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; FILE REFERENCE: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; CURRENT APPLICATION NUMBER: US/10/303,664A
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 1917
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-303-664A-35

Query Match          3.4%; Score 19; DB 6; Length 1917;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy          365 AGAGAAATACAAAAGTGAT 383
|||||
Db          764 AGAGAAATACAAAAGTGAT 782

RESULT 24
US-10-369-493-27237/c
; Sequence 27237, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
```



```

; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27237
; LENGTH: 2301
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27237

Query Match          3.4%; Score 19; DB 6; Length 2301;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      382 ATTGTTGGGATTAATTCTA 400
DB      1245 ATTGTTGGGATTAATTCTA 1227

RESULT 25
US-09-795-651-100
; Sequence 100, Application US/09795651
; Publication No. US20020049176A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Cleverger, William
; APPLICANT: Becker, K. David
; APPLICANT: Grako, Kathryn
; TITLE OF INVENTION: MODULATION OF MITOCHONDRIAL MASS AND FUNCTION
; TITLE OF INVENTION: FOR THE TREATMENT OF DISEASES AND FOR TARGET AND
; FILE REFERENCE: 660088,429C1
; CURRENT APPLICATION NUMBER: US/09/795,651
; CURRENT FILING DATE: 2001-02-27
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 100
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-795-651-100

Query Match          3.4%; Score 19; DB 3; Length 4661;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      365 AGAGAAATACAAAGTGAT 383
DB      917 AGAGAAATACAAAGTGAT 935

RESULT 26
US-10-172-118-17
; Sequence 17, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Robert, Chris
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118
; CURRENT FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 60/380,770
; PRIOR FILING DATE: 2002-05-14
```

```

; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 17
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: AB007896
; DATABASE ENTRY DATE: 2001-06-18
US-10-172-118-17

Query Match          3.4%; Score 19; DB 6; Length 4661;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      365 AGAGAAATACAAAGTGAT 383
DB      917 AGAGAAATACAAAGTGAT 935

RESULT 27
US-10-342-887-17
; Sequence 17, Application US/10342887
; Publication No. US20040058340A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: Linsley, Peter S.
; APPLICANT: Mao, Mao
; APPLICANT: Robert, Christopher J.
; APPLICANT: Van 't Veer, Laura Johanna
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-188-999
; CURRENT APPLICATION NUMBER: US/10/342,887
; CURRENT FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: 60/298,918
; PRIOR FILING DATE: 2001-06-18
; PRIOR APPLICATION NUMBER: 60/380,710
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 10/172,118
; PRIOR FILING DATE: 2002-06-14
; NUMBER OF SEQ ID NOS: 2699
; SEQ ID NO 17
; LENGTH: 4661
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-342-887-17

Query Match          3.4%; Score 19; DB 7; Length 4661;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      365 AGAGAAATACAAAGTGAT 383
DB      917 AGAGAAATACAAAGTGAT 935

RESULT 28
US-10-025-950-1
; Sequence 1, Application US/10025950
; Publication No. US20030096392A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: 21163, A No. US20030096392A1 Human Prollyl
; TITLE OF INVENTION: Oligopeptidase and Uses Therefor
; FILE REFERENCE: 035800/242196
; CURRENT APPLICATION NUMBER: US/10/025,950
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,736
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 6
```



```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 4959
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (451)...(2364)
US-10-025-950-1
```

```
Query Match          3.4%; Score 19; DB 5; Length 4959;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      365 AGAGAAATACAAAGTGAT 383
Db      1214 AGAGAAATACAAAGTGAT 1232
```

## RESULT 29

```
US-10-303-664A-34
; Sequence 34, Application US/10303664A
; Publication No. US20030153018A1
; GENERAL INFORMATION:
; APPLICANT: Hunter, John Joseph
; APPLICANT: Williamson, Mark W.
; APPLICANT: MacBeth, Kyle J.
; APPLICANT: Rudolph-Owen, Laura A.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR TREATING
; TITLE OF INVENTION: CANCER USING 2192, 2193, 6568, 8895, 9138, 9217, 9609,
; TITLE OF INVENTION: 9857, 9882, 10025, 20657, 21163, 25848, 25968, 32603, 32670,
; TITLE OF INVENTION: 33794, 54476 and 94710
; FILE REFERENCE: MP12001-29093R (M)
; CURRENT APPLICATION NUMBER: US/10/303,664A
; CURRENT FILING DATE: 2002-11-25
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 4959
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (451)...(2367)
US-10-303-664A-34
```

```
Query Match          3.4%; Score 19; DB 6; Length 4959;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      365 AGAGAAATACAAAGTGAT 383
Db      1214 AGAGAAATACAAAGTGAT 1232
```

## RESULT 30

```
US-10-437-963-17397
; Sequence 17397, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
```

```
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 17397
; LENGTH: 5970
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_23053C.1
US-10-437-963-17397
```

```
Query Match          3.4%; Score 19; DB 7; Length 5970;
Best Local Similarity 100.0%; Pred. No. 60;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      119 ATTGAGGACGAGCACT 137
Db      3758 ATTGAGGACGAGCACT 3776
```

## RESULT 31

```
US-09-764-869-1390
; Sequence 1390, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1390
; LENGTH: 10093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-764-869-1390
```

```
Query Match          3.4%; Score 19; DB 3; Length 10093;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      493 GATGAGGAACAGCATTC 511
Db      3174 GATGAGGAACAGCATTC 3192
```

## RESULT 32

```
US-10-091-504-1390
; Sequence 1390, Application US/10091504
; Publication No. US2003005908A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007C1
; CURRENT APPLICATION NUMBER: US/10/091,504
; CURRENT FILING DATE: 2002-03-07
; NUMBER OF SEQ ID NOS: 2442
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1390
; LENGTH: 10093
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-091-504-1390
```

```
Query Match          3.4%; Score 19; DB 5; Length 10093;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy      493 GATGAGGAACAGCATTC 511
Db      3174 GATGAGGAACAGCATTC 3192
```



RESULT 33  
US-10-227-577-1390  
; Sequence 1390, Application US/10227577  
; Publication No. US20040005575A1  
; GENERAL INFORMATION:  
; APPLICANT: Rosen et al.  
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies  
; FILE REFERENCE: PC007C2  
; CURRENT APPLICATION NUMBER: US/10/227,577  
; CURRENT FILING DATE: 2002-08-26  
; PRIOR APPLICATION NUMBER: 10/091,504  
; PRIOR FILING DATE: 2002-03-07  
; PRIOR APPLICATION NUMBER: 09/764,869  
; PRIOR FILING DATE: 2001-01-17  
; PRIOR APPLICATION NUMBER: 60/179,065  
; PRIOR FILING DATE: 2000-01-31  
; PRIOR APPLICATION NUMBER: 60/180,628  
; PRIOR FILING DATE: 2000-02-04  
; PRIOR APPLICATION NUMBER: 60/214,886  
; PRIOR FILING DATE: 2000-06-28  
; PRIOR APPLICATION NUMBER: 60/217,487  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,758  
; PRIOR FILING DATE: 2000-08-14  
; PRIOR APPLICATION NUMBER: 60/220,963  
; PRIOR FILING DATE: 2000-07-26  
; PRIOR APPLICATION NUMBER: 60/217,496  
; PRIOR FILING DATE: 2000-07-11  
; PRIOR APPLICATION NUMBER: 60/225,447  
; PRIOR FILING DATE: 2000-08-14  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 242  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1390  
; LENGTH: 10093  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-227-577-1390

Query Match 3.4%; Score 19; DB 6; Length 10093;  
Best Local Similarity 100.0%; Pred. No. 62;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 493 GATGAGAAACGACATTC 511  
DB 3174 GATGAGAAACGACATTC 3192

RESULT 34  
US-10-221-613-250/C  
; Sequence 250, Application US/10221613  
; Publication No. US20040029123A1  
; GENERAL INFORMATION:  
; APPLICANT: OLEK, Alexander  
; APPLICANT: FIEBENROCK, Christian  
; APPLICANT: BERLIN, Kurt  
; TITLE OF INVENTION: Diagnosis of Diseases Associated with Cell Cycle  
; FILE REFERENCE: 5013.1004  
; CURRENT APPLICATION NUMBER: US/10/221,613  
; CURRENT FILING DATE: 2002-09-13  
; PRIOR APPLICATION NUMBER: PCT/EP01/02945  
; DE 10013847.00  
; DE 10019058.8  
; DE 10019173.8  
; DE 10033529.7  
; DB 10043826.1  
; PRIOR FILING DATE: 2001-03-15  
; 2000-03-15  
; 2000-04-06  
; 2000-04-07  
; 2000-06-30

2000-09-01  
; NUMBER OF SEQ ID NOS: 428  
; SEQ ID NO 250  
; LENGTH: 10872  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURES:  
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)  
US-10-221-613-250

Query Match 3.4%; Score 19; DB 7; Length 10872;  
Best Local Similarity 100.0%; Pred. No. 63;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 175 ATTATCTCCAAATATAA 193  
DB 8782 ATTATCTCCAAATATAA 8764

RESULT 35  
US-09-754-468-14/C  
; Sequence 14, Application US/09754468  
; Publication No. US20050192237A1  
; GENERAL INFORMATION:  
; APPLICANT: Iversen, Patrick L.  
; TITLE OF INVENTION: Antisense Antibacterial Cell Division  
; FILE REFERENCE: 0450-0033.30  
; CURRENT APPLICATION NUMBER: US/09/754,468  
; CURRENT FILING DATE: 2001-01-04  
; PRIOR APPLICATION NUMBER: US 60/174,484  
; PRIOR FILING DATE: 2000-01-04  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 14  
; LENGTH: 13311  
; TYPE: DNA  
; ORGANISM: Salmonella typhimurium  
US-09-754-468-14

Query Match 3.4%; Score 19; DB 3; Length 13311;  
Best Local Similarity 100.0%; Pred. No. 64;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 485 TTGGGATTGATGAGGAAC 503  
DB 5411 TTGGGATTGATGAGGAAC 5393

RESULT 36  
US-09-070-927A-399  
; Sequence 399, Application US/09070927A  
; Patent No. US20020120116A1  
; GENERAL INFORMATION:  
; APPLICANT: Charles A. Kunesh  
; APPLICANT: Patrick J. Dillon  
; APPLICANT: Steven Barash  
; TITLE OF INVENTION: Enterococcus faecialis Polynucleotides and Polypeptides  
; NUMBER OF SEQUENCES: 962  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Human Genome Sciences, Inc.  
; STREET: 9410 Key West Avenue  
; CITY: Rockville  
; STATE: Maryland  
; COUNTRY: USA  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage  
; COMPUTER: HP Vectra 486/33  
; OPERATING SYSTEM: MSDOS version 6.2  
; SOFTWARE: ASCII Text  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/070,927A



```

; FILING DATE: 04-May-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/046,655
; FILING DATE: 1997-05-16
; APPLICATION NUMBER: 60/044,031
; FILING DATE: 1997-05-06
; APPLICATION NUMBER: 60/066,009
; FILING DATE: 1997-11-14
; ATTORNEY/AGENT INFORMATION:
; NAME: Kenley K. Hoover
; REGISTRATION NUMBER: 40,302
; REFERENCE/DOCKET NUMBER: PB369
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8512
; INFORMATION FOR SEQ ID NO: 399:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 32768 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 399:
US-09-070-927A-399

Query Match          3.4%; Score 19; DB 3; Length 32768;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      114 TCGTGATTAGACGAGAA 132
Db      27385 TGCTGATTAGACGAGAA 27403

RESULT 37
US-10-312-841-2
; Sequence 2, Application US/10312841
; Publication No. US20030186277A1
; GENERAL INFORMATION:
; APPLICANT: Epigenomics AG
; TITLE OF INVENTION: Diagnose von bedeutenden genetischen Parametern innerhalb des MHC
; FILE REFERENCE: E01/1208/WO
; CURRENT APPLICATION NUMBER: US/10/312,841
; CURRENT FILING DATE: 2002-12-30
; NUMBER OF SEQ ID NOS: 2
; SEQ ID NO 2
; LENGTH: 3673778
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: chemically treated genomic DNA (Homo sapiens)
; NAME/KEY: unsure
; LOCATION: (379615)
US-10-312-841-2

Query Match          3.4%; Score 19; DB 6; Length 3673778;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      216 GATTGTAATGTTTAGAA 234
Db      2041066 GATTGTAATGTTTAGAA 2041084

RESULT 38
US-10-068-238-2/c
; Sequence 2, Application US/10068238
; Publication No. US20030082563A1
; GENERAL INFORMATION:
; APPLICANT: Bell, Constance A.
; APPLICANT: Uhl, James
; APPLICANT: Cockerill, Franklin
```

```

; TITLE OF INVENTION: Detection of Bacillus Anthracis
; FILE REFERENCE: 07039-372001
; CURRENT APPLICATION NUMBER: US/10/068,238
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: US 60/329,826
; PRIOR FILING DATE: 2001-10-15
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 18
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Oligonucleotide
US-10-068-238-2

Query Match          3.2%; Score 18; DB 5; Length 18;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      141 TTGTGAATGTTGCGACT 158
Db      18 TTGTGAATGTTGCGACT 1

RESULT 39
US-10-681-773-116813/c
; Sequence 116813, Application US/10681773
; Publication No. US20040146890A1
; GENERAL INFORMATION:
; APPLICANT: Matsuzaki, Hajime
; APPLICANT: Mei, Rui
; APPLICANT: Shen, Mei-Mei
; APPLICANT: Kennedy, Giulia
; TITLE OF INVENTION: Methods for Genotyping Polymorphisms in Humans
; FILE REFERENCE: 3522.2
; CURRENT APPLICATION NUMBER: US/10/681,773
; CURRENT FILING DATE: 2003-10-07
; PRIOR APPLICATION NUMBER: 60/470,475
; PRIOR FILING DATE: 2002-05-14
; PRIOR APPLICATION NUMBER: 60/417,190
; PRIOR FILING DATE: 2002-10-08
; NUMBER OF SEQ ID NOS: 124031
; SOFTWARE: Microarray Probe Sequence Listing Generator V 1.1
; SEQ ID NO 116813
; LENGTH: 25
; TYPE: DNA
; ORGANISM: Homo sapien
US-10-681-773-116813

Query Match          3.2%; Score 18; DB 7; Length 25;
Best Local Similarity 100.0%; Pred. No. 1,4e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      184 CAAATAAATGATTCAA 201
Db      22 CAAATAAATGATTCAA 5

RESULT 40
US-09-925-065A-539145/c
; Sequence 539145, Application US/09925065A
; Publication No. US20050228172A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
```



```
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: fastseq for windows Version 4.0
; SEQ ID NO 539145
; LENGTH: 369
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-539145
```

```
Query Match 117 TGATTGAGCAGCAGC 134 3.2%; Score 18; DB 4; Length 369;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 117 TGATTGAGCAGCAGC 134
Db 238 TGATTGAGCAGCAGC 221
```

```
Search completed: April 12, 2006, 06:04:08
Job time : 1547.89 secs
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